

```
RESULT 2
S43467
nef protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C:Accession: S43467
R:Freund, J.; Kellner, R.; Houthaeve, T.; Kalbitzer, H.R.
Eur. J. Biochem. 221, 811-819, 1994
A:Title: Stability and proteolytic domains of Nef protein from human immunodeficiency vi
A:Reference number: S43467; MUID:94229079
A:Accession: S43467
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-205 <PRE>
C:Superfamily: AIDS nef protein

Query Match 66.1%; Score 1115; DB 2; Length 205;
Best Local Similarity 99.0%; Pred. No. 3.2e-85;
Matches 203; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GKGKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 61
|||||
DB 1 GKGKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
|||||
QY 62 EEEVGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGLIHSQRQDILDLYHTQGYF 121
|||||
DB 61 EEEVGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGLIHSQRQDILDLYHTQGYF 120
|||||
QY 122 PDWQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREVL 181
|||||
DB 121 PDWQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREVL 180
|||||
QY 182 EWRFDLSRLAFHHVARELHPEYFKNC 206
|||||
DB 181 EWRFDLSRLAFHHVARELHPEYFKNC 205
|||||

RESULT 3
S03244
nef protein (clone HX82) - human immunodeficiency virus type 1
N:Alternate names: 3'-orf protein
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
C:Accession: S03244
R:Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettawa
Nucleic Acids Res. 13, 8219-8229, 1985
A:Title: Polymorphism of the 3' open reading frame of the virus associated with the acqu
A:Reference number: S03244; MUID:86067228
A:Accession: S03244
A:Molecule type: DNA
A:Residues: 1-206 <RAT>
A:Cross-References: EMBL:X03187
A:Note: the in-frame stop codon at residue 124, shown as 'X', may be suppressed
C:Genetics:
A:Gene: nef; 3'-orf; orf-F
C:Superfamily: AIDS nef protein

Query Match 66.1%; Score 1115; DB 2; Length 206;
Best Local Similarity 98.5%; Pred. No. 3.2e-85;
Matches 203; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGGKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
|||||
DB 1 MGGKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
|||||
QY 61 QEEVGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGLIHSQRQDILDLYHTQGY 120
|||||
DB 61 QEEVGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGLIHSQRQDILDLYHTQGY 120
|||||
QY 121 FPDWQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180
|||||
```

```
DB 121 FPDWQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180
QY 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206
|||||
DB 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206
|||||

RESULT 4
ASLJVL
nef protein - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: 3'-orf protein; orf-F protein
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A04007
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr
A:Reference number: A93355; MUID:85111157
A:Accession: A04007
A:Molecule type: DNA
A:Residues: 1-206 <MUE>
A:Cross-References: GB:K02083; NID:G555008; PIDN:AAB59874.1; PID:G328560
C:Genetics:
A:Gene: nef; 3'-orf; orf-F
C:Superfamily: AIDS nef protein
C:Keywords: AIDS; immunodeficiency

Query Match 66.0%; Score 1114; DB 1; Length 206;
Best Local Similarity 97.6%; Pred. No. 3.8e-85;
Matches 201; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGGKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
|||||
DB 1 MGGKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
|||||
QY 61 QEEVGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGLIHSQRQDILDLYHTQGY 120
|||||
DB 61 QEEVGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGLIHSQRQDILDLYHTQGY 120
|||||
QY 121 FPDWQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180
|||||
DB 121 FPDWQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180
|||||
QY 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206
|||||
DB 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206
|||||

RESULT 5
ASLJ12
nef protein - human immunodeficiency virus type 1 (isolate HTLV-III, 12)
N:Alternate names: 3'-orf protein; orf-F protein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C:Accession: A04006
R:Arya, S.K.; Gallo, R.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986
A:Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity
A:Reference number: A94093; MUID:86177573
A:Accession: A04006
A:Molecule type: DNA
A:Residues: 1-206 <ARY>
A:Cross-References: EMBL:M11840; NID:G328453; PIDN:AAA5001.1; PID:G328458
C:Genetics:
A:Gene: nef; 3'-orf; orf-F
C:Superfamily: AIDS nef protein
C:Keywords: AIDS; immunodeficiency

Query Match 65.6%; Score 1108; DB 1; Length 206;
Best Local Similarity 97.1%; Pred. No. 1.2e-84;
```

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2002, 08:08:31 ; Search time 50.45 Seconds  
(Without alignments)  
575.203 Million cell updates/sec

Title: US-09-509-239-13  
Perfect score: 1688  
Sequence: 1 MGGKWSKVVGWPTVRM.....QSRDPTGPKTSGHHHHH 302

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1130	66.9	206	1 ASLJFV	nef protein - huma
2	1115	66.1	205	2 S43467	nef protein - huma
3	1115	66.1	206	2 S03244	nef protein (clone
4	1114	66.0	206	1 ASLJVL	nef protein - huma
5	1108	65.6	206	1 ASLJ12	nef protein - huma
6	1097	65.0	206	2 JC5400	nef protein - huma
7	1096	64.9	206	2 S03245	nef protein (clone
8	1096	64.9	206	2 S33986	nef protein - huma
9	1081.5	64.1	205	1 ASLJH3	nef protein - huma
10	1019	60.4	204	2 S43985	nef protein - huma
11	1019	60.4	218	1 ASLJBR	nef protein - huma
12	1007	59.7	206	2 S25937	nef protein - huma
13	997	59.1	210	1 ASLJ02	nef protein - huma
14	991.5	58.7	214	1 I44001	nef protein - huma
15	987	58.5	182	2 S03247	nef protein (clone
16	987	58.5	204	2 S03246	nef protein - huma
17	911	54.0	212	1 QQLJ2R	nef protein - huma
18	903.5	53.5	207	1 B44963	nef protein - huma
19	837	49.6	205	1 QQLJND	nef protein - huma
20	834.5	49.4	209	2 T01673	nef protein - huma
21	832	49.3	205	1 ASLJIK	nef protein - huma
22	486	28.8	86	2 S33982	nef protein - simi
23	478	28.3	95	1 TNLJ12	trans-activating t
24	470	27.8	86	2 A25700	trans-activating t
25	443	26.2	225	2 S46333	trans-activating t
26	439.5	26.0	97	2 S54385	nef protein - simi
27	437	25.9	101	2 T09446	nef protein - huma
28	434	25.7	101	1 E44001	tat protein - huma
29	429.5	25.4	309	2 S07993	trans-activating t

## ALIGNMENTS

## RESULT 1

ASLJFV

nef protein - human immunodeficiency virus type 1 (isolate LAV-la)

N:Alternate names: 3'-orf protein; orf-F protein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999

C:Accession: A04008: S14609

R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.

Cell 40, 9-17, 1985

A:Title: Nucleotide sequence of the AIDS virus, LAV.

A:Reference number: A30866; MUID:85099333

A:Accession: A04008

A:Molecule type: DNA

A:Residues: 1-206 &lt;WAT&gt;

A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59752.1; PID:g326425

A:Experimental source: isolate LAV-la

R:Ciccarelli, R.B.

Submitted to the EMBL Data Library, March 1991

A:Reference number: S14607

A:Accession: S14609

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-206 &lt;CIC&gt;

A:Cross-references: EMBL:X58780; NID:g60113; PIDN:CAA41585.1; PID:g60114

C:Genetics:

A:Gene: nef; 3'-orf; orf-F

C:Superfamily: AIDS nef protein

C:Keywords: AIDS; immunodeficiency; phosphoprotein

Query Match

Best Local Similarity 66.9%; Score 1130; DB 1; Length 206;

Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGGKWSKVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60

Db 1 MGGKWSKVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60

Qy 61 QEEVEGVPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWVHTQGY 120

Db 61 QEEVEGVPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWVHTQGY 120

Qy 121 FPDQNYTPGPGVRYPLTFGCYKLVPPDPKVEANKGENTSLHPVSLHGMDPEREV 180

Db 121 FPDQNYTPGPGVRYPLTFGCYKLVPPDPKVEANKGENTSLHPVSLHGMDPEREV 180

Qy 181 LEWRFDLSLAFHHVARELHPEYFKNC 206

Db 181 LEWRFDLSLAFHHVARELHPEYFKNC 206

Matches 200; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
 Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRODILDLYIHTQGY 120  
 Db 61 QEEKVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRODILDLYIHTQGY 120

QY 121 FPDQNYTPGQVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDPPERV 180  
 Db 121 FPDQNYTPGQVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDPPERV 180

QY 181 LEWRDLSRLAFHHVARELHPEYFKNK 206  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNK 206

RESULT 6  
 JC5400  
 nef protein - Human immunodeficiency virus type 1, HIV-1  
 C:Species: Human immunodeficiency virus type 1, HIV-1  
 C:Date: 07-Jul-1997 #sequence\_revision 18-Jul-1997 #text\_change 31-Oct-1997  
 C:Accession: JC5400  
 R:Macreadie, I.G.; Lowe, M.G.; Curtain, C.C.; Hewish, D.; Azad, A.A.  
 Biochem. Biophys. Res. Commun. 232, 707-711, 1997  
 A:Title: Cytotoxicity resulting from addition of HIV-1 Nef N-terminal peptides to yeast  
 A:Reference number: JC5400; MUID:97271389  
 A:Accession: JC5400  
 A:Molecule type: protein  
 A:Residues: 1-206 <MAC>  
 C:Comment: The amino-terminal part possesses membrane-perturbing and fusogenic activities.  
 C:Superfamily: AIDS nef protein  
 F:2-206/Product: nef protein #status predicted <MAT>

Query Match 65.0%; Score 1097; DB 2; Length 206;  
 Best Local Similarity 97.1%; Pred. No. 9.9e-84;  
 Matches 200; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
 Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRODILDLYIHTQGY 120  
 Db 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRODILDLYIHTQGY 120

QY 121 FPDQNYTPGQVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDPPERV 180  
 Db 121 FPDQNYTPGQVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDPPERV 180

QY 181 LEWRDLSRLAFHHVARELHPEYFKNK 206  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNK 206

RESULT 7  
 S03245  
 nef protein (clone HXB3) - human immunodeficiency virus type 1  
 N:Alternate names: 3'-orf protein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 20-Sep-1999  
 C:Accession: S03245  
 R:Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, K.J.; Petteway  
 Nucleic Acids Res. 13, 8219-8229, 1985  
 A:Title: Polymorphism of the 3' open reading frame of the virus associated with the acqu  
 A:Reference number: S03244; MUID:86067228  
 A:Accession: S03245  
 A:Molecule type: DNA  
 A:Residues: 1-206 <RAT>

A:Cross-references: EMBL:X03188; NID:g61556; PIDN:CAA26947.1  
 C:Genetics:  
 A:Gene: nef; 3'-orf; orf-F  
 C:Superfamily: AIDS nef protein

Query Match 64.9%; Score 1096; DB 2; Length 206;  
 Best Local Similarity 96.6%; Pred. No. 1.2e-83;  
 Matches 199; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
 Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRODILDLYIHTQGY 120  
 Db 61 QEEKVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRODILDLYIHTQGY 120

QY 121 FPDQNYTPGQVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDPPERV 180  
 Db 121 FPDQNYTPGQVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDPPERV 180

QY 181 LEWRDLSRLAFHHVARELHPEYFKNK 206  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNK 206

RESULT 8  
 S33986  
 nef protein - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Sep-1999  
 C:Accession: S33986  
 R:Carlini, F.  
 submitted to the EMBL Data Library, November 1991  
 A:Reference number: S33979  
 A:Accession: S33986  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-206 <CAR>  
 A:Cross-references: EMBL:L11530; NID:g60192; PIDN:CAA77629.1; PID:g60200  
 C:Superfamily: AIDS nef protein

Query Match 64.9%; Score 1096; DB 2; Length 206;  
 Best Local Similarity 96.6%; Pred. No. 1.2e-83;  
 Matches 199; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
 Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRODILDLYIHTQGY 120  
 Db 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRODILDLYIHTQGY 120

QY 121 FPDQNYTPGQVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDPPERV 180  
 Db 121 FPDQNYTPGQVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDPPERV 180

QY 181 LEWRDLSRLAFHHVARELHPEYFKNK 206  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNK 206

RESULT 9  
 ASLJH3  
 nef protein - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)  
 N:Alternate names: 3'-orf protein; orf-F protein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 31-Jan-1997  
 C:Accession: A04005

Streicher,

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RESULT 12
S25937 net protein - human immunodeficiency virus type 1
C-species: human Immunodeficiency virus type 1, HIV-1
C-date: 25-Feb-1994 #sequence_revision 01-Dec-1995
C-accession: S25937
R-Guo, H.G.; Chermann, J.-C.; Waters, D.; Hall, L.; Louie, A.; Gallo, R.C.;
Nature 349, 745-746, 1991
A-title: Sequence analysis of original HIV-1.

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A:Reference number: S25937; MUID:91156044  
A:Accession: S25937  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: nucleic acid  
A:Residues: 1-206 <GUO>  
A:Cross-references: EMBL:X57465; NID:g60217; PIDN:CAA40702.1; PID:g60218  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1991  
C:Superfamily: AIDS nef protein

Query Match 59.7%; Score 1007; DB 2; Length 206;  
Best Local Similarity 85.9%; Pred. No. 2.9e-76;  
Matches 177; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

QY 1 MGCKWKSXSVVGVPTVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
DB 1 MGCKWKSXSVVGVPTVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 61 QEEVEYGFVPTVPQVPLRPMYTKAADVLSHFLKKGGLGGLIHSQRQDILDLWIYHTQGY 120  
DB 61 QEEVEYGFVPTVPQVPLRPMYTKAADVLSHFLKKGGLGGLIHSQRQDILDLWIYHTQGY 120

QY 121 FPDWQNTPGVGYPLTFCWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPEREV 180  
DB 121 FPDWQNTPGVGYPLTFCWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPEREV 180

QY 181 LEWRFSRLAFHVAHRELHPEYKNC 206  
DB 181 LEWRFSRLAFHVAHRELHPEYKNC 206

RESULT 13  
ASLJO2  
nef protein - human immunodeficiency virus type 1 (isolate ARV-2)  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A04009  
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Sch  
Science 227, 484-492, 1985  
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
A:Reference number: A04003; MUID:85090453  
A:Accession: A04009  
A:Molecule type: DNA  
A:Residues: 1-210 <SAN>  
A:Cross-references: GB:K02007; NID:g328658; PIDN:AAB59883.1; PID:g328667  
C:Genetics:  
A:Gene: nef; 3'-orf; orf-F  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; Immunodeficiency

Query Match 59.1%; Score 997; DB 1; Length 210;  
Best Local Similarity 85.2%; Pred. No. 2e-75;  
Matches 179; Conservative 16; Mismatches 11; Indels 4; Gaps 1;

QY 1 MGCKWKSXSVVGVPTVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAAC 56  
DB 1 MGCKWKSXSVVGVPTVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAAC 56

QY 57 WLEAQEEVEYGFVPTVPQVPLRPMYTKAADVLSHFLKKGGLGGLIHSQRQDILDLWIYH 116  
DB 61 WLEAQEEVEYGFVPTVPQVPLRPMYTKAADVLSHFLKKGGLGGLIHSQRQDILDLWIYH 120

QY 117 TQGYFPDQWNTPGVGYPLTFCWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDP 176  
DB 121 TQGYFPDQWNTPGVGYPLTFCWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDP 180

QY 177 EREVLEWRFSRLAFHVAHRELHPEYKNC 206  
DB 181 EREVLEWRFSRLAFHVAHRELHPEYKNC 210

RESULT 14  
I44001  
nef protein - human immunodeficiency virus type 1 (strain YU-2)  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 23-Feb-1997  
C:Accession: I44001  
R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.  
J. Virol. 66, 6587-6600, 1992  
A:Title: Complete nucleotide sequence, genome organization, and biological properties  
A:Reference number: A44001; MUID:93021387  
A:Accession: I44001  
A:Molecule type: DNA  
A:Residues: 1-214 <LIY>  
A:Cross-references: GB:M93258  
C:Genetics:  
A:Gene: nef; 3'-orf; orf-F  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; Immunodeficiency

Query Match 58.7%; Score 991.5; DB 1; Length 214;  
Best Local Similarity 84.2%; Pred. No. 5.9e-75;  
Matches 181; Conservative 12; Mismatches 11; Indels 11; Gaps 2;

QY 1 MGCKWKSXSVVGVPTVR-----ERMRAEPAADGVGAASRDLEKKGAISSNTAA 50  
DB 1 MGCKWKSXSVVGVPTVR-----ERMRAEPAADGVGAASRDLEKKGAISSNTAA 60

QY 51 TNAACAWLEAQEEVEYGFVPTVPQVPLRPMYTKAADVLSHFLKKGGLGGLIHSQRQDIL 110  
DB 61 TNAACAWLEAQEEVEYGFVPTVPQVPLRPMYTKAADVLSHFLKKGGLGGLIHSQRQDIL 120

QY 111 DLWIYHTQGYFPDQWNTPGVGYPLTFCWCYKLVPEPDKVEEANKGENTSLHPVSL 170  
DB 121 DLWIYHTQGYFPDQWNTPGVGYPLTFCWCYKLVPEPDKVEEANKGENTSLHPVSL 179

QY 171 HGMDPEREVLEWRFSRLAFHVAHRELHPEYKNC 205  
DB 180 HGMDPEREVLEWRFSRLAFHVAHRELHPEYKNC 214

RESULT 15  
S03247  
nef protein (clone C15) - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: 3'-orf protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 20-Jun-2000  
C:Accession: S03247  
R:Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pett  
Nucleic Acids Res. 13, 8219-8229, 1985  
A:Title: Polymorphism of the 3' open reading frame of the virus associated with the a  
A:Reference number: S03244; MUID:86067228  
A:Accession: S03247  
A:Molecule type: mRNA  
A:Residues: 1-182 <PAT>  
A:Cross-references: EMBL:X03189; NID:g61552; PIDN:CAA26948.1; PID:g1335562  
C:Genetics:  
A:Gene: nef; 3'-orf; orf-F  
C:Superfamily: AIDS nef protein

Query Match 58.5%; Score 987; DB 2; Length 182;  
Best Local Similarity 98.4%; Pred. No. 1.2e-74;  
Matches 179; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 25 PAADGVGAASRDLEKKGAISSNTAATNAACAWLEAQEEVEYGFVPTVPQVPLRPMYKAA 84  
DB 1 PAADGVGAASRDLEKKGAISSNTAATNAACAWLEAQEEVEYGFVPTVPQVPLRPMYKAA 60

QY 85 VDLSHFLKKGGLGGLIHSQRQDILDLWIYHTQGYFPDQWNTPGVGYPLTFCWCYK 144

Db 61 VDLSHFLKEGKGLGLIHSQRQDILDWYHTQGYFPDQWNYTPGCVRYPLTFGWCYK 120  
QY 145 LVPVDPKVEEANKGENTSLHVPVSLHGMDDPEREVLEWRDLSRLAFHHVARELHPEYFK 204  
Db 121 LVPVDPKVEEANKGENTSLHVPVSLHGMDDPEREVLEWRDLSRLAFHHVARELHPEYFK 180  
QY 205 NC 206  
Db 181 NC 182

RESULT 16  
S03246  
nef protein (clone HAT3) - human immunodeficiency virus type 1  
N:Alternate names: 3'-orf protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 20-Sep-1999  
C:Accession: S03246  
R:Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettawa  
Nucleic Acids Res. 13, 8219-8229, 1985  
A:Title: Polymorphism of the 3' open reading frame of the virus associated with the acqu  
A:Reference number: S03244; MUID:86067228  
A:Accession: S03246  
A:Molecule type: DNA  
A:Residues: 1-204 <RAT>  
A:Cross-references: EMBL:X03190; NID:g61550; PIDN:CAA26949.1; PID:g61551  
A:Note: the authors translated the codon AGT for residue 11 as Gly  
C:Genetics:  
A:Gene: nef; 3'-orf; orf-F  
C:Superfamily: AIDS nef protein

Query Match 58.5%; Score 987; DB 2; Length 204;  
Best Local Similarity 84.5%; Pred. No. 1.3e-74; Mismatches 14; Indels 2; Gaps 1;  
Matches 174; Conservative 16;  
QY 1 MGGKWSKSSVVGWPTVVRMRRAEPAADGVGAASRDLEKHGAIITSSNTAATNAACAWLEA 60  
Db 1 MGGKWSKSKMGPWPAVRERMQRAEPAADGVGAASRDLEKHGAIITSSNT--NNAACTWLEA 58  
QY 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEGKGLGLIHSQRQDILDWYHTQY 120  
Db 59 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEGKGLGLIHSQRQDILDWYHTQY 118  
QY 121 FPDQWNYTPGCVRYPLTFGWCYKLVPEVPDKEVEANKGENTSLHVPVSLHGMDDPEREV 180  
Db 119 FPDQWNYTPGCVRYPLTFGWCYKLVPEVPDKEVEANKGENTSLHVPVSLHGMDDPEREV 178  
QY 181 LEWRDLSRLAFHHVARELHPEYFKNC 206  
Db 179 LVNKFDSRLAFHHVARELHPEYFKNC 204

RESULT 17  
QOLJZR  
nef protein - human immunodeficiency virus Zr-6  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: human immunodeficiency virus Zr-6  
C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999  
C:Accession: F26192  
R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu  
Gene 52, 71-82, 1987  
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotid  
A:Reference number: A26192; MUID:87248097  
A:Accession: F26192  
A:Molecule type: DNA  
A:Residues: 1-212 <SRI>  
A:Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45381.1; PID:g329404  
C:Genetics:  
A:Gene: nef; 3'-orf; orf-F  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; immunodeficiency

Query Match 54.0%; Score 911; DB 1; Length 212;  
Best Local Similarity 77.4%; Pred. No. 2.8e-68;  
Matches 164; Conservative 23; Mismatches 19; Indels 6; Gaps 2;

QY 1 MGGKWSKSSVVGWPTVVRMRRAEPAADGVGAASRDLEKHGAIITSSNTAATNAAC 55  
Db 1 MGGKWSKSSVVGWPAIRERIRRTDPAADGVGAASRDLEKHGAIITSSNTRDTNADC 60  
QY 56 AWLEAQEE-BEVGFPVTPQVPLRPMTYKAADVLSHFLKEGKGLGLIHSQRQDILDWY 114  
Db 61 AWLEAQEESEVGPVPLRPMTYKLAVDLSHFLKEGKGLGLIHSQRQDILDWY 120  
QY 115 YHTQGYFPDQWNYTPGCVRYPLTFGWCYKLVPEVPDKEVEANKGENTSLHVPVSLHGM 174  
Db 121 YNTQGIFFDQWNYTPGCGIRYPLTFGWCYKLVPEVPDKEVEATEGETNCLLHPVCOHGM 180  
QY 175 DPREVLEWRDLSRLAFHHVARELHPEYFKNC 206  
Db 181 DTEREVLEWRDLSRLAFHHVARELHPEYFKNC 212

RESULT 18  
QOLJND  
nef protein - human immunodeficiency virus type 1 (isolate NDK)  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999  
C:Accession: JQ0068  
R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe,  
Gene 81, 275-284, 1989  
A:Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human in  
A:Reference number: JQ0065; MUID:90034200  
A:Accession: JQ0068  
A:Molecule type: DNA  
A:Residues: 1-207 <SPI>  
A:Cross-references: GB:M27323; NID:g328154; PIDN:AAA44874.1; PID:g328163  
C:Genetics:  
A:Gene: nef  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; immunodeficiency

Query Match 53.5%; Score 903.5; DB 1; Length 207;  
Best Local Similarity 77.3%; Pred. No. 1.1e-67;  
Matches 160; Conservative 25; Mismatches 21; Indels 1; Gaps 1;  
QY 1 MGGKWSKSSVVGWPTVVRMRRAEPAADGVGAASRDLEKHGAIITSSNTAATNAACAWLEA 60  
Db 1 MGGKWSKSLVGVWPAIRERIRKTDPADGVGAASRDLEKHGAIITSSNTASTNDTCWLEA 60  
QY 61 QEE-BEVGFPVTPQVPLRPMTYKAADVLSHFLKEGKGLGLIHSQRQDILDWYHTQ 119  
Db 61 QEESEVGPVPLRPMTYKAVDLSHFLKEGKGLGLIHSQRQDILDWYHTQ 120  
QY 120 YPDQWNYTPGCVRYPLTFGWCYKLVPEVPDKEVEANKGENTSLHVPVSLHGMDDPERE 179  
Db 121 IPDQWNYTPGCGIRYPLTFGWCYKLVPEVPDKEVEATEGETNCLLHPVCOHGM 180  
QY 180 VLEWRDLSRLAFHHVARELHPEYFKNC 206  
Db 181 VLMWRDLSRLAFHHVARELHPEYFKNC 207

RESULT 19  
B44963  
nef protein - human immunodeficiency virus type 1 (isolate Z321)  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 28-May-1999

C:Accession: B44963  
R:Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J.  
AIDS Res. Hum. Retroviruses 5, 121-129, 1989  
A:Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nu  
A:Reference number: A44963; MUID:89228766  
A:Accession: B44963  
A:Molecule type: DNA  
A:Residues: 1-205 <SR>  
A:Cross-references: GB:M15896; NID:g329392; PIDN:AAB53951.1; PID:g329397  
C:Genetics:  
A:Gene: nef; 3'-orf; orf-F  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; immunodeficiency

Query Match 49.6%; Score 837; DB 1; Length 205;  
Best Local Similarity 73.2%; Pred. No. 3.8e-62;  
Matches 153; Conservative 23; Mismatches 25; Indels 8; Gaps 3;

QY 1 MGKWSKSSVVGWPTVRRMR---AEPADGVGAASRDLEKHGAISSNTAATNAACAW 57  
DB 1 MNKWSK----GWPVRRIRTPPAPPAEGVGAASQDLAKHGAISSNTATNPDCAM 56  
QY 58 LEAQEE-EVGFPTVTPQVPLRPMYKAAVDLSHFLKEKGLGLIHSQRQDILDWYH 116  
DB 57 LEAQEESEVGFPPVPLRPMYKAAVDLSHFLKEKGLGLIHSQRQDILDWYH 116  
QY 117 TQGYFPDQNYTPGCVRPPLTFGCWYKLVPEPKVEANKGENTSLHPVSLHGMDDP 176  
DB 117 TQGYFPDQNYTPGCVRPPLTFGCWYKLVPEPKVEANKGENTSLHPVSLHGMDDP 176  
QY 177 EREVLEWRFDSSLARHVAELHPEYFKN 205  
DB 177 EREVLEWRFDSSLARHVAELHPEYFKN 205

## RESULT 20

T01673  
nef protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 21-Jul-2000  
C:Accession: T01673  
R:Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.  
Cell 46, 63-74, 1986  
A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol  
A:Reference number: Z14389; MUID:86245056  
A:Accession: T01673  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-209 <ALI>  
A:Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28017.1; PID:g60235  
C:Superfamily: AIDS nef protein

Query Match 49.4%; Score 834.5; DB 2; Length 209;  
Best Local Similarity 70.1%; Pred. No. 6.2e-62;  
Matches 148; Conservative 26; Mismatches 30; Indels 7; Gaps 2;

QY 1 MGKWSKSSVVGWPTVRRMRRAEPADGVG-----AASRDLEKHGAISSNTAATNAAC 55  
DB 1 MGKWSKSSVVGWPKIRIRRRTPPTGTGAVSQDAVSQDLKCGAAASSSPAANNASC 60  
QY 56 AWEAQEESEVGFPTVTPQVPLRPMYKAAVDLSHFLKEKGLGLIHSQRQDILDWYH 115  
DB 61 E--PPEEESEVGFPPVPLRPMYKAAVDLSHFLKEKGLGLIHSQRQDILDWYH 118  
QY 116 HTQGYFPDQNYTPGCVRPPLTFGCWYKLVPEPKVEANKGENTSLHPVSLHGMDD 175  
DB 119 HTQGYFPDQNYTPGCVRPPLTFGCWYKLVPEPKVEANKGENTSLHPVSLHGMDD 178  
QY 176 PEREVLWRFDSSLARHVAELHPEYFKN 206  
DB 179 AEREVLKWKFDSSLARHVAELHPEYFKN 209

## RESULT 21

nef protein - simian immunodeficiency virus SIVcpz  
ASLJK  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: simian immunodeficiency virus SIVcpz  
A:Note: host Pan troglodytes (chimpanzee)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999  
C:Accession: S09991  
R:Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.  
Nature 345, 356-359, 1990  
A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.  
A:Reference number: S09983; MUID:90259077  
A:Accession: S09991  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-205 <HUR>  
A:Cross-references: EMBL:X52154; NID:g58866; PIDN:CAA36408.1; PID:g58877  
C:Genetics:  
A:Gene: nef  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; immunodeficiency

Query Match 49.3%; Score 832; DB 1; Length 205;  
Best Local Similarity 70.2%; Pred. No. 9.8e-62;  
Matches 144; Conservative 27; Mismatches 34; Indels 0; Gaps 0;

QY 1 MGKWSKSSVVGWPTVRRMRRAEPADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60  
DB 1 MGTWSKSSLVGWPVEVRRIRREAPTAAGVGEVSKDLERHGAITSRTPTQTALWEE 60  
QY 61 QEEVEVGFPTVTPQVPLRPMYKAAVDLSHFLKEKGLGLIHSQRQDILDWYHQTQY 120  
DB 61 MDNEEVGFPPVPLRPMYKAAVDLSHFLKEKGLGLIHSQRQDILDWYHQTQY 120  
QY 121 FPDQNYTPGCVRPPLTFGCWYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
DB 121 FPDQNYTPGCVRPPLTFGCWYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
QY 181 LEWRFDSSLARHVAELHPEYFKN 205  
DB 181 LEWRFDSSLARHVAELHPEYFKN 205

## RESULT 22

S33982  
Trans-activating transcription regulator - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 06-Oct-1994 #sequence\_revision 23-Feb-1996 #text\_change 20-Sep-1999  
C:Accession: S33982; S26385; S19864  
R:Carlini, F.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33982  
A:Molecule type: DNA  
A:Residues: 1-86 <CAR>  
A:Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77625.1; PID:g60196  
R:Siderovski, D.P.; Matsuyama, T.; Frigerio, E.; Chui, S.; Min, X.; Erfle, H.; Sumner  
Nucleic Acids Res. 20, 5311-5320, 1992  
A:Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activato  
A:Reference number: S26385; MUID:93065196  
A:Accession: S26385  
A:Molecule type: nucleic acid  
A:Residues: 1-86 <SID>  
A:Cross-references: EMBL:X64650; NID:g60144; PIDN:CAA45921.1; PID:g60145  
C:Genetics:  
A:Gene: tat  
A:Introns: 72/2  
C:Superfamily: AIDS trans-activating transcription regulator  
C:Keywords: AIDS; immunodeficiency

```
Query Match      28.8%; Score 486; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 EPVDPRLPKHPGSPKTAICTNCKYKCCFHCQVCFITKALGISYGRKKRRRRPPQG 268
      |||||
Db 2 EPVDPRLPKHPGSPKTAICTNCKYKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61
      |||||

QY 269 SOTHQVSLSKOPTSQSRGDPGTPGKE 293
      |||||
Db 62 SOTHQVSLSKOPTSQSRGDPGTPGKE 86
      |||||

RESULT 23
TNLJ12
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate)
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 02-Jul-1998
C:Accession: A04017
R:Araya, S.K.; Gallo, R.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986
A:Title: Three novel genes of human T-lymphotropic virus type III: Immune reactivity of
A:Reference number: A94093; MUID:86177573
A:Accession: A04017
A:Molecule type: DNA
A:Residues: 1-95 <ARY>
C:Genetics:
A:Gene: tat
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS: immunodeficiency; transcription regulation

Query Match      28.3%; Score 478; DB 1; Length 95;
Best Local Similarity 98.8%; Pred. No. 1e-32;
Matches 84; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 209 EPVDPRLPKHPGSPKTAICTNCKYKCCFHCQVCFITKALGISYGRKKRRRRPPQG 268
      |||||
Db 11 EPVDPRLPKHPGSPKTAICTNCKYKCCFHCQVCFITKALGISYGRKKRRRRPPQG 70
      |||||

QY 269 SOTHQVSLSKOPTSQSRGDPGTPGKE 293
      |||||
Db 71 SOTHQVSLSKOPTSQSRGDPGTPGKE 95
      |||||

RESULT 24
A25700
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 02-Jul-1998
C:Accession: A25700
R:Sodroski, J.; Patarca, R.; Rosen, C.; Wong-Staal, F.; Haseltine, W.
Science 229, 74-77, 1985
A:Reference number: A25700; MUID:85244627
A:Accession: A25700
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-86 <SOD>
C:Superfamily: AIDS trans-activating transcription regulator

Query Match      27.8%; Score 470; DB 2; Length 86;
Best Local Similarity 96.5%; Pred. No. 4.2e-32;
Matches 82; Conservative 0; Mismatches 3; Indels 0; Caps 0;

QY 209 EPVDPRLPKHPGSPKTAICTNCKYKCCFHCQVCFITKALGISYGRKKRRRRPPQG 268
      |||||
Db 2 EPVDPRLPKHPGSPKTAICTNCKYKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61
      |||||

QY 269 SOTHQVSLSKOPTSQSRGDPGTPGKE 293
      |||||
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```
Db 62 SOTHQVSLSKOPTSQSRGDPGTPGKE 86

RESULT 25
S46353
nef protein - simian immunodeficiency virus SIVagm (isolate SAB-1)
C:Species: simian immunodeficiency virus SIVagm
A:Variety: isolate SAB-1
C:Date: 25-Dec-1994 #sequence_revision 14-Feb-1997 #text_change 20-Sep-1999
C:Accession: S46353
R:Jin, M.J.; Hui, H.; Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; Hirsch, V.
EMBO J. 13, 2935-2947, 1994
A:Title: Mosaic genome structure of simian immunodeficiency virus from West African
A:Reference number: S46353; MUID:94298785
A:Accession: S46353
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-226 <JIN>
A:Cross-references: EMBL:U04005; NID:9466229; PIDN:AAA21511.1; PID:9466237
A:Experimental source: isolate SAB-1; sabaesus monkey
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
C:Genetics:
A:Gene: nef
C:Superfamily: AIDS nef protein

Query Match      26.2%; Score 443; DB 2; Length 226;
Best Local Similarity 44.1%; Pred. No. 2.1e-29;
Matches 98; Conservative 30; Mismatches 70; Indels 24; Gaps 6;

QY 1 MGKWSKS-----SVVGWPTVRR-MRRAPADGVAASRDLE-----KHGATSSNT 48
      |||||
Db 1 MGKSSKQQQRHSLWLWKLQAPVIQYDMLADPLGLQSGSHIQEACAKSLRDGLIRQGS 60
      |||||

QY 49 AATNAAC-----AWLEAOEEVEVGPVTPQVPLRPMTYKAAVDLSHFLKEKGLG 99
      |||||
Db 61 SRTSEGVKMKHOGQPSWYD-EDEEVGFPVRCPLPRANTYKLAIDFGHFLKEKGLG 119
      |||||

QY 100 LIHSQRRQDILDMWYHTQGYFPDMQNYTPGCVRYPLTFGMICYKLVVPVDPKVEANKG 159
      |||||
Db 120 IYVSERRKKILDYALNENGVIDGMQNYTDGPGTRYPKCGMCKLVPV--DLSEEA 177
      |||||

QY 160 ENTSLLHPVSLHGMDDPEREVLWRFDLSLAFHHVARELHPE 201
      |||||
Db 178 ENHCLLHPAQVAYEDDANKETLVKFDPLLAVDYVAVRLHPE 219
      |||||

RESULT 26
S54385
nef protein - human immunodeficiency virus type 1 (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
C:Accession: S54385
R:Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A:Reference number: S54377
A:Accession: S54385
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-97 <THE>
A:Cross-references: EMBL:M22639; NID:g329377; PIDN:AAA5371.1; PID:g555045
C:Superfamily: AIDS nef protein

Query Match      26.0%; Score 439.5; DB 2; Length 97;
Best Local Similarity 84.5%; Pred. No. 1.6e-29;
Matches 82; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MGKWSKSSVVGWPTVRRMRRAEPADGVGAASRDLEKHGATSSNTAATNACAWLEA 60
      |||||
Db 1 MGRWSKSSIVGVPAIRIRIRTRDPAADGVGAVSRDLEKHGATSSNTRGTNADCAWLEA 60
      |||||

QY 61 QEE-EVGFPTVQVPLRPMTYKAAVDLSHFLKEKGG 96
```







DR HIV; K02013; NEFSBRU.  
DR HIV; M19921; NEFSNL43.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; Myristate; GTP-binding; Phosphorylation; 3D-structure.  
FT LIPID 2 MYRISTATE.  
FT MOD\_RES 15 15 PHOSPHORYLATION (BY PKC).  
FT VARIANT 11 11 V -> I (IN CLONE PNL4-3).  
FT VARIANT 15 15 T -> A (IN CLONE PNL4-3).  
FT VARIANT 33 33 A -> V (IN CLONE PNL4-3).  
FT VARIANT 51 51 T -> N (IN CLONE PNL4-3).  
SQ SEQUENCE 206 AA; 23342 MW; 77453FC80B6004F2 CRC64;

Query Match 66.9%; Score 1130; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. 9.3e-92;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGATSSNTAATNAACAWLEA 60  
DB 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGATSSNTAATNAACAWLEA 60  
QY 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKGGLGSLHSORRODILDLWIYHTQGY 120  
DB 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKGGLGSLHSORRODILDLWIYHTQGY 120  
QY 121 FPDQNTYTPGPGVRYPLTFGCWYKLVPEPKVVEEANKGENTSLHPVSLHGMDPPERV 180  
DB 121 FPDQNTYTPGPGVRYPLTFGCWYKLVPEPKVVEEANKGENTSLHPVSLHGMDPPERV 180  
QY 181 LEWRFDSRLAFHHVARELHPEYFKNC 206  
DB 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 2  
NEF\_HVIPV  
ID NEF\_HVIPV STANDARD; PRT; 206 AA.  
AC P03405;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
GN NEF.  
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11700;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85111157; PubMed=2982104;  
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,  
FA Capon D.J.;  
RT Nucleic acid structure and expression of the human  
RT AIDS/lymphadenopathy retrovirus.";  
RL Nature 313:450-458(1985).  
RN [2]  
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.  
RX MEDLINE=88039140; PubMed=3118220;  
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,  
RA Montagnier L., Lecocq J.-P.;  
RT "HIV F/3" orf encodes a phosphorylated GTP-binding protein resembling  
RT an oncogene product.";  
RL Nature 330:266-269(1987).  
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
CC  
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CC  
DR EMBL; K02083; AAB59874.1; -  
DR EMBL; X01762; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A04007; ASLJVL.  
DR HSSP; P03406; IEFN.  
DR HIV; K02083; NEFSVP22.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; Myristate; GTP-binding.  
FT LIPID 2 MYRISTATE.  
SQ SEQUENCE 206 AA; 23352 MW; EDE64281A17C6735 CRC64;

Query Match 66.0%; Score 1114; DB 1; Length 206;  
Best Local Similarity 97.6%; Pred. No. 2.3e-90;  
Matches 201; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGATSSNTAATNAACAWLEA 60  
DB 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGATSSNTAATNAACAWLEA 60  
QY 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKGGLGSLHSORRODILDLWIYHTQGY 120  
DB 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKGGLGSLHSORRODILDLWIYHTQGY 120  
QY 121 FPDQNTYTPGPGVRYPLTFGCWYKLVPEPKVVEEANKGENTSLHPVSLHGMDPPERV 180  
DB 121 FPDQNTYTPGPGVRYPLTFGCWYKLVPEPKVVEEANKGENTSLHPVSLHGMDPPERV 180  
QY 181 LEWRFDSRLAFHHVARELHPEYFKNC 206  
DB 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 3

NEF\_HVILW  
ID NEF\_HVILW STANDARD; PRT; 206 AA.  
AC Q70627;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
GN NEF.  
OS Human immunodeficiency virus type 1 (LW12.3 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=82834;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95127297; PubMed=7826699;  
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,  
RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker  
RT infected with HIV type 1 (HTLV type IIIB).";  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [2]  
RP STRUCTURE BY NMR OF 56-206.  
RX MEDLINE=97337445; PubMed=9194185;  
RA Grzesiek S., Bax A., Hu J.S., Kaufman J., Palmer I., Stahl S.J.,  
RA Tjandra N., Wingfield P.T.;  
RT "Refined solution structure and backbone dynamics of HIV-1 Nef.";  
RL Protein Sci. 6:1248-1263(1997).  
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
CC  
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EMBL; U12055; AAA76691.1; -



DR PDB: 2NEF; 07-JUL-97.  
 DR InterPro: IPR001558; F-protein.  
 DR Pfam: PF00469; F-protein; 1.  
 KW AIDS; Myristate; GTP-binding; 3D-structure.  
 FT LIPID 2 MYRISTATE.  
 SQ SEQUENCE 206 AA; 23414 MW; ED81F68F6B61279E CRC64;

Query Match 65.8%; Score 1111; DB 1; Length 206;  
 Best Local Similarity 97.1%; Pred. No. 4.3e-90;  
 Matches 200; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
 Db 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
 Qy 61 QEEEGVGPVTPQVPLRPMTYKAAVDLSHFLKKEGGLSHQSRQDILDLIWIHTQGY 120  
 Db 61 QEEEGVGPVTPQVPLRPMTYKAAVDLSHFLKKEGGLSHQSRQDILDLIWIHTQGY 120  
 Qy 121 FPDQWNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHHPVSLHGMDDPEREV 180  
 Db 121 FPDQWNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHHPVSLHGMDDPEREV 180  
 Qy 181 LEWRFDSRLAFHHVARELHPEYFKNC 206  
 Db 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 4  
 NEF\_HV112 STANDARD; PRT; 206 AA.  
 ID NEF\_HV112  
 AC P04324;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
 GN NEF.  
 OS Human immunodeficiency virus type 1 (clone 12) (HIV-1).  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11679;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86177573; PubMed=3008154;  
 RA Arya S.K., Gallo R.C.;  
 RT "Three novel genes of human T-lymphotropic virus type III: Immune  
 RT reactivity of their products with sera from acquired immune  
 RT deficiency syndrome patients."  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).  
 RN [2]  
 RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.  
 RX MEDLINE=88039140; PubMed=3118220;  
 RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,  
 RA Montagnier L., Lecocq J.-P.;  
 RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling  
 RT an oncogene product."  
 RL Nature 330:266-269(1987).  
 CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 CC  
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 CC  
 CC EMBL; M11840; AAA45001.1;  
 DR PIR; A04006; ASLJ12.  
 DR HSSP; P03406; IEFN.  
 DR HIV; M11840; NEFSPC12.  
 DR InterPro; IPR001558; F-protein.

DR Pfam: PF00469; F-protein; 1.  
 KW AIDS; Myristate; GTP-binding.  
 FT LIPID 2 MYRISTATE.  
 SQ SEQUENCE 206 AA; 23366 MW; 218F5B2980F79A46 CRC64;

Query Match 65.6%; Score 1108; DB 1; Length 206;  
 Best Local Similarity 97.1%; Pred. No. 7.8e-90;  
 Matches 200; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
 Db 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
 Qy 61 QEEEGVGPVTPQVPLRPMTYKAAVDLSHFLKKEGGLSHQSRQDILDLIWIHTQGY 120  
 Db 61 QEEEGVGPVTPQVPLRPMTYKAAVDLSHFLKKEGGLSHQSRQDILDLIWIHTQGY 120  
 Qy 121 FPDQWNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHHPVSLHGMDDPEREV 180  
 Db 121 FPDQWNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHHPVSLHGMDDPEREV 180  
 Qy 181 LEWRFDSRLAFHHVARELHPEYFKNC 206  
 Db 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 5  
 NEF\_HV1B8 STANDARD; PRT; 205 AA.  
 ID NEF\_HV1B8  
 AC P05855;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
 GN NEF.  
 OS Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11684;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85111123; PubMed=2578615;  
 RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,  
 RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,  
 RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,  
 RA Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,  
 RA Wong-Staal F.;  
 RT "Complete nucleotide sequence of the AIDS virus, HTLV-III."  
 RL Nature 313:277-284(1985).  
 RN [2]  
 RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.  
 RX MEDLINE=88039140; PubMed=3118220;  
 RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,  
 RA Montagnier L., Lecocq J.-P.;  
 RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling  
 RT an oncogene product."  
 RL Nature 330:266-269(1987).  
 CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 CC  
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 CC  
 CC EMBL; K02011; -; NOT\_ANNOTATED\_CDS.  
 DR HSSP; P03406; IEFN.  
 DR HIV; K02011; NEF5B8.  
 DR InterPro; IPR001558; F-protein.  
 DR Pfam; PF00469; F-protein; 1.

KW AIDS: Myristate; GTP-binding.  
FT LIPID 2 MYRISTATE  
SQ SEQUENCE 205 AA; 23305 MW; 8EC12F6650DD111 CRC64;

Query Match 64.5%; Score 1088.5; DB 1; Length 205;  
Best Local Similarity 96.6%; Pred. No. 3.9e-88;  
Matches 199; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 1 MGGKWSKSSVVGWPTVTRMRRAEPAADGVGAASRDLEKKGALTSNTAATNAACAWLEA 60  
Dy 1 MGGKWSKSSVVGWPTVTRMRRAEPAADGVGAASRDLEKKGALTSNTAATNAACAWLEA 60  
Qy 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKKEGGLIHSORRODILDLWIHTQGY 120  
Dy 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKKEGGLIHSORRODILDLWIHTQGY 120  
Qy 121 FPDQNYTPGCVRYPLTFGVCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPREV 180  
Dy 121 FPDQNYTPGCVRYPLTFGVCYKLVPEPK-EEANKGENTSLHPVSLHGMDDPREV 179  
Qy 181 LEWRDLSRLAFHHVARELHPEYFKNC 206  
Dy 180 LEWRDLSRLAFHHVARELHPEYFKNC 205

## RESULT 6

NEF\_HV1BN STANDARD; PRT; 218 AA.  
AC P12479;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
GN NEF.  
OS Human immunodeficiency virus type 1 (LBR isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11693;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89083613; PubMed=2789516;  
RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P.,  
Dandekar S.  
RT "Biological and molecular characterization of human immunodeficiency  
virus (HIV-LBR) from the brain of a patient with progressive  
dementia".  
RL Virology 168:79-89(1989).  
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
CC -!- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS  
HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.  
CC -----  
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CC -----  
DR EMBL; M21098; AAA44222.1; -.  
DR PIR; D31667; ASLJBR.  
DR HSP; P03406; 1EPN.  
DR HIV; M21098; NEFSBRVA.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 2.  
KW AIDS: Myristate; GTP-binding.  
FT LIPID 2 MYRISTATE (BY SIMILARITY).  
SQ SEQUENCE 218 AA; 25032 MW; FCADAE1045C460E CRC64;  
  
Query Match 60.4%; Score 1019; DB 1; Length 218;  
Best Local Similarity 84.1%; Pred. No. 5e-82;

Matches 185; Conservative 12; Mismatches 7; Indels 16; Gaps 2;  
Qy 1 MGGKWSKSSVVGWPTVTRMRRAEPAADGVGAASRDLEKKGALTSNTAATNAACAWLEA 106  
Dy 1 MGGKWSKSSVVGWPTVTRMRRAEPAADGVGAASRDLEKKGALTSNTAATNAACAWLEA 106  
Qy 47 NTAATNAACAWLEAEEVEGFPVTPQVPLRPMTYKAADVLSHFLKKEGGLIHSORRODILDLWIHTQGY 118  
Dy 59 NTAATNAACAWLEAEEVEGFPVTPQVPLRPMTYKAADVLSHFLKKEGGLIHSORRODILDLWIHTQGY 118  
Qy 107 QDILDLWIHTQGYFPDQNYTPGCVRYPLTFGVCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPREV 166  
Dy 119 QDILDLWIHTQGYFPDQNYTPGCVRYPLTFGVCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPREV 178  
Qy 167 PVSLLHGMDDPREVLEWRDLSRLAFHHVARELHPEYFKNC 206  
Dy 179 PMSQGMDDPDERVLEWRDLSRLAFHHVARELHPEYFKNC 218

## RESULT 7

NEF\_HV1S3 STANDARD; PRT; 205 AA.  
AC P19545;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
GN NEF.  
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90317906; PubMed=2370688;  
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;  
RT "Human immunodeficiency virus type 1 cellular host range,  
replication, and cytopathicity are linked to the envelope region of  
the viral genome".  
RL J. Virol. 64:4016-4020(1990).  
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
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CC -----  
DR EMBL; M38427; AAA45068.1; -.  
DR HSP; P03406; 1EPN.  
DR HIV; M38427; NEFSF33.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS: Myristate; GTP-binding.  
FT LIPID 2 MYRISTATE (BY SIMILARITY).  
SQ SEQUENCE 205 AA; 23318 MW; FFB419A1C5DFC9F3 CRC64;  
  
Query Match 59.6%; Score 1005.5; DB 1; Length 205;  
Best Local Similarity 86.4%; Pred. No. 7e-81;  
Matches 178; Conservative 19; Mismatches 8; Indels 1; Gaps 1;  
Qy 1 MGGKWSKSSVVGWPTVTRMRRAEPAADGVGAASRDLEKKGALTSNTAATNAACAWLEA 60  
Dy 1 MGGKWSKSK-MGPAVRERMRRAEPAADGVGAASRDLEKKGALTSNTAATNAACAWLEA 59  
Qy 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKKEGGLIHSORRODILDLWIHTQGY 120  
Dy 60 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKKEGGLIHSORRODILDLWIHTQGY 119  
Qy 121 FPDQNYTPGCVRYPLTFGVCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPREV 180



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AC P05858;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11701;
RN [1]
RP SEQUENCE FROM N.A.
RA Starich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S.,
RA Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
RA Wong-Staal F.;
RL Submitted (XXX-1987) to the HIV data bank.
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC
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CC
CC EMBL; M17451; AAA45058.1;
CC HSP; P03406; IEFN.
CC InterPro: IPR001558; F-protein.
CC Pfam: PF00469; F-protein; 1.
CC ADS; Myristate; GTP-binding.
FT LPID 2
SQ SEQUENCE 208 AA; 23532 MW; 8F836FE980F084C CRC64;

Query Match 58.9%; Score 994; DB 1; Length 208;
Best Local Similarity 84.6%; Pred. No. 7.3e-80;
Matches 176; Conservative 16; Mismatches 14; Indels 2; Gaps 1;

QY 1 MGGKWSKSSVVGWPTVR-----ERMRAEPAADGVGAASRDLEKKGGLIHSQRQDIL 60
DB 1 MGGKWSKSKMGWPAVRERMQAEPADGVGAASRDLEKKGGLIHSQRQDIL 60
QY 61 Q-EEVEGFPVTPQVPLRPMTHKAAVDLSHFLKEKGLIHSQRQDIL 118
DB 61 QEEDEEVEGFPVTPQVPLRPMTHKAAVDLSHFLKEKGLIHSQRQDIL 120
QY 119 GFYFDQWNTPGVRYPLTFTGWCYKLVPEPKVEEANKGENTSLHHPVSL 178
DB 121 GFYFDQWNTPGVRYPLTFTGWCYKLVPEPKVEEANKGENTSLHHPVSL 180
QY 179 EVLEWRDLSRLAFHVAHELHPEYKNC 206
DB 181 EVLVKWDLSRLAFHVAHELHPEYKDC 208

RESULT 11
NEF_HV1Y2
ID NEF_HV1Y2 STANDARD; PRT; 214 AA.
AC P35959;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=36377;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,

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RA Shaw G.M.;
RT Complete nucleotide sequence, genome organization, and biological
RT properties of human immunodeficiency virus type 1 in vivo: evidence
RT for limited defectiveness and complementation.
RL J. Virol. 66:6587-6600(1992).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC
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CC
CC EMBL; M93258; -; NOT_ANNOTATED_CDS.
CC PIR; I44001; I44001.
CC HSP; P03406; IEFN.
CC InterPro: IPR001558; F-protein.
CC Pfam: PF00469; F-protein; 1.
CC ADS; Myristate; GTP-binding.
FT LPID 2
SQ SEQUENCE 214 AA; 24532 MW; E188D43D7B084D04 CRC64;

Query Match 58.7%; Score 991.5; DB 1; Length 214;
Best Local Similarity 84.2%; Pred. No. 1.2e-79;
Matches 181; Conservative 12; Mismatches 11; Indels 11; Gaps 2;

QY 1 MGGKWSKSSVVGWPTVR-----ERMRAEPAADGVGAASRDLEKKGGLIHSQRQDIL 50
DB 1 MGGKWSKSKMGWPAVRERMQAEPADGVGAASRDLEKKGGLIHSQRQDIL 60
QY 51 TNAACAWLEAQEEEEVEGFPVTPQVPLRPMTHKAAVDLSHFLKEKGLIHSQRQDIL 110
DB 61 TNADCAWLEAQEEEEVEGFPVTPQVPLRPMTHKAAVDLSHFLKEKGLIHSQRQDIL 120
QY 111 DLWYHTQGYFPDQWNTPGVRYPLTFTGWCYKLVPEPKVEEANKGENTSLHHPVSL 170
DB 121 DLWYHTQGYFPDQWNTPGVRYPLTFTGWCYKLVPEPKVEEANKGENTSLHHPVSL 179
QY 171 HGMDDEPEREVLWRDLSRLAFHVAHELHPEYKNC 205
DB 180 HGMDDEPEREVLWRDLSRLAFHVAHELHPEYKNC 214

RESULT 12
NEF_HV1JR
ID NEF_HV1JR STANDARD; PRT; 216 AA.
AC P20867;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (JRCSE isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen I.S.Y.;
RL Submitted (DEC-1988) to the HIV data bank.
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC
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CC      EMBL; M38429; AAB03750.1; -.
DR      HSSP; P03406; 1EFN.
DR      HIV; M38429; NEFSJRCSF.
DR      InterPro; IPR001558; F-protein.
DR      Pfam; PF00469; F-protein; 1.
DR      AIDS; Myristate; GTP-binding.
KW      AIDS; Myristate; GTP-binding.
FT      LIPID 2
SQ      SEQUENCE 216 AA; 24567 MW; D163FFA8C71529DC CRC64;

Query Match      58.1%; Score 981; DB 1; Length 216;
Best Local Similarity 81.9%; Pred. No. 1e-78;
Matches 177; Conservative 15; Mismatches 14; Indels 10; Gaps 1;

QY      1  MGKWKSGVGVGPTVRERMRRAEPAAD-----GVGAASRDLEKKGAISSNTAA 50
DB      1  MGCKWSKHSVPGWSTVRERMRRAEPATDRVQTPEAAVGVGAVSRDLEKKGAISSNTAA 60

QY      51  TNAACAWLEAQEEVEGFVTPQVPLRPMTYKAAVDLSHLFKEGGLEGLHSORRQDIL 110
DB      61  TNADCAWLEAYEDEVGFVPRPQVPLRPMTYKAAIDLSHLFKEGGLEGLIYSOKRQDIL 120

QY      111 DLWYHTQGVFPDQWNTPGGVRYPLTFGCYKLVPEVPDKEEANKGENTSLLLHPVSL 170
DB      121 DLWYHTQGVFPDQWNTAGGVRYPLTFGCWFKLVDPDPEKVEEANGENNCLLHPMSQ 180

QY      171 HGMDPPEVLEWRFSRLAFPHHVARELHPEYFKNC 206
DB      181 HGMDPEKEVLYNKFDSKLLALHHVARELHPEYKYDC 216

RESULT 13
NEF_HV1S1
ID      NEF_HV1S1      STANDARD;      PRT;      208 AA.
AC      P19546;
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN      NEF.
OS      Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC      Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID=11691;
RN      [1]
RS      SEQUENCE FROM N.A.
RX      MEDLINE=90347835; PubMed=2384920;
RA      Cheng-Mayer C., Qulroga M., Tung J.W., Dina D., Levy J.;
RT      "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT      macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL      J. Virol. 64:4390-4398(1990).
CC      -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC      ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC      -----
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CC      or send an email to license@isb-sib.ch.
CC      -----
EMBL; M65024; AAA45073.1; -.
HSSP; P03406; 1EFN.
HIV; M38428; NEFSF162.
InterPro; IPR001558; F-protein.
DR      Pfam; PF00469; F-protein; 1.
KW      AIDS; Myristate; GTP-binding.
FT      LIPID 2
SQ      SEQUENCE 208 AA; 23684 MW; AOB1007D14E46E32 CRC64;
MYRISTATE (BY SIMILARITY).

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Query Match 57.7%; Score 974; DB 1; Length 208;

```

Best Local Similarity 84.2%; Pred. No. 4.1e-78;
Matches 176; Conservative 16; Mismatches 13; Indels 4; Gaps 2;

Qy 1 MGGKWSKSSVVGWPTVRRMR---ABPAADGVGAASRDLEKHGCAITSSNTAATAACAW 57
      |||||  || |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 MGGKWSK-RWSGWSAVRERKRAEPAEPAADGVGAASRDLEKHGCAITSSNTAANNACAW 59

Qy 58 LEAQEESEVGPVTPQVPLRPMTYKAAVDLSHFUKKEGGLGLTHSORRDILDIWYHT 117
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 60 LEAQEDEDVGPVPQVPLRPMTYKAAVDLSHFUKKEGGLGLTHSORRDILDIWYHT 119

Qy 118 QGYEPDQNTPGPGVAYPLTFGWCYKLVLPVEPKVGEANKGENTSLHPVSLHGMDDPE 177
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 120 QGYEPDQNTPGPGIRYPLTFGWCFLKLVLPVDPDVEANAGENNLSLHPMSQHGMDPE 179

Qy 178 REVLEWFDSRLAFHHVARELHPEYFKNC 206
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 180 KEVLVWFDSRLAFHHMARELHPEYKDC 208

RESULT 14
NEF_HVIEL
ID ID NEF_HVIEL STANDARD; PRT; 206 AA.
AC P04604;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86245056; PubMed=2424612;
RA Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
of two isolates from African patients.";
RL Cell 46:63-74(1986).
RN [2]
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
RX MEDLINE=88039140; PubMed=3118220;
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
RA Montagnier L., Lecocq J.-P.;
RT "HIV F3'orf encodes a phosphorylated GTP-binding protein resembling
an oncogene product.";
RL Nature 330:286-289(1987).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
-----
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-----
CC EMBL; K03454; AAA4330.1; -
CC DR EMBL; A07108; CAA00617.1; -
CC DR HSSP; P03406; IEFN.
CC DR HIV; K03454; NEF$ELI.
CC DR InterPro; IPR001558; F-protein.
CC DR Pfam; PF00469; F-protein; 1.
CC DR AIDS; Myristate; GTP-binding.
CC FT LIPID 2
SQ SEQUENCE 206 AA; 23612 MW; 4CFF9F18AEB503C CRC64;
MYRISTATE.

```

Query Match 54.9%; Score 927.5; DB 1; Length 206;  
Best Local Similarity 79.1%; Pred. No. 4.7e-74;  
Matches 163; Conservative 24; Mismatches 18; Indels 1

QY 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNACAWLEA 60  
DB 1 MGGKWSKSSVVGWPAIRIRIRRTNPAADGVGAASRDLEKKGAISSNTASTNADCAWLEA 60  
QY 61 QEE-EEVGFPPVTPQVPLRPMTYKAADVLSHFLKKEGGLGLIHSORRODILDWIYHTQG 119  
DB 61 QEESEVGFPPVTPQVPLRPMTYKAADVLSHFLKKEGGLGLIHSORRODILDWIYHTQG 120  
QY 120 YFPDQNYTPGPGVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPERE 179  
DB 121 IFPDQNYTPGPGIRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPERE 180  
QY 180 VLEWRDRLAFHVAARELHPEYKNC 205  
DB 181 VLKWRFRNSRLAFEHKAREMHPEFYKNC 206

RESULT 15  
ID\_NEF\_HV126 STANDARD; PRT; 212 AA.  
AC P04602;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
GN NEF.  
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11708;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87248097; PubMed=3036660;  
RA Srinivasan A., Anand R., York D., Ranganathan P., Feorino P.,  
RA Sanchetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,  
RA Sanchez-Pescador R.;  
RT "Molecular characterization of human immunodeficiency virus from  
RT Zaire: nucleotide sequence analysis identifies conserved and variable  
RT domains in the envelope gene."  
RL Gene 52:71-82(1987).  
RN [2]  
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.  
RX MEDLINE=88039140; PubMed=3118220;  
RA Guy B., Kleny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,  
RA Montagnier L., Lecocq J.-P.;  
RT "HIV E3' orf encodes a phosphorylated GTP-binding protein resembling  
RT an oncogene product."  
RL Nature 330:266-269(1987).  
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

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DR EMBL; K03458; AAA45381.1; -  
DR PIR; F26192; QOLJZR.  
DR HSP; P03406; 1EFN.  
DR HIV; K03458; NEFS26.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
DR AIDS; Myristate; GTP-binding.  
KW Lipid  
FT Lipid  
SQ SEQUENCE 212 AA; 24415 MW; EC095A1B263047CF CRC64;

Query Match 54.0%; Score 911; DB 1; Length 212;  
Best Local Similarity 77.4%; Pred. No. 1.3e-72;  
Matches 164; Conservative 23; Mismatches 19; Indels 6; Gaps 2;

QY 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAC 55  
DB 1 MGGKWSKSSVVGWPAIRIRIRRTNPAADGVGAASRDLEKKGAISSNTAATNAC 60  
QY 56 AWLEAQEE-EEVGFPPVTPQVPLRPMTYKAADVLSHFLKKEGGLGLIHSORRODILDWI 114  
DB 61 AWLEAQEESEVGFPPVTPQVPLRPMTYKAADVLSHFLKKEGGLGLIHSORRODILDWI 120  
QY 115 YHOGYPPDQNYTPGPGVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDD 174  
DB 121 YHOGYPPDQNYTPGPGIRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDD 180  
QY 175 DPEREVLEWRDRLAFHVAARELHPEYKNC 206  
DB 181 DTEREVLEWRDRLAFHVAARELHPEYKNC 212

RESULT 16  
ID\_NEF\_HVIND STANDARD; PRT; 207 AA.  
AC P18801;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
GN NEF.  
OS Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11695;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90034200; PubMed=2806917;  
RA Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F.,  
RA Hampe A., Chermann J.C.;  
RT "Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the  
RT human immunodeficiency virus."  
RL Gene 81:275-284(1989).  
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
CC -!- MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH  
CC AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.

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DR EMBL; M27323; AAA44874.1; -  
DR PIR; JQ0068; QOLJND.  
DR HSP; P03406; 1EFN.  
DR HIV; M27323; NEFSNDK.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
DR AIDS; Myristate; GTP-binding.  
KW Lipid  
FT Lipid  
SQ SEQUENCE 207 AA; 23748 MW; 09036C2F81D45D5E CRC64;

Query Match 53.5%; Score 903.5; DB 1; Length 207;  
Best Local Similarity 77.3%; Pred. No. 5.9e-72;  
Matches 160; Conservative 25; Mismatches 21; Indels 1; Gaps 1;

QY 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNACAWLEA 60  
DB 1 MGGKWSKSSVVGWPAIRIRIRRTNPAADGVGAASRDLEKKGAISSNTASTNADCAWLEA 60  
QY 61 QEE-EEVGFPPVTPQVPLRPMTYKAADVLSHFLKKEGGLGLIHSORRODILDWIYHTQG 119  
DB 61 QEESEVGFPPVTPQVPLRPMTYKAADVLSHFLKKEGGLGLIHSORRODILDWIYHTQG 120

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QY 120 YFPDQNYTPGQVRYPLTFCWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPERE 179
Db 121 IFPDQNTTPGQIRYPTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPERQ 180
QY 180 VLEWRFDSRLAFHHVARELHPEYFKNC 206
Db 181 VLMWRFNSRLALEHKARELHPEYFKDC 207

RESULT 17
NEF_HV104
ID NEF_HV104 STANDARD; PRT: 205 AA.
AC P24741;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (strain Ugandan / isolate U455)
OS (HIV-1).
OS Viruses; Retrovirdae; Lentivirus.
OC NCBI_TaxID=11703;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91090981; PubMed=2265025;
RA Oram J.D., Downing R.G., Roff M., Clegg J.C.S., Serwadda D.,
RA Carswell J.W.;
RT "Nucleotide sequence of a Ugandan HIV-1 provirus reveals genetic
RT diversity from other HIV-1 isolates."
RL AIDS Res. Hum. Retroviruses 6:1073-1078(1990).
CC -|- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -----
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CC -----
DR EMBL; M62320; AAA75023.1; -
DR HSP; P03406; IEPN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 205 AA; 23253 MW; 869AB03E6E7893C4 CRC64;

Query Match 51.7%; Score 872; DB 1; Length 205;
Best Local Similarity 75.1%; Pred. No. 3.3e-69;
Matches 154; Conservative 24; Mismatches 27; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVWGVTVRMRRAEPAADGVGAASRDLEKHGATSSNTAATNAACAWLEA 60
Db 1 MGGKWSKSRVPEVKRMRTPAARKGVAGVQDLKYGAVTSSNTSNAACAWLEA 60
QY 61 QEEEEYGFVTPQVPLRPMYTKAAVDLSHFLKKEGGLIHSQRQDILDLYIHTQGY 120
Db 61 QEEGDVGFPVPQVPLRPMYTKAAFDLSFLKKEGGLDGLIHSQRQDILDLYIHTQGF 120
QY 121 FPDQNYTPGQVRYPLTFCWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180
Db 121 FPDQNYTPGQIRYPTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREY 180
QY 181 LEWRFDSRLAFHHVARELHPEYFKN 205
Db 181 LMKWFDSTALKHAYELHPEYFKD 205

RESULT 18
NEF_HV1MN
ID NEF_HV1MN STANDARD; PRT: 182 AA.
AC P05856;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OS Viruses; Retrovirdae; Lentivirus.
OC NCBI_TaxID=11696;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates."
RL Virology 164:531-536(1988).
CC -|- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -|- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
CC PATIENT IN 1984.
CC -----
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CC -----
DR EMBL; M17449; AAA44858.1; -
DR HSP; P03406; IEPN.
DR HIV; M17449; NEFSMN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 182 AA; 20632 MW; 2C5B5A6E3EF13B26 CRC64;

Query Match 49.9%; Score 842; DB 1; Length 182;
Best Local Similarity 87.4%; Pred. No. 1.2e-66;
Matches 153; Conservative 11; Mismatches 7; Indels 4; Gaps 2;

QY 1 MGGKWSKSSVWGVTVRMRRAEPAADGVGAASRDLEKHGATSSNTAATNAACAW 57
Db 1 MGGKWSK-RVTGMPTVRMRRAEPAELAADGVGAASRDLEKHGATSSNTAATNADCAW 59
QY 58 LEAQEEYGFVTPQVPLRPMYTKAAVDLSHFLKKEGGLIHSQRQDILDLYIHT 117
Db 60 LEAQEEYGFVTPQVPLRPMYTKAALDLSHFLKKEGGLDGLIYSQRQDILDLYIHT 119
QY 118 QGYFPDQNYTPGQVRYPLTFCWCYKLVPEPKVEEANKGENTSLHPVSLHGM 172
Db 120 QGYFPDQNYTPGQIRYPTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGM 174

RESULT 19
NEF_HV12H
ID NEF_HV12H STANDARD; PRT: 205 AA.
AC P05859;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (Zaire H2321 isolate) (HIV-1).
OS Viruses; Retrovirdae; Lentivirus.
OC NCBI_TaxID=11692;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89228766; PubMed=2713163;
RA Srinivasan A., York D., Butler D. Jr., Jannoun-Nasr R., Getchell J.,

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RA McCormick J., Ou C.Y., Myers G., Smith T., Chen E.;
RT "Molecular characterization of HIV-1 isolated from a serum collected
RT in 1976: nucleotide sequence comparison to recent isolates and
RT generation of hybrid HIV.";
RL AIDS Res. Hum. Retroviruses 5:121-129(1989).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -----
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CC -----
DR EMBL; M15896; AAB53951.1; -
DR PIR; B44963; B44963.
DR HSP; P03406; IEFN.
DR HIV; M15896; NEFSZ321.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 205 AA; 23306 MW; EA55B18AF412A9D0 CRC64;
-----
Query Match 49.6%; Score 837; DB 1; Length 205;
Best Local Similarity 73.2%; Pred. No. 3.8e-66;
Matches 153; Conservative 23; Mismatches 25; Indels 8; Gaps 3;
QY 1 MGGKWSKSVGWPTVRRMR---AEPADGVGAASRDLEKHGALTSSNTAATNAACAW 57
DB 1 MGNKSK-----GWPAVREIRTPAPPAREGVGAASQDLAKHGALSSNTATNPDCAW 56
QY 58 LEAQEE-EVGFPPVTPQVPLRPMTYKAAVDLSHFLKEKGLGEGLIHSORRQDILDWYH 116
DB 57 LEAQEESEVGFPPVTPQVPLRPMTYKGAFLDFFLKEKGLDGLIYSKKRQIIDLWYH 116
QY 117 TGGYFPDMQNYTPGCVRYPLTFGCWYKLVPEPKVEEANKGENTSLHHPVSLHGMDDP 176
DB 117 TGGFFPDHNYTPGCGTRPLCGWCFLVDPVPEVEEANTGNNCLLHPMSHQGMDD 176
QY 177 EREVLWRFDSRLAFHVAHRELHPEYFKN 205
DB 177 EREVLWKFDDSLARKHLAREHHPYK 205
RESULT 20
NEF_HV1MA
ID NEF_HV1MA STANDARD; PRT; 209 AA.
AC P04603.
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11697;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86245056; PubMed=2424612;
RA Alison M., Wain-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
RT of two isolates from African patients.";
RL Cell 46:63-74(1986).
RN [2]
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
RX MEDLINE=88039140; PubMed=3118220;
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
RA Montagnier L., Lecocq J.-P.;
RT "Hiv F/3' orf encodes a phosphorylated GTP-binding protein resembling
an oncogene product.";
RL Nature 330:266-269(1987).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -----
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CC -----
DR EMBL; X04415; CAA28017.1; -
DR EMBL; A07116; CAA00624.1; -
DR HSP; P03406; IEFN.
DR HIV; K03456; NEFSMAL.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 209 AA; 23644 MW; D0B30A2442C8CC44 CRC64;
-----
Query Match 49.4%; Score 834.5; DB 1; Length 209;
Best Local Similarity 70.1%; Pred. No. 6.4e-66;
Matches 148; Conservative 26; Mismatches 30; Indels 7; Gaps 2;
QY 1 MGGKWSKSVGWPTVRRMRRAEPAADGVG-----AASRDLEKHGALTSSNTAATNAAC 55
DB 1 MGGKWSKSIVGWPKIRIRPTPTETGVGAVSQDVLKCGAAASSSPAANNASC 60
QY 56 AWLEAQEEVEEFGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGEGLIHSORRQDILDWY 115
DB 61 E---PPEEEVEEFGFPVTPQVPLRPMTYKGAFLDLSHFLKEKGLDGLVMSKPKRQIIDLWY 118
QY 116 HTQGYFPDMQNYTPGCVRYPLTFGCWYKLVPEPKVEEANKGENTSLHHPVSLHGMDD 175
DB 119 HTQGYFPDMQNYTPGCGTRPLCGWCFLVPEPKVEEANKGENTSLHHPVSLHGMDD 178
QY 176 PEREVLWRFDSRLAFHVAHRELHPEYFKN 206
DB 179 AEREVLWKFDDSLARKHLAREHHPYKDC 209
RESULT 21
NEF_SIVCZ
ID NEF_SIVCZ STANDARD; PRT; 205 AA.
AC P17664.
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90259077; PubMed=2188136;
RA Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
RT "Genetic organization of a chimpanzee lentivirus related to HIV-1.";
RL Nature 345:356-359(1990).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -----
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CC -----
DR EMBL; X52154; CAA36408.1;
DR PIR; S09991; ASLJIK.
DR HSP; P03406; IEFN.
DR HIV; X52154; NEFSCP2.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 205 AA; 23850 MW; 21E0A3EC99F1811F CRC64;

Query Match 49.3%; Score 832; DB 1; Length 205;
Best Local Similarity 70.2%; Pred. No. 1e-65;
Matches 144; Conservative 27; Mismatches 34; Indels 0; Gaps 0;

QY 1 MGKSKSSVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTATNAACAWLEA 60
DB 1 MGKSKSSVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTATNAACAWLEA 60
QY 61 QEEVEGVFPVTPQVPLRPMTYKAADVLSHFLKEKGLGSLHSORQDILDLWIYHTQGY 120
DB 61 QEEVEGVFPVTPQVPLRPMTYKAADVLSHFLKEKGLGSLHSORQDILDLWIYHTQGY 120
QY 121 FPDQNYTTPGVRPLTFGWCYKLVPEPKVPEANKGENTSLHPVSLHGMDDPEREV 180
DB 121 FPDQNYTTPGVRPLTFGWCYKLVPEPKVPEANKGENTSLHPVSLHGMDDPEREV 180
QY 181 LEWRFDSRLAFHVAELHPEYKNC 205
DB 181 LEWRFDSRLAFHVAELHPEYKNC 205
QY 181 LVWRFDSRLAFHVAELHPEYKNC 205
DB 181 LVWRFDSRLAFHVAELHPEYKNC 205

RESULT 22
NEF_HV1SC STANDARD; PRT; 239 AA.
AC P03857;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgu C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988).
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
CC 1984 IN SOUTHERN CALIFORNIA.
CC -----
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CC -----
CC EMBL; M17450; AAA5064.1;
CC HSP; P03406; IEFN.
CC HIV; M17450; NEFSCP.
CC InterPro; IPR001558; F-protein.
CC Pfam; PF00469; F-protein; 1.
KW AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 239 AA; 26799 MW; 704A17E54763A99B CRC64;

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CC -----
DR EMBL; X52154; CAA36408.1;
DR PIR; S09991; ASLJIK.
DR HSP; P03406; IEFN.
DR HIV; X52154; NEFSCP2.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 205 AA; 23850 MW; 21E0A3EC99F1811F CRC64;

Query Match 48.5%; Score 819; DB 1; Length 239;
Best Local Similarity 75.5%; Pred. No. 1.7e-64;
Matches 157; Conservative 16; Mismatches 31; Indels 4; Gaps 2;

QY 1 MGKSKSSVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTATNAACAWLEA 60
DB 1 MGKSKSSVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTATNAACAWLEA 60
QY 61 QEEVEGVFPVTPQVPLRPMTYKAADVLSHFLKEKGLGSLHSORQDILDLWIYHTQGY 120
DB 61 QEEVEGVFPVTPQVPLRPMTYKAADVLSHFLKEKGLGSLHSORQDILDLWIYHTQGY 118
QY 121 FPDQNYTTPGVRPLTFGWCYKLVPEPKVPEANKGENTSLHPVSLHGMDDPER 178
DB 121 FPDQNYTTPGVRPLTFGWCYKLVPEPKVPEANKGENTSLHPVSLHGMDDPER 178
QY 179 EVLEWRFDSRLAFHVAELHPEYKNC 206
DB 179 EVLEWRFDSRLAFHVAELHPEYKNC 206
QY 179 EVLEWRFDSRLAFHVAELHPEYKNC 206
DB 179 EVLEWRFDSRLAFHVAELHPEYKNC 206

RESULT 23
NEF_HV1H2 STANDARD; PRT; 123 AA.
AC P04601; O09780;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
RT virus.";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]
RP REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
RX MEDLINE=88039140; PubMed=3118220;
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
RA Montagnier L., Lecocq J.-P.;
RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
RT an oncogene product.";
RL Nature 330:266-269(1987).
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -1- MISCELLANEOUS: IN THIS ISOLATE A MUTATION IN POSITION 124 ADDS A
CC STOP CODON AND THE PROTEIN IS MUCH SHORTER THAN IN OTHER ISOLATES
CC (210 AA).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K03455; AAB50263.1;
CC HSP; AF033819; AAC82597.1;
CC HSP; Q70627; 2NEF.

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DR HIV: K03455; NEFSHXB2.  
 DR InterPro: IPR001558; F-protein.  
 DR Pfam: PF00469; F-protein; 1.  
 KW AIDS: Myristate; GTP-binding; Phosphorylation.  
 FT LIPID 2 MYRISTATE.  
 FT MOD\_RES 15 15 PHOSPHORYLATION (BY PKC).  
 SQ SEQUENCE 123 AA; 13692 MW; B5007753CCD244CF CRC64;

Query Match 38.2%; Score 645; DB 1; Length 123;  
 Best Local Similarity 98.4%; Pred. No. 1.2e-49;  
 Matches 121; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGKSKSSVVGWPTVVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 DB 1 MGKSKSSVVGWPTVVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 QY 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSORQDILDWIYHTQGY 120  
 DB 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSORQDILDWIYHTQGY 120  
 QY 121 FPD 123  
 DB 121 FPD 123

RESULT 24  
 ID NEF\_HV1B1 STANDARD; PRT; 123 AA.  
 AC P03404;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
 GN NEF.  
 OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1), and  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OC NCBI\_Taxid=11678;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=85111123; PubMed=2578615;  
 RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,  
 RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,  
 RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,  
 RA Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,  
 RA Wong-Staal F.;  
 RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";  
 RL Nature 313:277-284(1985).  
 RN [2]  
 RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.  
 RX MEDLINE=88039140; PubMed=3118220;  
 RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,  
 RA Montagnier L., Lecocq J.-P.;  
 RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling  
 RT an oncogene product.";  
 RL Nature 330:266-269(1987).  
 CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 CC -1- MISCELLANEOUS: IN THIS ISOLATE A MUTATION IN POSITION 124 ADDS A  
 CC STOP CODON AND THE PROTEIN IS MUCH SHORTER THAN IN OTHER ISOLATES  
 CC (210 AA).  
 CC -----  
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 CC -----  
 CC EMBL: M15654; AAA44206.1;  
 DR PIR: A04005; ASLJH3.  
 DR HSP; Q70627; 2NEF.

DR HIV: M15654; NEFSBH102.  
 DR InterPro: IPR001558; F-protein.  
 DR Pfam: PF00469; F-protein; 1.  
 KW AIDS: Myristate; GTP-binding.  
 FT LIPID 2 MYRISTATE.  
 SQ SEQUENCE 123 AA; 13606 MW; 0811735345F0EB8B CRC64;

Query Match 37.8%; Score 638; DB 1; Length 123;  
 Best Local Similarity 97.6%; Pred. No. 5.1e-49;  
 Matches 120; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGKSKSSVVGWPTVVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 DB 1 MGKSKSSVVGWPTVVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 QY 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSORQDILDWIYHTQGY 120  
 DB 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSORQDILDWIYHTQGY 120  
 QY 121 FPD 123  
 DB 121 FPD 123

RESULT 25  
 ID TAT\_HV1B1 STANDARD; PRT; 86 AA.  
 AC P04506;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE TAT protein (Transactivating regulatory protein).  
 GN TAT.  
 OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1), and  
 OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OC NCBI\_Taxid=11678, 11707;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-ISOLATE BH10;  
 RX MEDLINE=85111123; PubMed=2578615;  
 RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,  
 RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,  
 RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,  
 RA Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,  
 RA Wong-Staal F.;  
 RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";  
 RL Nature 313:277-284(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN-ISOLATE HXB3;  
 RX MEDLINE=85228248; PubMed=2988795;  
 RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,  
 RA Shaw G.M., Wong-Staal F., Reddy E.P.;  
 RT "HTLV-III env gene products synthesized in E. coli are recognized by  
 RT antibodies present in the sera of AIDS patients.";  
 RL Cell 41:979-986(1985).  
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE  
 CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND  
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR  
 CC PROMOTER.  
 CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.  
 CC -1- MISCELLANEOUS: THE TWO ISOLATES TAT SEQUENCE ARE IDENTICAL.  
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 CC -----

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CC EMBL; M14100; AAA44676.1; -
DR EMBL; M15654; AAA44199.1; -
DR HIV; M15654; TAT$BH102.
DR HIV; M14100; TAT$HXB3.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 86 AA; 9784 MW; 4DD609415FAF9015 CRC64;

Query Match 28.8%; Score 486; DB 1; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.4e-36;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 209 EPVDPRLPEWPKHGPSQPKTACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRPPQG 268
Db 2 EPVDPRLPEWPKHGPSQPKTACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRPPQG 61

Qy 269 SOTHQVSLSKOPTSQSRGDPGPK 293
Db 62 SOTHQVSLSKOPTSQSRGDPGPK 86

RESULT 26
TAT_HV1P
ID TAT_HV1P STANDARD; PRT; 86 AA.
AC P04607;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11700;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511157; PubMed=2982104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
RT AIDS/lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC [1]
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CC -----
CC EMBL; M11840; AAA44999.1; -
CC PIR; A04017; TNLJ12.
CC HIV; M11840; TAT$PCV12.
CC InterPro: IPR001831; HIV_Tat.
CC Pfam; PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 86 AA; 9794 MW; 4DD5C6415FAF9015 CRC64;

Query Match 28.5%; Score 481; DB 1; Length 86;
TAT_HV1B
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Best Local Similarity 98.8%; Pred. No. 1.7e-35;
Matches 84; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 209 EPVDPRLPEWPKHGPSQPKTACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRPPQG 268
Db 2 EPVDPRLPEWPKHGPSQPKTACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRPPQG 61

Qy 269 SOTHQVSLSKOPTSQSRGDPGPK 293
Db 62 SOTHQVSLSKOPTSQSRGDPGPK 86

RESULT 27
TAT_HV12
ID TAT_HV12 STANDARD; PRT; 86 AA.
AC P04326;
DT 20-MAR-1987 (Rel. 04, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (clone 12) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11679;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177573; PubMed=3008154;
RA Arya S.K., Gallo R.C.;
RT "Three novel genes of human T-lymphotropic virus type III: Immune
RT reactivity of their products with sera from acquired immune
RT deficiency syndrome patients.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
CC EMBL; M11840; AAA44999.1; -
CC PIR; A04017; TNLJ12.
CC HIV; M11840; TAT$PCV12.
CC InterPro: IPR001831; HIV_Tat.
CC Pfam; PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 86 AA; 9758 MW; 4DD609414FBE9115 CRC64;

Query Match 28.3%; Score 478; DB 1; Length 86;
Best Local Similarity 98.8%; Pred. No. 3.2e-35;
Matches 84; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 209 EPVDPRLPEWPKHGPSQPKTACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRPPQG 268
Db 2 EPVDPRLPEWPKHGPSQPKTACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRPPQG 61

Qy 269 SOTHQVSLSKOPTSQSRGDPGPK 293
Db 62 SOTHQVSLSKOPTSQSRGDPGPK 86

RESULT 28
TAT_HV1B
```

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ID AC P04610; STANDARD; PRT; 86 AA.
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]
RP SEQUENCE FROM N.A. (CLONE PNL4-3).
RX MEDLINE=8509333; PubMed=2981635;
RA Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
RT "Nucleotide sequence of the AIDS virus, LAV.";
RL Cell 40:9-17(1985).
RN [2]
RP SEQUENCE FROM N.A. (CLONE PNL4-3).
RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
RL Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; K02013; AA059745.1; -.
CC EMBL; M19921; AA04985.1; -.
CC HIV; K02013; TATSBRU.
CC HIV; M19921; TATSBL43.
CC InterPro: IPR001831; HIV_Tat.
CC Pfam: PF00539; Tat; 1.
CC PRINTS: PR00055; HIVTATDOMAIN.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC
CC FT VARIANT 24 24 T -> N (IN CLONE PNL4-3).
CC FT VARIANT 39 39 T -> M (IN CLONE PNL4-3).
CC FT VARIANT 58 61 PPQG -> AHON (IN CLONE PNL4-3).
CC FT VARIANT 67 67 V -> A (IN CLONE PNL4-3).
CC FT VARIANT 77 77 P -> S (IN CLONE PNL4-3).
CC SEQUENCE 86 AA; 9769 MW; 9B1BA4915FAF8A14 CRC64;

Query Match 27.8%; Score 470; DB 1; Length 86;
Best Local Similarity 96.5%; Pred. No. 1.6e-34;
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 209 EPVDRLEPWKHPGSPKTCACVCKCCFHCQVCFITKALGISYGRKKRRRPPG 268
DB 2 EPVDRLEPWKHPGSPKTCACVCKCCFHCQVCFITKALGISYGRKKRRRPPG 61
QY 269 SOTHQVSLSKQPTSSRSGDPTGPK 293
DB 62 SOTHQVSLSKQPTSSRSGDPTGPK 86

RESULT 29
TAT_HVIRH
ID TAT_HVIRH STANDARD; PRT; 102 AA.
AC P05508;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).

```

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GN OS
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11701;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86218077; PubMed=2423250;
RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S.,
RA Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
RA Wong-Staal F.;
RT "Identification and characterization of conserved and variable
RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of
RT AIDS.";
RL Cell 45:637-648(1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC
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CC
CC EMBL; M17451; AAA45050.1; -.
CC HIV; M17451; TATSBRF.
CC InterPro: IPR001831; HIV_Tat.
CC Pfam: PF00539; Tat; 1.
CC PRINTS: PR00055; HIVTATDOMAIN.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC SEQUENCE 102 AA; 11538 MW; 3EACFB843C5195BD CRC64;

Query Match 27.3%; Score 461; DB 1; Length 102;
Best Local Similarity 91.9%; Pred. No. 1.2e-33;
Matches 79; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 209 EPVDRLEPWKHPGSPKTCACVCKCCFHCQVCFITKALGISYGRKKRRRPPG 268
DB 2 EPVDRLEPWKHPGSPKTCACVCKCCFHCQVCFITKALGISYGRKKRRRPPG 61
QY 269 SOTHQVSLSKQPTSSRSGDPTGPK 294
DB 62 SOTHQVSLSKQPTSSRSGDPTGPK 87

RESULT 30
TAT_HVIRH
ID TAT_HVIRH STANDARD; PRT; 86 AA.
AC P04608; O09778;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
RT virus.";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]

```

Search completed: August 26, 2002, 08:15:41  
Job time: 345 sec

GenCore version 4.5  
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# OM protein - protein search, using sw model

Run on: August 26, 2002, 08:08:32 ; Search time 86.53 Seconds  
(without alignments)  
603.773 Million cell updates/sec

Title: US-09-509-239-13  
Perfect score: 1688  
Sequence: 1 MCGKWSKSSVGVGPTVRERM.....QSRGDTGPKETSGHHHHH 302

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum Match 100%  
Listing first 45 summaries

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL.19.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriaph.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1129	66.9	206	15 Q9WM24	Q9wm24 human immun
2	1124	66.6	206	15 Q9WLM4	Q9wlm4 human immun
3	1119	66.3	206	15 Q40177	Q40177 human immun
4	1115	66.1	206	15 Q90VU7	Q90vu7 human immun
5	1108	65.6	206	15 Q9PXW9	Q9pxw9 human immun
6	1105	65.5	206	15 Q9WM16	Q9wm16 human immun
7	1104	65.4	206	15 Q9WM30	Q9wm30 human immun
8	1101	65.2	206	15 Q9PXW8	Q9pxw8 human immun
9	1096	64.9	206	15 Q90179	Q90179 human immun
10	1096	64.9	206	15 Q85588	Q85588 aids-associ
11	1096	64.9	206	15 Q78244	Q78244 human immun
12	1092	64.7	206	15 Q9WLM7	Q9wlm7 human immun
13	1090	64.6	206	15 Q74905	Q74905 human immun
14	1087	64.4	206	15 Q89561	Q89561 human immun
15	1085	64.3	206	15 Q74913	Q74913 human immun
16	1080	64.0	206	15 Q74917	Q74917 human immun

17	1079	63.9	206	15 Q74914	Q74914 human immun
18	1079	63.9	206	15 Q74915	Q74915 human immun
19	1077	63.8	206	15 Q74909	Q74909 human immun
20	1076	63.7	202	15 Q9QPN3	Q9qpn3 human immun
21	1072	63.5	206	15 Q9Q596	Q9q596 human immun
22	1072	63.5	206	15 Q9Q595	Q9q595 human immun
23	1071	63.4	208	15 Q9YU09	Q9yyu9 human immun
24	1068	63.3	206	15 Q9W7X3	Q9w7x3 human immun
25	1065	63.1	206	15 Q9W7X2	Q9w7x2 human immun
26	1064	63.0	206	15 Q9W7U0	Q9w7u0 human immun
27	1062	62.9	206	15 Q93010	Q93010 human immun
28	1061	62.9	206	15 Q93012	Q93012 human immun
29	1060	62.8	206	15 Q9Q597	Q9q597 human immun
30	1057	62.6	206	15 Q9W7X2	Q9w7x2 human immun
31	1054	62.4	206	15 Q9Q594	Q9q594 human immun
32	1053	62.4	206	15 Q9Q5A3	Q9q5a3 human immun
33	1053	62.4	206	15 Q9DQF9	Q9dqt9 human immun
34	1052	62.3	205	15 Q74823	Q74823 human immun
35	1051	62.3	206	15 Q74824	Q74824 human immun
36	1050	62.2	206	15 Q9QR05	Q9qrd5 human immun
37	1050	62.2	206	15 Q9Q599	Q9q599 human immun
38	1049	62.1	206	15 Q89630	Q89630 human immun
39	1049	62.1	206	15 Q71956	Q71956 human immun
40	1048	62.1	206	15 Q9Q5A8	Q9q5a8 human immun
41	1048	62.1	206	15 Q72421	Q72421 human immun
42	1047	62.0	206	15 Q89537	Q89537 human immun
43	1047	62.0	206	15 Q9Q5D3	Q9q5d3 human immun
44	1047	62.0	206	15 Q72985	Q72985 human immun
45	1047	62.0	210	15 P90275	P90275 human immun

## ALIGNMENTS

RESULT 1  
Q9WM24 ID Q9WM24 PRELIMINARY; PRT: 206 AA.  
AC Q9WM24;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=12-IT;  
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,  
RA Johansson B., Vahine A., Sonnerborg A.;  
RT "HIV-1 nef mutations and clinical long-term non progression: a  
RT molecular epidemiology study."  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
CC -I- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES; IT SEEMS TO DOWN-REGULATE THE CD4(74) ANTIGEN.  
DR EMBL; F0111480; AAD01458.1;  
DR HSSP; P03406; 1EFN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW Aids; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23328 MW; FCC69458158FIA03 CRC64;

Query Match 66.9%; Score 1129; DB 15; Length 206;  
Best Local Similarity 99.5%; Pred. No. 8.7e-95;  
Matches 205; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MCGKWSKSSVGVGPTVRERMRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60  
|||||  
Db 1 MCGKWSKSSVGVGPTVRERMRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60  
QY 61 QEEVEVGFPTVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLSQRQDILDLIWIYHTQGY 120

```

Db 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGSLHSQRQDILDLMWYHTQY 120
QY 121 FPDWQNTTGGVRYPLTFTGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPDEREV 180
Db 121 FPDWQNTTGGVRYPLTFTGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPDEREV 180
QY 181 LEWRDLSRLAFHHVARELHPEYFKNC 206
Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

RESULT 2
Q9WLM4 PRELIMINARY: PRT: 206 AA.
AC Q9WLM4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=21-SW;
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,
RA Johansson B., Vahne A., Sonnerborg A.;
RT "Hiv-1 nef mutations and clinical long-term non progression: a
RT molecular epidemiology study.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES; IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL: AF047087; AD02461.1; -
DR HSP: P03406; IEFN.
DR InterPro: IPR001558; F-protein.
DR Pfam: PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23341 MW; FCD22BICEB55BB9 CRC64;

Query Match 66.6%; Score 1124; DB 15; Length 206;
Best Local Similarity 99.0%; Pred. No. 2.5e-94;
Matches 204; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVGVWPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
Db 1 MGGKWSKSSVGVWPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
QY 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGSLHSQRQDILDLMWYHTQY 120
Db 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGSLHSQRQDILDLMWYHTQY 120
QY 121 FPDWQNTTGGVRYPLTFTGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPDEREV 180
Db 121 FPDWQNTTGGVRYPLTFTGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPDEREV 180
QY 181 LEWRDLSRLAFHHVARELHPEYFKNC 206
Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

RESULT 3
Q40177 PRELIMINARY: PRT: 206 AA.
AC Q40177;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.

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OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=PNL4-3;
RA Faug G., Weiser B., Visosky A., Burger H.;
RT "Constructing full-length chimeric HIV-1 molecular clones by PCR-
RT mediated recombination.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES; IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL: AF003887; AAB64279.1; -
DR HSP: P03406; IEFN.
DR InterPro: IPR001558; F-protein.
DR Pfam: PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23428 MW; 9F94AEB9CAFD6CF6 CRC64;

Query Match 66.3%; Score 1119; DB 15; Length 206;
Best Local Similarity 98.5%; Pred. No. 7e-94;
Matches 203; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVGVWPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
Db 1 MGGKWSKSSVGVWPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
QY 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGSLHSQRQDILDLMWYHTQY 120
Db 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGSLHSQRQDILDLMWYHTQY 120
QY 121 FPDWQNTTGGVRYPLTFTGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPDEREV 180
Db 121 FPDWQNTTGGVRYPLTFTGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPDEREV 180
QY 181 LEWRDLSRLAFHHVARELHPEYFKNC 206
Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

RESULT 4
Q90VU7 PRELIMINARY: PRT: 206 AA.
AC Q90VU7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEF PROTEIN.
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=NL4-3;
RX MEDLINE=96036482; PubMed=7483282;
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
RA Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes
RT from primary virus cultures using the polymerase chain reaction.";
RL Virology 213:80-86(1995).
RN [2]
RC STRAIN=NL4-3;
RX MEDLINE=86281827; PubMed=3016298;
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
RA Martin M.A.;
RT "Production of acquired immunodeficiency syndrome-associated
RT retrovirus in human and nonhuman cells transfected with an infectious
RT molecular clone.";
RL J. Virol. 59:284-291(1985).
DR EMBL: U26942; AAB60579.1; -
SQ SEQUENCE 206 AA; 23367 MW; 65AF3B6184DC2FE7 CRC64;

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Query Match 66.1%; Score 1115; DB 15; Length 206;  
Best Local Similarity 98.1%; Pred. No. 1.6e-93;  
Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGKSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGGLHSGRRQDILDWIYHTQGY 60  
DB 1 MGKSKSSVIGWPAVRRMRRAEPAADGVGAASRDLEKKGGLHSGRRQDILDWIYHTQGY 60

QY 61 QEEEEVGFPTPOVPLRPMTYKAADVLSHFLKEKGLGGLHSGRRQDILDWIYHTQGY 120  
DB 61 QEEEEVGFPTPOVPLRPMTYKAADVLSHFLKEKGLGGLHSGRRQDILDWIYHTQGY 120

QY 121 FPDQNTYTPGPGVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHHPVSLHGMDDPEREV 180  
DB 121 FPDQNTYTPGPGVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHHPVSLHGMDDPEREV 180

QY 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206  
DB 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206

RESULT 5

Q9PXW9 PRELIMINARY; PRT; 206 AA.

ID Q9PXW9  
AC Q9PXW9  
DT 01-MAY-2000 (TREMELrel. 13, Created)  
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RC SEQUENCE FROM N.A.  
RC STRAIN=7-IT;  
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,  
RA Johansson B., Vahne A., Sonnerborg A.;  
RT "HIV-1 nef mutations and clinical long-term non progression: a  
RT molecular epidemiology study";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4 (T4) ANTIGEN.  
DR EMBL: AF011494; AAD01472.1;  
DR HSSP: P03406; IEFN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23333 MW; 2EBF2A6A3ECAF5EA CRC64;

Query Match 65.5%; Score 1105; DB 15; Length 206;  
Best Local Similarity 97.1%; Pred. No. 1.3e-92;  
Matches 200; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGKSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGGLHSGRRQDILDWIYHTQGY 60  
DB 1 MGKSKSSVIGWPAVRRMRRAEPAADGVGAASRDLEKKGGLHSGRRQDILDWIYHTQGY 60

QY 61 QEEEEVGFPTPOVPLRPMTYKAADVLSHFLKEKGLGGLHSGRRQDILDWIYHTQGY 120  
DB 61 QEEEEVGFPTPOVPLRPMTYKAADVLSHFLKEKGLGGLHSGRRQDILDWIYHTQGY 120

QY 121 FPDQNTYTPGPGVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHHPVSLHGMDDPEREV 180  
DB 121 FPDQNTYTPGPGVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHHPVSLHGMDDPEREV 180

QY 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206  
DB 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206

RESULT 7

Q9WM30 PRELIMINARY; PRT; 206 AA.

ID Q9WM30  
AC Q9WM30  
DT 01-NOV-1999 (TREMELrel. 12, Created)  
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)  
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RC SEQUENCE FROM N.A.  
RC STRAIN=8-IT;  
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,  
RA Johansson B., Vahne A., Sonnerborg A.;  
RT "HIV-1 nef mutations and clinical long-term non progression: a  
RT molecular epidemiology study";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4 (T4) ANTIGEN.





OC Viruses; Retroviral viruses; Retroviridae.  
 OX NCBI\_TaxID=11966;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86067228; PubMed=2999715;  
 RA Ratner L., Starcich B., Josephs S.F., Hahn B.H., Reddy E.P., Arya S.K.,  
 RA Livak K.J., Petteway S.R.Jr., Pearson M.L., Haseltine W.A., Arya S.K.,  
 RA Wong-staal F.;  
 RT "Polymorphism of the 3' open reading frame of the virus associated  
 RT with the acquired immune deficiency syndrome, human T-lymphotropic  
 RT virus type III.";  
 RL Nucleic Acids Res. 13:8219-8229(1985).  
 CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 DR EMBL; X03188; CAA26947.1; -  
 DR HSSP; P03406; 1EFN.  
 DR InterPro; IPR001558; F-protein.  
 DR Pfam; PF00469; F-protein; 1.  
 DR AIDS; GTP-binding; Myristate.  
 KW AIDS; GTP-binding; Myristate.  
 SQ SEQUENCE 206 AA; 23419 MW; 3B25EB332A479A46 CRC64;

Query Match 64.9%; Score 1096; DB 15; Length 206;  
 Best Local Similarity 96.6%; Pred. No. 8.6e-92;  
 Matches 199; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGKWSKSSVVGWPTVVRMRRAEPAADGGAASRDLEKKGAISSNTAATNAACAWLEA 60  
 Db 1 MGGKWSKSSVVGWPTVVRMRRAEPAADGGAASRDLEKKGAISSNTAATNAACAWLEA 60  
 Qy 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLIHSQRQDILDWIYHTQGY 120  
 Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLIHSQRQDILDWIYHTQGY 120  
 Qy 121 FPDQNTYTPGVRPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
 Db 121 FPDQNTYTPGVRPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
 Qy 181 LEWRFDLSLAFHHVARELHPEYFKNK 206  
 Db 181 LEWRFDLSLAFHHVARELHPEYFKNK 206

RESULT 11  
 Q78244 ID Q78244 PRELIMINARY; PRT; 206 AA.  
 AC Q78244;  
 DT 01-NOV-1996 (TReMBLrel. 01. Created)  
 DT 01-NOV-1996 (TReMBLrel. 01. Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19. Last annotation update)  
 DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
 GN NEF.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carlini F., Federici M., Equestre M., Ricci S., Ratti G., Zibai Q.,  
 RA Verani P., Rossi G.B.;  
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
 RT chronically infected HUT-78 cellular clone.";  
 RL J. Viral Diseases 1:40-55(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89352106; PubMed=2765297;  
 RA Federici M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 RA Macchi B., Mangiano N., Verani P., Rossi G.;  
 RT "Biological and molecular characterization of producer and non  
 RT producer clones from HUT-78 infected with a patient HIV isolate.";  
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Titti F., Federici M., Butto S., Orecchia A., Carlini F., Taddeo B.,

RA Borsetti A., Saggio I., Verani P., Rossi G.;  
 RT "Variability of HIV-1 virus: characteristics of an infected but not  
 RT productive clone.";  
 RL Int. J. Immunopharmacol. 3:17-23(1990).  
 CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 DR EMBL; Z11530; CAA77629.1; -  
 DR HSSP; P03406; 1EFN.  
 DR InterPro; IPR001558; F-protein.  
 DR Pfam; PF00469; F-protein; 1.  
 DR AIDS; GTP-binding; Myristate.  
 KW AIDS; GTP-binding; Myristate.  
 SQ SEQUENCE 206 AA; 23398 MW; A31CC7244BBB2B43 CRC64;

Query Match 64.9%; Score 1096; DB 15; Length 206;  
 Best Local Similarity 96.6%; Pred. No. 8.6e-92;  
 Matches 199; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGGKWSKSSVVGWPTVVRMRRAEPAADGGAASRDLEKKGAISSNTAATNAACAWLEA 60  
 Db 1 MGGKWSKSSVVGWPTVVRMRRAEPAADGGAASRDLEKKGAISSNTAATNAACAWLEA 60  
 Qy 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLIHSQRQDILDWIYHTQGY 120  
 Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLIHSQRQDILDWIYHTQGY 120  
 Qy 121 FPDQNTYTPGVRPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
 Db 121 FPDQNTYTPGVRPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
 Qy 181 LEWRFDLSLAFHHVARELHPEYFKNK 206  
 Db 181 LEWRFDLSLAFHHVARELHPEYFKNK 206

RESULT 12  
 Q9WLM7 ID Q9WLM7 PRELIMINARY; PRT; 206 AA.  
 AC Q9WLM7;  
 DT 01-NOV-1999 (TReMBLrel. 12. Created)  
 DT 01-NOV-1999 (TReMBLrel. 12. Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19. Last annotation update)  
 DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
 GN NEF.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=18-SW;  
 RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,  
 RA Johansson B., Vahne A., Sonnerborg A.;  
 RT "HIV-1 nef mutations and clinical long-term non progression: a  
 RT molecular epidemiology study.";  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 DR EMBL; AF047084; AAD02458.1; -  
 DR HSSP; P03406; 1EFN.  
 DR InterPro; IPR001558; F-protein.  
 DR Pfam; PF00469; F-protein; 1.  
 DR AIDS; GTP-binding; Myristate.  
 KW AIDS; GTP-binding; Myristate.  
 SQ SEQUENCE 206 AA; 23512 MW; E09E3BEF828A83C0 CRC64;

Query Match 64.7%; Score 1092; DB 15; Length 206;  
 Best Local Similarity 95.6%; Pred. No. 2e-91;  
 Matches 197; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGGKWSKSSVVGWPTVVRMRRAEPAADGGAASRDLEKKGAISSNTAATNAACAWLEA 60  
 Db 1 MGGKWSKSSVVGWPTVVRMRRAEPAADGGAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGGLIHSORRQDILDLDWIYHTQY 120  
|||||  
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGGLIHSORRQDILDLDWIYHTQY 120  
|||||  
QY 121 FPDWQNTYTPGQVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
|||||  
Db 121 FPDWQNTYTPGQVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
|||||  
QY 181 LEWRDSDSLAFHHVARELHPEYFKNC 206  
|||||  
Db 181 LEWRDSDSLAFHHVARELHPEYFKNC 206  
|||||  
RESULT 13  
Q74905 PRELIMINARY: PRT: 206 AA.  
AC Q74905;  
DT 01-NOV-1996 (TremBLrel. 01, Created)  
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentiviridae;  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96400183; PubMed=8806559;  
RA Ratner L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,  
Hahn B., Powderly W., Arens M.,  
RT "Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects  
at different stages of disease."  
RL Virology 223:245-250(1996).  
CC -|- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23617 MW; 5CAAB09C4730C38A CRC64;

Query Match 64.6%; Score 1090; DB 15; Length 206;  
Best Local Similarity 95.1%; Pred. No. 3e-91;  
Matches 196; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MGGKWSKSSVGVPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNACAWLEA 60  
|||||  
Db 1 MGGKWSKSSVGVPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNACAWLEA 60  
|||||  
QY 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGGLIHSORRQDILDLDWIYHTQY 120  
|||||  
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGGLIHSORRQDILDLDWIYHTQY 120  
|||||  
QY 121 FPDWQNTYTPGQVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
|||||  
Db 121 FPDWQNTYTPGQVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
|||||  
QY 181 LEWRDSDSLAFHHVARELHPEYFKNC 206  
|||||  
Db 181 LEWRDSDSLAFHHVARELHPEYFKNC 206  
|||||  
RESULT 14  
Q89561 PRELIMINARY: PRT: 206 AA.  
AC Q89561;  
DT 01-NOV-1996 (TremBLrel. 01, Created)  
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.

OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentiviridae;  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Arens M.O., Ratner L., Joseph T., Bandres J.,  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
CC -|- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23629 MW; BF467FB1B7147CDE CRC64;

Query Match 64.4%; Score 1087; DB 15; Length 206;  
Best Local Similarity 94.7%; Pred. No. 5.7e-91;  
Matches 195; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MGGKWSKSSVGVPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNACAWLEA 60  
|||||  
Db 1 MGGKWSKSSVGVPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNACAWLEA 60  
|||||  
QY 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGGLIHSORRQDILDLDWIYHTQY 120  
|||||  
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGGLIHSORRQDILDLDWIYHTQY 120  
|||||  
QY 121 FPDWQNTYTPGQVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
|||||  
Db 121 FPDWQNTYTPGQVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
|||||  
QY 181 LEWRDSDSLAFHHVARELHPEYFKNC 206  
|||||  
Db 181 LEWRDSDSLAFHHVARELHPEYFKNC 206  
|||||

RESULT 15  
Q74913 PRELIMINARY: PRT: 206 AA.  
AC Q74913;  
DT 01-NOV-1996 (TremBLrel. 01, Created)  
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentiviridae;  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96400183; PubMed=8806559;  
RA Ratner L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,  
Hahn B., Powderly W., Arens M.,  
RT "Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects  
at different stages of disease."  
RL Virology 223:245-250(1996).  
CC -|- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23649 MW; E5B97FA0B70FC175 CRC64;

Query Match 64.3%; Score 1085; DB 15; Length 206;  
Best Local Similarity 95.6%; Pred. No. 8.6e-91;  
Matches 196; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGGKSKSVVGVPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
DB 1 MGGKSKSVVGVPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
QY 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGGLIHSQRQDILDWVHTQY 120  
DB 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGGLIHSQRQDILDWVHTQY 120  
QY 121 FPDWNYTPGQVRYPLTFGWCYKLVPEPDKEANKGENTSLHHPVSLHGMDDPEREV 180  
DB 121 FPDWNYTPGQVRYPLTFGWCYKLVPEPDKEANKGENTSLHHPVSLHGMDDPEREV 180  
QY 181 LEWRDSDRLAFHHVARELHPEYFKN 205  
DB 181 LEWRDSDRLAFHHVARELHPEYFKN 205  
RESULT 16  
Q74917 PRELIMINARY; PRT; 206 AA.  
AC Q74917;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RX MEDLINE=96400183; PubMed=8806559;  
RA Hahn B., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,  
Hahn B., Powderly W., Arens M.;  
RT "Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects  
at different stages of disease."  
RL Virology 223:245-250(1996).  
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL: U44460; AAB38210.1; -;  
DR HSP; P03406; IEFN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23562 MW; 478BBFA675CB203 CRC64;

Query Match 64.0%; Score 1080; DB 15; Length 206;  
Best Local Similarity 94.7%; Pred. No. 2.5e-90;  
Matches 195; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MGGKSKSVVGVPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
DB 1 MGGKSKSVVGVPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
QY 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGGLIHSQRQDILDWVHTQY 120  
DB 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGGLIHSQRQDILDWVHTQY 120  
QY 121 FPDWNYTPGQVRYPLTFGWCYKLVPEPDKEANKGENTSLHHPVSLHGMDDPEREV 180  
DB 121 FPDWNYTPGQVRYPLTFGWCYKLVPEPDKEANKGENTSLHHPVSLHGMDDPEREV 180  
QY 181 LEWRDSDRLAFHHVARELHPEYFKN 206  
DB 181 LEWRDSDRLAFHHVARELHPEYFKN 206  
RESULT 17  
Q74914 PRELIMINARY; PRT; 206 AA.  
AC Q74914;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RX MEDLINE=96400183; PubMed=8806559;  
RA Hahn B., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,  
Hahn B., Powderly W., Arens M.;  
RT "Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects  
at different stages of disease."  
RL Virology 223:245-250(1996).  
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL: U44454; AAB38206.1; -;  
DR HSP; P03406; IEFN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23615 MW; 08D97FA0B70FC17D CRC64;  
Query Match 63.9%; Score 1079; DB 15; Length 206;  
Best Local Similarity 95.1%; Pred. No. 3e-90;  
Matches 195; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 1 MGGKSKSVVGVPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
DB 1 MGGKSKSVVGVPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
QY 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGGLIHSQRQDILDWVHTQY 120  
DB 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGGLIHSQRQDILDWVHTQY 120  
QY 121 FPDWNYTPGQVRYPLTFGWCYKLVPEPDKEANKGENTSLHHPVSLHGMDDPEREV 180  
DB 121 FPDWNYTPGQVRYPLTFGWCYKLVPEPDKEANKGENTSLHHPVSLHGMDDPEREV 180  
QY 181 LEWRDSDRLAFHHVARELHPEYFKN 205  
DB 181 LEWRDSDRLAFHHVARELHPEYFKN 205  
RESULT 18  
Q74915 PRELIMINARY; PRT; 206 AA.  
AC Q74915;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RX MEDLINE=96400183; PubMed=8806559;  
RA Hahn B., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,  
Hahn B., Powderly W., Arens M.;  
RT "Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects  
at different stages of disease."  
RL Virology 223:245-250(1996).  
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL: U44455; AAB38207.1; -;  
DR HSP; P03406; IEFN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.



RL AIDS 0.0-0.0(2000).  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
DR EMBL: AF203197; AAF25320.1; -.  
DR HSSP: P03406; IEFN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS: GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23510 MW; 081DF3A125A7576 CRC64;

Query Match 63.5%; Score 1072; DB 15; Length 206;  
Best Local Similarity 94.7%; Pred. No. 1.3e-89;  
Matches 195; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGKAITSSNTAATNAACAWLEA 60  
DB 1 MGKWSKSGDGGWPAVRMRRAEPAADGVGAASRDLEKHGKAITSSNTAATNAACAWLEA 60  
QY 61 QEEEEVGFPTVPPVLRPMPTKYAAVDLSHFLKKGGLIHSQRQDILDWYHTQGY 120  
DB 61 QEEEEVGFPTVPPVLRPMPTKYAAVDLSHFLKKGGLIHSQRQDILDWYHTQGY 120  
QY 121 FPDQNTTGGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPER 180  
DB 121 FPDQNTTGGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPER 180  
QY 181 LEWRFDRLAFHHVARELHPEYFKNC 206  
DB 181 LEWRFDRLAFHHVARELHPEYFKNC 206

RESULT 22  
ID Q9Q595 PRELIMINARY; PRT: 206 AA.  
AC Q9Q595;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-8-IT;  
RA Visco Comandini U.; Yun Z.; Paganelli R.; Orlandi P.; Salotti A.;  
RT Johansson B.; Vahine A.; Sonnerborg A.;  
RT "HIV-1 nef mutations and clinical long-term non progression: a  
molecular epidemiology study";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL: AF011470; AAD01448.1; -.  
DR HSSP: P03406; IEFN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS: GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23681 MW; 1C891C3AD230C6A8 CRC64;

Query Match 63.4%; Score 1071; DB 15; Length 208;  
Best Local Similarity 94.2%; Pred. No. 1.6e-89;  
Matches 196; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 1 MGKWSKSSVVGWPTVRRMRRAEPA--ADGVGAASRDLEKHGKAITSSNTAATNAACAWL 58  
DB 1 MGKWSKRSVIGWPAVRMRRAEPAARXGAVSRDLEKHGKAITSSNTAATNAACAWL 60  
QY 59 EAQEEVGFPTVPPVLRPMPTKYAAVDLSHFLKKGGLIHSQRQDILDWYHTQ 118  
DB 61 EAQEEVGFPTVPPVLRPMPTKYAAVDLSHFLKKGGLIHSQRQDILDWYHTQ 120  
QY 119 GYFPDQNTTGGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPER 178  
DB 121 GYFPDQNTTGGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPER 180  
QY 179 EVLEWRFDRLAFHHVARELHPEYFKNC 206  
DB 181 KVLEWRFDRLAFHHVARELHPEYFKNC 208

Query Match 63.5%; Score 1072; DB 15; Length 206;  
Best Local Similarity 93.7%; Pred. No. 1.3e-89;  
Matches 193; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGKAITSSNTAATNAACAWLEA 60  
DB 1 MGKWSKRSVVGWPAVRMRRAEPAADGVGAASRDLEKHGKAITSSNTAATNAACAWLEA 60  
QY 61 QEEEEVGFPTVPPVLRPMPTKYAAVDLSHFLKKGGLIHSQRQDILDWYHTQGY 120  
DB 61 QEEEEVGFPTVPPVLRPMPTKYAAVDLSHFLKKGGLIHSQRQDILDWYHTQGY 120

RP SEQUENCE FROM N.A.  
 RC STRAIN-PATIENT 27;  
 RA McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,  
 RA Pemberton L., Brew B.J.;  
 RT "Anomalies in Nef expression within the central nervous system of HIV-  
 RT 1 positive individuals/AIDS patients with or without AIDS dementia  
 RT complex.";  
 RL J. Neurovirol. 4:0-0(1998).  
 CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 DR EMBL; AF064676; AAC18377.1; -;  
 DR HSP; P03406; 1EPN.  
 DR InterPro; IPR001558; F-protein.  
 DR Pfam; PF00469; F-protein; 1.  
 DR AIDS; GTP-binding; Myristate.  
 KW AIDS; GTP-binding; Myristate.  
 SQ SEQUENCE 206 AA; 23499 MW; DEE21CAF05891D6B CRC64;

Query Match 63.3%; Score 1068; DB 15; Length 206;  
 Best Local Similarity 91.7%; Pred. No. 3e-89;  
 Matches 189; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 Db 1 MGGKWSKSSVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 QY 61 QEEEEVGPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTQY 120  
 Db 61 QEEEEVGPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTQY 120  
 QY 121 FPDWQNTYTPGCVRYPLTFGCWCKLVPEPKVEANKGENTSLHPVSLHGMDPDERV 180  
 Db 121 FPDWQNTYTPGCVRYPLTFGCWCKLVPEPKVEANKGENTSLHPVSLHGMDPDERV 180  
 QY 181 LEWRDLSRLAFHHVARELHPEYFKNC 206  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206  
 QY 181 LEWRDLSRLAFHHVARELHPEYFKNC 206  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

Query Match 63.3%; Score 1068; DB 15; Length 206;  
 Best Local Similarity 91.7%; Pred. No. 3e-89;  
 Matches 189; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 Db 1 MGGKWSKSSVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 QY 61 QEEEEVGPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTQY 120  
 Db 61 QEEEEVGPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTQY 120  
 QY 121 FPDWQNTYTPGCVRYPLTFGCWCKLVPEPKVEANKGENTSLHPVSLHGMDPDERV 180  
 Db 121 FPDWQNTYTPGCVRYPLTFGCWCKLVPEPKVEANKGENTSLHPVSLHGMDPDERV 180  
 QY 181 LEWRDLSRLAFHHVARELHPEYFKNC 206  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206  
 QY 181 LEWRDLSRLAFHHVARELHPEYFKNC 206  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

Query Match 63.1%; Score 1065; DB 15; Length 206;  
 Best Local Similarity 93.2%; Pred. No. 5.7e-89;  
 Matches 192; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 Db 1 MGGKWSKSSVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 QY 61 QEEEEVGPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTQY 120  
 Db 61 QEEEEVGPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTQY 120  
 QY 121 FPDWQNTYTPGCVRYPLTFGCWCKLVPEPKVEANKGENTSLHPVSLHGMDPDERV 180  
 Db 121 FPDWQNTYTPGCVRYPLTFGCWCKLVPEPKVEANKGENTSLHPVSLHGMDPDERV 180  
 QY 181 LEWRDLSRLAFHHVARELHPEYFKNC 206  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

Query Match 63.0%; Score 1064; DB 15; Length 206;  
 Best Local Similarity 91.7%; Pred. No. 7e-89;  
 Matches 189; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 Db 1 MGGKWSKSSVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 QY 61 QEEEEVGPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTQY 120  
 Db 61 QEEEEVGPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTQY 120  
 QY 121 FPDWQNTYTPGCVRYPLTFGCWCKLVPEPKVEANKGENTSLHPVSLHGMDPDERV 180  
 Db 121 FPDWQNTYTPGCVRYPLTFGCWCKLVPEPKVEANKGENTSLHPVSLHGMDPDERV 180  
 QY 181 LEWRDLSRLAFHHVARELHPEYFKNC 206  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

Query Match 63.0%; Score 1064; DB 15; Length 206;  
 Best Local Similarity 91.7%; Pred. No. 7e-89;  
 Matches 189; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 Db 1 MGGKWSKSSVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 QY 61 QEEEEVGPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTQY 120  
 Db 61 QEEEEVGPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTQY 120  
 QY 121 FPDWQNTYTPGCVRYPLTFGCWCKLVPEPKVEANKGENTSLHPVSLHGMDPDERV 180  
 Db 121 FPDWQNTYTPGCVRYPLTFGCWCKLVPEPKVEANKGENTSLHPVSLHGMDPDERV 180  
 QY 181 LEWRDLSRLAFHHVARELHPEYFKNC 206  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

Query Match 63.0%; Score 1064; DB 15; Length 206;  
 Best Local Similarity 91.7%; Pred. No. 7e-89;  
 Matches 189; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

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ID O93010 PRELIMINARY; PRT; 206 AA.
AC O93010:
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 9;
RX MEDLINE-98097260; PubMed-9436760;
RA Kang M.R., Cho Y.K., Chun J., Kim Y.B., Lee I., Lee H.J., Kim S.H.,
RA Kim Y.K., Yoon K., Yang J.M., Kim J.M., Shin Y.O., Kang C., Lee J.S.,
RA Choi K.W., Kim D.G., Fitch W.M., Kim S.;
RT "Phylogenetic analysis of the nef gene reveals a distinctive
RT monophyletic clade in Korean HIV-1 cases."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 17:58-68(1998).
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF063922; AAC17893.1;
DR HSSP; P03406; 1EFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23348 MW; 4D5AEDF55FAE93E3 CRC64;

Query Match 62.9%; Score 1062; DB 15; Length 206;
Best Local Similarity 94.6%; Pred. No. 1.1e-88;
Matches 194; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGGKWSKSVVGVPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60
D 1 MGGKWSKSVVGVPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60
QY 61 QEEVEGVPVTPQVPLRPMTYKAAVDLSHFLKEKGLGGLIHSQRQDILDWIYHTQY 120
D 61 QEEVEGVPVTPQVPLRPMTYKAAVDLSHFLKEKGLGGLIHSQRQDILDWIYHTQY 120
QY 121 FPDWQNTYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180
D 121 FPDWQNTYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180
QY 181 LEWRDSDSLAFHHVARELHPEYFKN 205
D 181 LEWRDSDSLAFHHVARELHPEYFKN 205
D 181 LEWRDSDSLAFHHVARELHPEYKDC 206

RESULT 28
Q93012
ID O93012 PRELIMINARY; PRT; 206 AA.
AC O93012:
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 27;
RA McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,
RA Pemberton L., Brew B.J.;
RT "Anomalies in Nef expression within the central nervous system of HIV-
RT 1 positive individuals/AIDS patients with or without AIDS dementia
RT complex."
RL J. Neurovirol. 4:0-0(1998).
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
```

```
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF064673; AAC18374.1;
DR HSSP; P03406; 1EFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23472 MW; 2255A447ECE85456 CRC64;

Query Match 62.9%; Score 1061; DB 15; Length 206;
Best Local Similarity 91.7%; Pred. No. 1.3e-88;
Matches 189; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGGKWSKSVVGVPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60
D 1 MGGKWSKSVVGVPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60
QY 61 QEEVEGVPVTPQVPLRPMTYKAAVDLSHFLKEKGLGGLIHSQRQDILDWIYHTQY 120
D 61 QEEVEGVPVTPQVPLRPMTYKAAVDLSHFLKEKGLGGLIHSQRQDILDWIYHTQY 120
QY 121 FPDWQNTYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180
D 121 FPDWQNTYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180
QY 181 LEWRDSDSLAFHHVARELHPEYFKN 206
D 181 LEWRDSDSLAFHHVARELHPEYKDC 206

RESULT 29
Q90597
ID Q90597 PRELIMINARY; PRT; 206 AA.
AC Q90597:
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang B., Sakseena N.K.;
RT "HIV-1 Strains from a cohort of American subjects reveal the presence
RT of a V2 region extension unique to slow progressors; and non-
RT progressors."
RL AIDS 0:0-0(2000).
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF203196; AAF25318.1;
DR HSSP; P03406; 1EFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23599 MW; 9C887A58541A9905 CRC64;

Query Match 62.8%; Score 1060; DB 15; Length 206;
Best Local Similarity 92.7%; Pred. No. 1.6e-88;
Matches 191; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGGKWSKSVVGVPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60
D 1 MGGKWSKSVVGVPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60
QY 61 QEEVEGVPVTPQVPLRPMTYKAAVDLSHFLKEKGLGGLIHSQRQDILDWIYHTQY 120
D 61 QEEVEGVPVTPQVPLRPMTYKAAVDLSHFLKEKGLGGLIHSQRQDILDWIYHTQY 120
QY 121 FPDWQNTYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180
D 121 FPDWQNTYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180
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Db 121 FPDQNYTPGCGIRYPLTFGNCYKLVPEQEKYKANEGKNTSLHPSLHGMDDPREV 180  
 Qy 181 LEWREDSRLAFHHVARELHPEYFKNC 206  
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 Db 181 LEWREDSRLAFHHVARELHPEYFKNC 206

RESULT 30  
 Q9W7X2 PRELIMINARY; PRT; 206 AA.  
 AC Q9W7X2;  
 DT 01-NOV-1999 (Tremblrel. 12, Created)  
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
 GN NEF.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID-11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PATIENT 27;  
 RA McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,  
 RA Pemberton L., Brew B.J.;  
 RT "Anomalies in Nef expression within the central nervous system of HIV-  
 RT 1 positive individuals/AIDS patients with or without AIDS dementia  
 RT complex.";  
 RL J. Neurovirol. 4:0-0(1998).  
 CC -|- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 DR EMBL; AF064677; AAC18378.1;  
 DR HSP; F03406; IEFN.  
 DR InterPro; IPR001358; F-protein.  
 DR Pfam; PF00469; F-protein; 1.  
 KW AIDS; GTP-binding; Myristate.  
 SQ SEQUENCE 206 AA; 23442 MW; DC6A96AF05891D6B CRC64;

Query Match 62.6%; Score 1057; DB 15; Length 206;  
 Best Local Similarity 91.3%; Pred. No. 3e-88;  
 Matches 188; Conservative 13; Mismatches 5; Indels 0; Gaps 0;  
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 ||||||||||||||||||  
 Db 1 MCGKWSKSSVVGWPTVRRMRRAEPAADGVAASRDLEKKGALTSNTAATNAACAWLEA 60  
 ||||||||||||||||||  
 Qy 61 QEEEEVFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDLMYHTQGY 120  
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 Db 61 QEEEEVFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDLMYHTQGY 120  
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 Qy 121 FPDQNYTPGCGIRYPLTFGNCYKLVPEQEKYKANEGKNTSLHPSLHGMDDPREV 180  
 ||||||||||||||||||  
 Db 121 FPDQNYTPGCGIRYPLTFGNCYKLVPEQEKYKANEGKNTSLHPSLHGMDDPREV 180  
 ||||||||||||||||||  
 Qy 181 LEWREDSRLAFHHVARELHPEYFKNC 206  
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 Db 181 LEWREDSRLAFHHVARELHPEYFKNC 206

Search completed: August 26, 2002, 08:14:55  
 Job time: 383 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 08:12:25 ; Search time 99.16 Seconds  
(without alignments)  
460.380 Million cell updates/sec

Title: US-09-509-239-17  
Perfect score: 2255  
Sequence: 1 CSHSSNMANTQMSDKIII.....QSRGDPGPKETSGHHHHH 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11107396 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
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22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2255	100.0	411	22 AAG63235	Amino acid sequenc
2	2246	99.6	413	20 AAY02355	A representative L
3	2246	99.6	413	22 AAG63237	Amino acid sequenc
4	2242	99.4	411	20 AAY02353	A representative L
5	1706.5	75.7	324	20 AAY02352	A representative L
6	1706.5	75.7	324	22 AAG63234	Amino acid sequenc
7	1697.5	75.3	326	20 AAY02354	A representative L
8	1697.5	75.3	326	22 AAG63236	Amino acid sequenc
9	1688	74.9	302	20 AAY02351	A representative H
10	1688	74.9	302	22 AAG63233	Amino acid sequenc
11	1675	74.3	302	20 AAY02357	A representative H

12	1675	74.3	302	22 AAG63239	Amino acid sequenc
13	1139.5	50.5	215	20 AAY02349	A representative H
14	1139.5	50.5	215	22 AAG63231	Amino acid sequenc
15	1120	49.7	206	21 AAY50795	Human NEF protein/
16	1116	49.5	206	14 AAR38893	Nef protein of HIV
17	1115	49.4	206	21 AAB10054	HIV-1 nef protein.
18	1114	49.4	206	20 AAG9326	HIV-1 nef protein
19	1111	49.3	206	7 AAP61515	Sequence of E' pro
20	1107	49.1	216	7 AAP60423	Sequence of LAV v1
21	1092	48.4	206	20 AAW90179	HTLV-III E' protei
22	1011	44.8	216	22 AAE04960	HIV-1 Jrf1 Nef pro
23	997	44.2	210	19 AAW53113	Protein 6 containe
24	997	44.2	210	21 AAY77299	HIV-1 Jrf1 Nef (G2
25	996	44.2	217	22 AAE04962	HIV-1 Jrf1 Nef (G2
26	983	43.6	210	12 AAR12262	Human tpa leader p
27	978	43.4	237	22 AAE04961	Human tpa leader p
28	968	42.9	237	22 AAE04963	HIV-1 non-subtype
29	952	42.2	206	21 AAB69363	HIV-1 non-subtype
30	948.5	42.1	3025	22 AAB86169	HIV-1 non-subtype
31	934	41.4	206	21 AAB69361	Sequence encoded b
32	927.5	41.1	206	9 AAP81859	HIV-1 non-subtype
33	910.5	40.4	207	21 AAB69359	Sequence deduced f
34	903.5	40.1	207	11 AAR08407	HIV-1 non-subtype
35	901.5	40.0	207	21 AAB69364	HIV-1 non-subtype
36	891.5	40.0	208	21 AAB69356	HIV-1 non-subtype
37	895.5	39.7	219	21 AAB69362	HIV-1 non-subtype
38	893.5	39.6	217	21 AAB69365	HIV-1 non-subtype
39	885.5	39.3	207	21 AAB69366	HIV-1 non-subtype
40	878.5	39.0	207	21 AAB69357	HIV-1 non-subtype
41	867	38.4	206	21 AAB69358	HIV-1 non-subtype
42	860	38.1	206	21 AAB69360	HIV-1 non-subtype
43	834.5	37.0	209	19 AAW72998	HIV isolate LAV.MA
44	831.5	36.9	209	9 AAP81866	Sequence encoded b
45	796	35.3	212	19 AAW68481	HIV-1 strain YBF30

## ALIGNMENTS

## RESULT 1

AAG63235  
ID AAG63235 standard; Protein; 411 AA.  
AC AAG63235;  
XX  
XX 01-OCT-2001 (first entry)  
XX  
XX Amino acid sequence of a His tagged LipD-Nef-Tat linked protein.  
XX HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.  
XX  
XX Synthetic.  
OS Human immunodeficiency virus.  
XX  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..109  
FT /note= "ProtD fusion partner"  
XX  
XX WO200154719-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 29-JAN-2001; 2001WO-EP00944.  
XX  
XX 31-JAN-2000; 2000GB-0002200.  
PR 14-APR-2000; 2000GB-0009336.  
PR 06-JUN-2000; 2000GB-0013806.  
PR 28-JUN-2000; 2000WO-EP05998.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
XX Voss G;  
XX

DR WPI: 2001-476172/51.  
 DR N-PSDB: AAH42879.  
 XX  
 PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
 PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
 PT protein or polynucleotide for the manufacture of a vaccine.  
 XX  
 PS Disclosure; Fig 1; 90pp; English.  
 XX  
 CC The present sequence represents a His-tagged Nef-Tat linked protein of  
 CC HIV, with a lipidation signal sequence (LipoD) which is removed after  
 CC processing and a ProD fusion partner. The protein is expressed in  
 CC Escherichia coli, and is used to produce the vaccine of the invention.  
 CC The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat;  
 CC and HIV gp120 in the manufacture of a vaccine. The vaccine is used for  
 CC the prophylactic or therapeutic immunization of humans against HIV.  
 CC Tat, Nef or Nef-Tat act in synergy with gp120 in the treatment and  
 CC prevention of HIV. The vaccine reduces the HIV viral load in HIV  
 CC infected humans and results in a maintenance of CD4+ levels over those  
 CC levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat  
 CC and HIV gp120.  
 XX  
 SQ Sequence 411 AA;  
 Query Match 100.0%; Score 2255; DB 22; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-205; Mismatches 0; Indels 0; Gaps 0;  
 Matches 411; Conservative 0;  
 QY 1 CSSHSSNMANTQMSKDKIIIAHRSAGSYLPEHTLESKALAFQAQADYLEQDLAMTKDGRLL 60  
 DB 1 CSSHSSNMANTQMSKDKIIIAHRSAGSYLPEHTLESKALAFQAQADYLEQDLAMTKDGRLL 60  
 QY 61 VVIHDFLDGLTDVAKKPPHRRKDGRIYVDFTLKEIQSLEMTNFETMGKWSKSSVY 120  
 DB 61 VVIHDFLDGLTDVAKKPPHRRKDGRIYVDFTLKEIQSLEMTNFETMGKWSKSSVY 120  
 QY 121 GWPTVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEVEGFPVT 180  
 DB 121 GWPTVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEVEGFPVT 180  
 QY 181 PVPURPMYKAAVDLSHFLKEGGLIHSQRQDILDWIIYHTQGYFPDQWNTTGP 240  
 DB 181 PVPURPMYKAAVDLSHFLKEGGLIHSQRQDILDWIIYHTQGYFPDQWNTTGP 240  
 QY 241 GVRYPITFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPEREVLHFRDRLAF 300  
 DB 241 GVRYPITFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPEREVLHFRDRLAF 300  
 QY 301 HHVARELHPEYFNKCTSEPVDPRLPEKHPGSGPKTACTNCTCYKCCFHCQVCFTKALG 360  
 DB 301 HHVARELHPEYFNKCTSEPVDPRLPEKHPGSGPKTACTNCTCYKCCFHCQVCFTKALG 360  
 QY 361 ISYGRKKRRQRRRPPQSGQTHQVSLSKOPTSOSRQDPTGPKETSGHHHHH 411  
 DB 361 ISYGRKKRRQRRRPPQSGQTHQVSLSKOPTSOSRQDPTGPKETSGHHHHH 411  
 RESULT 2  
 ID AAY02355 standard; Protein: 413 AA.  
 XX  
 AC AAY02355;  
 XX  
 DT 09-JUL-1999 (first entry)  
 XX  
 DE A representative LipoD-Tat fusion protein.  
 XX  
 DE HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
 KW vaccine; HIV infection; protein D.  
 XX  
 XX Synthetic.  
 OS Human immunodeficiency virus type 1.

XX WO9916884-A1.  
 PN  
 XX  
 PD 08-APR-1999.  
 XX  
 PF 17-SEP-1998; 98WO-EP06040.  
 XX  
 PR 26-SEP-1997; 97GB-0020585.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA  
 PI Bruck C, Godart SAG, Marchand M;  
 XX  
 XX WPI: 1999-302282/25.  
 DR N-PSDB: AAX35691.  
 XX  
 PT HIV Tat or Nef protein linked to a fusion partner  
 PS Disclosure; Fig 2; 66pp; English.  
 XX  
 CC The present sequence represents a fusion protein comprising LipoD-HIV-1  
 CC Tat. The protein is exemplified the fusion proteins of  
 CC the invention. The specification also describes fusion proteins  
 CC comprising HIV-1 Nef protein. The fusion protein can be used in a  
 CC vaccine to prevent HIV infection.  
 XX  
 SQ Sequence 413 AA;  
 Query Match 99.6%; Score 2246; DB 20; Length 413;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-204; Mismatches 0; Indels 0; Gaps 0;  
 Matches 410; Conservative 0;  
 QY 2 SSHSSNMANTQMSKDKIIIAHRSAGSYLPEHTLESKALAFQAQADYLEQDLAMTKDGRLL 61  
 DB 4 SSHSSNMANTQMSKDKIIIAHRSAGSYLPEHTLESKALAFQAQADYLEQDLAMTKDGRLL 63  
 QY 62 VVIHDFLDGLTDVAKKPPHRRKDGRIYVDFTLKEIQSLEMTNFETMGKWSKSSVY 121  
 DB 64 VVIHDFLDGLTDVAKKPPHRRKDGRIYVDFTLKEIQSLEMTNFETMGKWSKSSVY 123  
 QY 122 WPTVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEVEGFPVT 181  
 DB 124 WPTVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEVEGFPVT 183  
 QY 182 QVPLPMTYKAAVDLSHFLKEGGLIHSQRQDILDWIIYHTQGYFPDQWNTTGP 241  
 DB 184 QVPLPMTYKAAVDLSHFLKEGGLIHSQRQDILDWIIYHTQGYFPDQWNTTGP 243  
 QY 242 VRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPEREVLHFRDRLAF 301  
 DB 244 VRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPEREVLHFRDRLAF 303  
 QY 302 HVARELHPEYFNKCTSEPVDPRLPEKHPGSGPKTACTNCTCYKCCFHCQVCFTKALG 361  
 DB 304 HVARELHPEYFNKCTSEPVDPRLPEKHPGSGPKTACTNCTCYKCCFHCQVCFTKALG 363  
 QY 362 SYGRKKRRQRRRPPQSGQTHQVSLSKOPTSOSRQDPTGPKETSGHHHHH 411  
 DB 364 SYGRKKRRQRRRPPQSGQTHQVSLSKOPTSOSRQDPTGPKETSGHHHHH 413  
 RESULT 3  
 ID AAG63237 standard; Protein: 413 AA.  
 XX  
 AC AAG63237;  
 XX  
 DT 01-OCT-2001 (first entry)  
 XX  
 DE Amino acid sequence of a His tagged ProD-Nef-Tat fusion protein.  
 XX  
 KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.

XX Synthetic.  
OS Human immunodeficiency virus.  
FH Key Location/Qualifiers  
FT Peptide 1..111  
FT /note= "Protd fusion partner"  
XX WO200154719-A2.  
XX 02-AUG-2001.  
XX 29-JAN-2001; 2001WO-EP00944.  
XX 31-JAN-2000; 2000GB-0002200.  
XX 14-APR-2000; 2000GB-0009336.  
XX 06-JUN-2000; 2000GB-0013806.  
XX 28-JUN-2000; 2000WO-EP05998.  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX Voss G;  
PI WPI; 2001-476172/51.  
DR N-PSDB; AAH42881.  
XX New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
PT protein or polynucleotide for the manufacture of a vaccine -  
XX Disclosure; Fig 1; 90pp; English.  
XX The present sequence represents a His-tagged Protd-Nef-Tat fusion  
CC protein. The protein is expressed in Escherichia coli, and is used to  
CC produce the vaccine of the invention. The specification describes  
CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the  
CC manufacture of a vaccine. The vaccine is used for the prophylactic or  
CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
CC in synergy with gp120 in the treatment and prevention of HIV. The  
CC vaccine reduces the HIV viral load in HIV infected humans and results  
CC in a maintenance of CD4+ levels over those levels found in the absence  
CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.  
XX Sequence 413 AA;  
SQ

Query Match 99.6%; Score 2246; DB 22; Length 413;  
Best Local Similarity 100.0%; Pred. No. 1.3e-204;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSSNNMANTQMSKIIIAHRCASGYLPEHTLESKALAFQAQADYLEQDLAMTKDRLV 61  
DB 4 sssnsmantqmskiiiahragsylypehtleskalfagagadyleqdlamtkdrlv 63  
QY 62 VIHDFLDGLTDVAKKFPFHRHRKDGYYVIDFTLKEIQSLEMTENFETMGKWSKSSVVG 121  
DB 64 vihdhfdlgltdvakkfphrhrkdgyryvidftlkeiqslemtenfetmgkwsksvvg 123  
QY 122 WPTVRMRRAEPAADGVAASRDLEKHAITSNTAATNAACAWLEAQEEVEGFPVTP 181  
DB 124 wptvrermrraepaadvgaasrdlekhaitsntaatnaacawleaqeeveegfpvtp 183  
QY 182 QVPLRPMTYKAAVDLSHFLKEKGGLEGLTHSQRRQDILDWIYHTQGYFPDQWNYTPGPG 241  
DB 184 qvplrptykaavdlshflkekgleglthsqrrqdildwiyhtqgyfpdwqnytpgpg 243  
QY 242 VRYPLTFGCYKLVPEPDKVEANKGENTSLHPSVLSHGMDPPERLEWRFDSRLAFH 301  
DB 244 vrypltfgcylkvppepdkveankgentslhpsvlsghmdpperlewrfdsrldfh 303  
QY 302 HVARELHPEYFNCTSEPDRLPEPKHFGSQPKTACTNCKYKCCFHCQVCFITKALGI 361  
DB 304 hvarelhpeyfnctsepdrlpepkhfgsqpkactnckykccfhcqvcfitkalgi 363

QY 362 SYGRKKRRQRRRPOGQSTHQVLSKQPTSQSRGDPGTGPKETSGHHHHH 411  
DB 364 sygrkkrrqrrrrppgsgsthqvlskqptsqsrqsgdtpgpketsghhhhh 413  
RESULT 4  
AA02353  
ID AAY02353 standard; Protein; 411 AA.  
XX AAY02353;  
XX 09-JUL-1999 (first entry)  
XX A representative LipoD-Tat-His fusion protein.  
XX HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
XX vaccine; HIV infection; protein D.  
XX Synthetic.  
XX Human immunodeficiency virus type 1.  
XX WO9916884-A1.  
XX 08-APR-1999.  
XX 17-SEP-1998; 98WO-EP06040.  
XX 26-SEP-1997; 97GB-0020585.  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX Bruck C, Godart SAG, Marchand M;  
XX WPI; 1999-302282/25.  
DR N-PSDB; AAX35689.  
XX HIV Tat or Nef protein linked to a fusion partner  
PT Disclosure; Fig 2; 66pp; English.  
XX The present sequence represents a fusion protein comprising Lipod-HIV-1  
CC Tat-His. The protein is exemplified the fusion proteins of  
CC the invention. The specification also describes fusion proteins  
CC comprising HIV-1 Nef protein. The fusion protein can be used in a  
CC vaccine to prevent HIV infection.  
XX Sequence 411 AA;  
SQ

Query Match 99.4%; Score 2242; DB 20; Length 411;  
Best Local Similarity 99.8%; Pred. No. 3e-204;  
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSHSSNMANTQMSKIIIAHRCASGYLPEHTLESKALAFQAQADYLEQDLAMTKDRL 60  
DB 1 csshssnmantqmskiiiahragsylypehtleskalfagagadyleqdlamtkdgrl 60  
QY 61 VIHDFLDGLTDVAKKFPFHRHRKDGYYVIDFTLKEIQSLEMTENFETMGKWSKSSV 120  
DB 61 vihdhfdlgltdvakkfphrhrkdgyryvidftlkeiqslemtenfetmgkwsksv 120  
QY 121 GWPVTRMRRAEPAADGVAASRDLEKHAITSNTAATNAACAWLEAQEEVEGFPVTP 180  
DB 121 gwpvtrermrraepaadvgaasrdlekhaitsntaatnaacawleaqeeveegfpvt 180  
QY 181 PQVPLRPMTYKAAVDLSHFLKEKGGLEGLTHSQRRQDILDWIYHTQGYFPDQWNYTPGP 240  
DB 181 pqvplrptykaavdlshflkekgleglthsqrrqdildwiyhtqgyfpdwqnytpgp 240  
QY 241 GVRYPPLTFGCYKLVPEPDKVEANKGENTSLHPSVLSHGMDPPERLEWRFDSRLAF 300  
DB 241 gvryppltfgcylkvppepdkveankgentslhpsvlsghmdpperlewrfdsrldf 300

QY 301 HHVARELHPEYFKNCTSEPDRLPEWHPGSGPQKTACTIONCYCKKCCFHCQVCFITKALG 360  
 Db 301 hhvarelhpeyfkntsepdvrlpewkhpqsgpqtactnctcyckkccfchqvcfittkalg 360  
 QY 361 ISYGRKKRRRRPPGQSTHQSLSKOPTSOSRGPDPKPTSGHSHHHH 411  
 Db 361 isygrkkrrrrppgsgsthsqslskptsqsrpdpkptsgshshhh 411

RESULT 5  
 AAY02352  
 ID AAY02352 standard; Protein; 324 AA.  
 XX  
 AC AAY02352;  
 XX  
 DT 09-JUL-1999 (first entry)  
 XX  
 DE A representative LipD-Nef-His fusion protein.  
 XX  
 KW HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
 KW vaccine; HIV infection; protein D.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO9916884-A1.  
 XX  
 PD 08-APR-1999.  
 XX  
 PF 17-SEP-1998; 98WO-EP06040.  
 XX  
 PR 26-SEP-1997; 97GB-0020585.  
 XX

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA Bruck C, Godart SAG, Marchand M;  
 PI WPI; 1999-302282/25.  
 DR N-PSDB; AAX35688.  
 XX  
 PT HIV Tat or Nef protein linked to a fusion partner  
 XX  
 PS Disclosure; Fig 2; 66pp; English.  
 XX  
 CC The present sequence represents a fusion protein comprising LipD-HIV-1  
 CC Nef-His. The protein is exemplified by the fusion proteins of  
 CC the invention. The specification also describes fusion proteins  
 CC comprising HIV-1 Tat protein. The fusion protein can be used in a  
 CC vaccine to prevent HIV infection.  
 XX  
 SQ Sequence 324 AA;

Query Match 75.7%; Score 1706.5; DB 20; Length 324;  
 Best Local Similarity 78.8%; Pred. No. 1.6e-153;  
 Matches 324; Conservative 0; Mismatches 0; Indels 87; Gaps 1;  
 QY 1 CSSHSSNMANTQMSDKIIIAHAGSGLPEHTLESKALFAQAQADLEQDLAMTKDGR 60  
 Db 1 CSSHSSNMANTQMSDKIIIAHAGSGLPEHTLESKALFAQAQADLEQDLAMTKDGR 60  
 QY 61 VVIHDFLDGTLTVAKFPHPHRKDGRIYVIDFTLKEIQSLSEMTENTETGGKWSKSVV 120  
 Db 61 vvihdflldgtldvakkfphrhrkdgrivvidftlkeiqslsemtentetggkwsksv 120  
 QY 121 GWPTVREMRRAEPADGVGAASRDLEKHGAITSNTAATNAACAWLEAQEEEEVGFPVT 180  
 Db 121 gwptvremrraepadvgvgaasrdlekhgaitsntaataacawleaqeeeevgfpvt 180  
 QY 181 PQVLRPMYTKAAVDLSHFLKEKGLGLIHSQRQDILDWYHTQGYFDMQNYTPGP 240  
 Db 181 pqvlpmtkykaavdlshflkekglglisqrqddildwihtqgyfwdwnytpgp 240

QY 241 GVRYPITFGWCYKLYPVEPKVEANKGENTSLHHPVSLHGMDDPEREVLWRFDLSRLAF 300  
 Db 241 gvrypltifgwcylklypvepkveeankgentsllhpsvlhgmddperewlwrfdslrlaf 300  
 QY 301 HHVARELHPEYFKNCTSEPDRLPEWHPGSGPQKTACTIONCYCKKCCFHCQVCFITKALG 360  
 Db 301 hhvarelhpeyfkntsepdvrlpewkhpqsgpqtactnctcyckkccfchqvcfittkalg 360  
 QY 361 ISYGRKKRRRRPPGQSTHQSLSKOPTSOSRGPDPKPTSGHSHHHH 411  
 Db 361 isygrkkrrrrppgsgsthsqslskptsqsrpdpkptsgshshhh 411

RESULT 6  
 AAG63234  
 ID AAG63234 standard; Protein; 324 AA.  
 XX  
 AC AAG63234;  
 XX  
 DT 01-OCT-2001 (first entry)  
 XX  
 DE Amino acid sequence of a His tagged LipD-Nef of HIV.  
 XX  
 KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..109  
 ET /note= "ProtD fusion partner"  
 XX  
 PN WO200154719-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 29-JAN-2001; 2001WO-EP00944.  
 XX  
 PR 31-JAN-2000; 2000GB-0002200.  
 PR 14-APR-2000; 2000GB-0009336.  
 PR 06-JUN-2000; 2000GB-0013806.  
 PR 28-JUN-2000; 2000WO-EP05998.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Voss G;  
 XX  
 DR WPI; 2001-476172/51.  
 DR N-PSDB; AAH42878.  
 XX  
 PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
 PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
 PT protein or polynucleotide for the manufacture of a vaccine -  
 XX  
 PS Disclosure; Fig 1; 90pp; English.  
 XX

XX The present sequence represents a His-tagged Nef protein of HIV, with  
 CC a lipidation signal sequence (lipid) which is removed after processing.  
 CC The protein is expressed in Escherichia coli, and is used to  
 CC produce the vaccine of the invention. The specification describes  
 CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the  
 CC manufacture of a vaccine. The vaccine is used for the prophylactic or  
 CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
 CC in synergy with gp120 in the treatment and prevention of HIV. The  
 CC vaccine reduces the HIV viral load in HIV infected humans and results  
 CC in a maintenance of CD4+ levels over those levels found in the absence  
 CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.  
 XX

SQ Sequence 324 AA;

Query Match 75.7%; Score 1706.5; DB 22; Length 324;









XX OS Synthetic.  
 OS Human immunodeficiency virus.  
 XX PN WO200154719-A2.  
 XX XX  
 XX PD 02-AUG-2001.  
 XX XX  
 XX PF 29-JAN-2001; 2001WO-EP00944.  
 XX XX  
 XX PR 31-JAN-2000; 2000GB-0002200.  
 PR 14-APR-2000; 2000GB-0009336.  
 PR 06-JUN-2000; 2000GB-0013806.  
 PR 28-JUN-2000; 2000WO-EP05998.  
 XX XX  
 XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX PI  
 XX Voss G;  
 XX XX  
 DR WPI: 2001-476172/51.  
 DR N-PSDB; AAH42883.  
 XX XX  
 XX PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
 PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
 PT protein or polynucleotide for the manufacture of a vaccine -  
 XX PS  
 XX Disclosure; Fig 1; 90pp; English.  
 XX XX  
 CC The present sequence represents a His-tagged mutant His protein of HIV.  
 CC The protein is expressed in the yeast Pichia pastoris, and is used to  
 CC produce the vaccine of the invention. The specification describes  
 CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the  
 CC manufacture of a vaccine. The vaccine is used for the prophylactic or  
 CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
 CC in synergy with gp120 in the treatment and prevention of HIV. The  
 CC vaccine reduces the HIV viral load in HIV infected humans and results  
 CC in a maintenance of CD4+ levels over those levels found in the absence  
 CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.  
 XX XX  
 XX Sequence 302 AA;

Query Match 74.3%; Score 1675; DB 22; Length 302;  
 Best Local Similarity 99.0%; Pred. No. 1.4e-150;  
 Matches 299; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 110 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169  
 DB 1 mggkwsksvvgwptvrermraepaadvggaasrdlekghaltsntaatnaacawlea 60  
 QY 170 QEEEEVGFPTPOVPLRPMTYKAAVDLSHFLKEKGGLEGILHSQRRQDILDLYHTQGY 229  
 DB 61 qeeeevgfpvtpgvrplrpmtykaavdlshflkekgglegilhsqrrqdlldlyhtqgy 120  
 QY 230 FPDQNYTPGPGVRYPLTFGWCYKLVPEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 289  
 DB 121 fpdqnytpgpgvrypltfwgcyklyvpdpkveeankgentsllhpvs lhgmdperev 180  
 QY 290 LEWRFDSRLAFHVAHELHPEYFNKNTSEPVDPRLPEPKHPGQPKTACTNCYKCKCFH 349  
 DB 181 lewrfdsrlafhvharelhpeyfnkntsepvdp rlepkhpqsgpkactnccfhh 240  
 QY 350 CQVCFITKALGISYGRKKRRRPPQGSQTHQVSLSKQPTSOSRGDPTGPKETSGHHH 409  
 DB 241 cqvcfitaalgisygrkkrrppqgsqthqvs lskptsosrgdptgpketsgghhh 300  
 QY 410 HH 411  
 DB 301 hh 302  
 RESULT 13  
 AAY02349

ID AAY02349 standard; Protein; 215 AA.  
 XX AC AAY02349;  
 XX DT 09-JUL-1999 (first entry)  
 XX DE A representative HIV-1 Nef-His protein.  
 XX KW HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
 XX vaccine; HIV infection; protein D.  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX PN WO9916884-A1.  
 XX XX  
 XX PD 08-APR-1999.  
 XX PF 17-SEP-1998; 98WO-EP06040.  
 XX PR 26-SEP-1997; 97GB-0020585.  
 XX XX  
 XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX PI Bruck C, Godart SAG, Marchand M;  
 XX XX  
 DR WPI: 1999-302282/25.  
 DR N-PSDB; AAX35885.  
 XX XX  
 XX HIV Tat or Nef protein linked to a fusion partner  
 XX Disclosure; Fig 2; 66pp; English.  
 CC The present sequence represents a representative HIV-1 Nef-His protein.  
 CC The protein is used in the creation of the fusion proteins of  
 CC the invention, in conjunction with a fusion partner (e.g. protein D).  
 CC The specification also describes fusion proteins comprising HIV-1 Tat  
 CC protein. The fusion protein can be used in a vaccine to prevent HIV  
 CC infection.  
 XX XX  
 XX Sequence 215 AA;

Query Match 50.5%; Score 1139.5; DB 20; Length 215;  
 Best Local Similarity 71.2%; Pred. No. 6.4e-100;  
 Matches 215; Conservative 0; Mismatches 0; Indels 87; Gaps 1;  
 QY 110 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169  
 DB 1 mggkwsksvvgwptvrermraepaadvggaasrdlekghaltsntaatnaacawlea 60  
 QY 170 QEEEEVGFPTPOVPLRPMTYKAAVDLSHFLKEKGGLEGILHSQRRQDILDLYHTQGY 229  
 DB 61 qeeeevgfpvtpgvrplrpmtykaavdlshflkekgglegilhsqrrqdlldlyhtqgy 120  
 QY 230 FPDQNYTPGPGVRYPLTFGWCYKLVPEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 289  
 DB 121 fpdqnytpgpgvrypltfwgcyklyvpdpkveeankgentsllhpvs lhgmdperev 180  
 QY 290 LEWRFDSRLAFHVAHELHPEYFNKNTSEPVDPRLPEPKHPGQPKTACTNCYKCKCFH 349  
 DB 181 lewrfdsrlafhvharelhpeyfnkntsepvdp rlepkhpqsgpkactnccfhh 206  
 QY 350 CQVCFITKALGISYGRKKRRRPPQGSQTHQVSLSKQPTSOSRGDPTGPKETSGHHH 409  
 DB 207 -----tsghhhh 213  
 QY 410 HH 411  
 DB 214 hh 215  
 RESULT 14

Db	207	-----tsghhhh 213
Qy	410 HH 411	
Db	214 hh 215	
RESULT 15		
AA50795		
ID	AA50795 standard; protein; 206 AA.	
XX		
AC	AA50795;	
XX		
DT	17-FEB-2000 (first entry)	
XX		
XX	Human NEF protein/calmodulin binding inhibitor.	
DE		
XX		
KW	NEF protein; calmodulin; negative factor protein; binding inhibitor;	
KW	diagnosis; detection; infection; treatment; HIV.	
XX		
OS	Homo sapiens.	
XX		
PN	W09957136-A2.	
XX		
PD	11-NOV-1999.	
XX		
PF	06-MAY-1999; 99WO-EP03105.	
XX		
PR	06-MAY-1998; 98DE-1020224.	
XX		
PA	(SCHO/) SCHOTT M.	
PA	(SCHO/) SCHORR J.	
PA	(ANTZ/) ANTZ C.	
XX		
PI	Schott M, Schorr J, Antz C;	
XX		
DR	WPI; 2000-038789/03.	
XX		
PT	Binding agents used for treatment, prevention and diagnosis of human	
PT	immune deficiency virus infection.	
XX		
PS	Claim 3; Fig 1; 29pp; German.	
XX		
CC	This invention describes novel binding partners (A) (i) for negative	
CC	factor protein (Nef) that competitively inhibit binding of calmodulin (i)	
CC	to Nef, or (ii) for (i) that competitively inhibit binding of Nef to (i).	
CC	(A) are used for prevention, diagnosis (by specific detection of intra-	
CC	and/or extra-cellular Nef, including staging of infection), and/or	
CC	treatment of infections with human immune deficiency virus (HIV).	
XX		
SQ	Sequence 206 AA;	
	Query Match 49.7%; Score 1120; DB 21; Length 206;	
	Best Local Similarity 99.0%; Pred. No. 4.3e-98;	
	Matches 204; Conservative 0; Mismatches 2; Indels 0; Gaps	
Qy	110 MGGKWSKSSVVGWPTVRERMRRAEPAADGGAASRDLEKHGAITSNTAATNAACAWLEA 169	
Db	1 mggkwsksvvgwptvrermrreapaadggaasrdlekhgaitsntaannaacawlea 60	
Qy	170 QEEEEVGPVTPQVPLRPMTYKAADVLSHFLEKGGLEGGLHSQRQDILDWIYHTQGY 229	
Db	61 qeeeevfpvtqpvlrptmtykaadvlsfhfkeggleglilhsqrrqdildwlyhcggy 120	
Qy	230 FPDQNYTPGPGVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDPEREV 289	
Db	121 fpdqnytpgpgvrypltfwgcyklvppepkveeankgentsllhpvsllhgmdperev 180	
Qy	290 LEWRFDLSRLAFHHVARELHPEYFKNC 315	
Db	181 lewrfdlsrlafhhvarelhpeyfknc 206	

## RESULT 16

AAR38893  
ID AAR38893 standard; Protein: 206 AA.

XX AC AAR38893;

XX DT 10-NOV-1993 (first entry)

XX DE Nef protein of HIV-1.

XX KW AIDS: antibody; p25; gp110; gp41; assay; detection;  
XX KW immunity; vaccine.

XX OS Human immunodeficiency virus-1.

XX PN US221610-A.

XX PD 22-JUN-1993.

XX PF 26-MAY-1988; 88US-0199143.

XX PR 26-MAY-1988; 88US-0199143.

XX PR 04-SEP-1991; 91US-0754300.

XX PA (INRM) INST NAT SANTE & RECH MEDICALE.  
XX PA (INSP) INST PASTEUR.XX PI Bahraoui EM, Chamaret S, Ferris S, Granier C, Montagnier L;  
XX PI Rietschoten JV, Rochat H, Sabatier JM;

XX DR WPI; 1993-213434/26.

XX PT Diagnosis of HIV infection - by detecting HIV antibodies using  
XX PT antigenic polypeptide derived from nef protein of HIV-1

XX PS Disclosure; Fig 2; 15pp; English.

XX SS The nef protein comprises peptides which are expressed in vivo in HIV  
XX CC infected patients before detectable amts. of p25, gp110 and gp41 are  
XX CC expressed. Thus, they can be used in assays for early detection of HIV.  
XX CC They can also be used to raise antibodies for use in detection,  
XX CC to induce cellular immunity or to raise neutralising antibodies  
XX CC that either inactivate the AIDS virus or reduce the viability of  
XX CC the virus in vivo or destroy infected cells.  
XX CC The peptides may be used in viral vaccines.

XX SQ Sequence 206 AA;

Query Match 49.5%; Score 1116; DB 14; Length 206;  
Best Local Similarity 99.0%; Pred. No. 1e-97;  
Matches 204; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 110 MGGKSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 169

DB 1 mggkssksvvgwptvrrmrreapaaadvgvgaasrdlekhgaitssntaatnaacawlea 60

QY 170 QEEEEVGFPTVPQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSQRQDILDLMVHTQGY 229

DB 61 qeeeevgfptvpqvlrprmtyaavdlshflkekggleglshqrqrqldldlwyhtggy 120

QY 230 FPDWQNYTGPQGVRYPLTFCWCYKLVPEPDKVEANKGENTSLHPVSLHGMDDPERV 289

DB 121 fpdwnytpgpgvrypltfwcycylvpdpdkveeankgentsllhpvslhgmddperv 180

QY 290 LEWRDLSRLAFHHVARELHPEYFKNC 315

DB 181 lewrfdslafhhvarelhpeyfknc 206

## RESULT 17

## AAB10054

ID AAB10054 standard; Protein: 206 AA.

XX AC AAB10054;

XX DT 02-NOV-2000 (first entry)

XX DE HIV-1 nef protein.

XX KW Glycoprotein; gag; pol; GP-1; GP-2; anti-HIV; cytostatic;  
XX KW gene therapy; treatment; infectious disease; HIV; AIDS; neoplasm;  
XX KW carcinoma; melanoma; nef protein.

XX OS Human immunodeficiency virus type 1.

XX PN EP1006196-A2.

XX PD 07-JUN-2000.

XX PF 25-NOV-1999; 99EP-0250415.

XX PR 26-NOV-1998; 98DE-1056463.

XX PA (PETT-) PETTE INST HEINRICH.

XX PI Von Laer MD;

XX DR WPI; 2000-378268/33.

XX DR N-PSDB; AAA40298, AAB10053, AAB10054.

XX PT New retroviral packing cell useful as pharmaceutical carrier in gene  
XX PT therapy for treatment of HIV and neoplasms, comprises retroviral genes  
XX PT and glycoproteins -

XX PS Disclosure: Page 48; 69pp; German.

XX CC This invention describes a novel retroviral packing cell (I), comprising  
XX CC the retroviral genes gag, pol and glycoproteins GP-1 and GP-2 of the LCMV  
XX CC coding gene gp, or a part of these. The products of the invention have  
XX CC anti-HIV and cytostatic activity and can be used for gene therapy. (I) is  
XX CC useful for in vitro infection of cells, especially hematopoietic stem  
XX CC cells, for expression of transgenes in cells and as a pharmaceutical  
XX CC carrier for gene therapy. (I) is therefore useful in the treatment of  
XX CC infectious diseases (HIV or AIDS), neoplasms (carcinomas), melanomas and  
XX CC other diseases. This sequence represents the Human immunodeficiency virus  
XX CC (HIV-1) nef protein described in the method of the invention.

XX SQ Sequence 206 AA;

Query Match 49.4%; Score 1115; DB 21; Length 206;  
Best Local Similarity 98.1%; Pred. No. 1.3e-97;  
Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 110 MGGKSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 169

DB 1 mggkssksvvgwptvrrmrreapaaadvgvgaasrdlekhgaitssntaanaacawlea 60

QY 170 QEEEEVGFPTVPQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSQRQDILDLMVHTQGY 229

DB 61 qeeeevgfptvpqvlrprmtyaavdlshflkekggleglshqrqrqldldlwyhtggy 120

QY 230 FPDWQNYTGPQGVRYPLTFCWCYKLVPEPDKVEANKGENTSLHPVSLHGMDDPERV 289

DB 121 fpdwnytpgpgvrypltfwcycylvpdpdkveeankgentsllhpvslhgmddperv 180

QY 290 LEWRDLSRLAFHHVARELHPEYFKNC 315

DB 181 lewrfdslafhhvarelhpeyfknc 206

RESULT 18  
AAW89326

ID AAW89326 standard; Protein; 206 AA.  
XX  
AC AAW89326;  
XX  
DT 01-JUN-1999 (first entry)  
XX  
DE HIV-1 nef protein sequence.  
XX  
KW Antigenic composition; primate; lentivirus; nef gene; vaccine;  
KW infection; AIDS; HIV-1; nef protein.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN US5851813-A.  
XX  
PD 22-DEC-1998.  
XX  
PF 27-JAN-1994; 94US-0188583.  
XX  
PR 27-JAN-1994; 94US-0188583.  
PR 12-JUL-1990; 90US-0551945.  
PR 09-JUL-1991; 91US-0721494.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Destosiers RC;  
XX  
XX WPI; 1999-080408/07.  
DR N-PSDB; AAW81866.  
XX  
XX Lentivirus antigenic compositions - containing lentivirus with nef  
PT gene deletion  
XX  
PS Disclosure; Fig 2A-R; 93pp; English.  
XX  
CC The invention relates to an antigenic composition comprising an isolated  
CC primate lentivirus whose genome contains an engineered non-reversible  
CC null mutation in the nef gene, or an infectious DNA clone in a carrier.  
CC The antigenic composition is used in vaccines against infection by the  
CC lentivirus, e.g. AIDS.  
XX  
SQ Sequence 206 AA;  
  
Query Match 49.4%; Score 1114; DB 20; Length 206;  
Best Local Similarity 97.6%; Pred. No. 1.6e-97;  
Matches 201; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
QY 110 MGGKSKSSVGVGPTVRMRRAEPAADGVGAASRDLEKHGALTSSNTAATNAACAWLEA 169  
DB 1 mggksskssvlgvpavremrrraepaadvgaasrdlekhgaltssntaannaacawlea 60  
  
QY 170 QEEEEVGFVPTQVPLRPMYKAAVDLSHFLKEGGLIHSQRQDILDLMYHTQGY 229  
DB 61 qeeekvgfvtqvpvlpmtykaavdlshflkeggleghsqrqdlldlwyhtqgy 120  
  
QY 230 FPDWQNYTFPGVRYPLTFGWCKYKLVPEPDKVEEANKGENTSLLHPVSLHGMDPEREV 289  
DB 121 fpdwqnytpgpgirypvltfgwcyklyvpvdpkveeankgentsllhpvslhgmdperv 180  
  
QY 290 LEWRFDRLAFHHVARELHPEYFKNC 315  
DB 181 lewrfdslafhvharelhpeyfknc 206  
  
RESULT 19  
AAP61515  
ID AAP61515 standard; Protein; 206 AA.  
XX  
AC AAP61515;  
XX  
DT 08-JUN-1991 (first entry)  
XX

DE Sequence of E' protein.  
XX  
XX HIV; LAV; AIDS; diagnosis; vaccine.  
XX  
OS HTLV-IIIB/H9 cells (ATCC CRL 8543).  
XX  
PN EP187041-A.  
XX  
PD 09-JUL-1986.  
XX  
PF 23-DEC-1985; 85EP-0309454.  
XX  
PR 24-DEC-1984; 84US-0685272.  
PR 04-DEC-1985; 85US-0805069.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Capon DJ, Lasky LA;  
XX  
XX WPI; 1986-177602/28.  
DR N-PSDB; AAN60288.  
XX  
XX Acquired immune deficiency syndrome polypeptide(s) - obt'd. by  
PT molecular cloning etc. and used for diagnosis and in vaccines  
PT against virus disease  
XX  
PS Example; fig 2; 125pp; English.  
XX  
XX A comparison of AAN60287 with the cDNA of the HTLV-III genome  
CC revealed one particular clone, designated p7.11 which contained a  
CC DNA sequence encoding this peptide (AAP60308) sequence. This approx.  
CC 2.2 kilobase covers the precursor gag region and encodes, 5' to 3',  
CC p-12, p-15, p-24 a second p-15 protein, and approx. 300 extra base  
CC pairs 3' to the gag region (see AAN60288).  
XX  
SQ Sequence 206 AA;  
  
Query Match 49.3%; Score 1111; DB 7; Length 206;  
Best Local Similarity 97.1%; Pred. No. 3.1e-97;  
Matches 200; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
  
QY 110 MGGKSKSSVGVGPTVRMRRAEPAADGVGAASRDLEKHGALTSSNTAATNAACAWLEA 169  
DB 1 mggksskssvlgvpavremrrraepaadvgaasrdlekhgaltssntaannaacawlea 60  
  
QY 170 QEEEEVGFVPTQVPLRPMYKAAVDLSHFLKEGGLIHSQRQDILDLMYHTQGY 229  
DB 61 qeeekvgfvtqvpvlpmtykaavdlshflkeggleghsqrqdlldlwyhtqgy 120  
  
QY 230 FPDWQNYTFPGVRYPLTFGWCKYKLVPEPDKVEEANKGENTSLLHPVSLHGMDPEREV 289  
DB 121 fpdwqnytpgpgirypvltfgwcyklyvpvdpkveeankgentsllhpvslhgmdperv 180  
  
QY 290 LEWRFDRLAFHHVARELHPEYFKNC 315  
DB 181 lewrfdslafhvharelhpeyfknc 206  
  
RESULT 20  
AAP60423  
ID AAP60423 standard; Protein; 216 AA.  
XX  
AC AAP60423;  
XX  
DT 20-AUG-1991 (first entry)  
XX  
DE Sequence of LAV virus ORF F protein.  
XX  
KW AIDS vaccine; diagnosis; immunoassay; HIV; HTLV-III.  
XX  
OS Lymphadenopathy virus.  
XX

PN WO8602383-A.  
 XX  
 PD 24-APR-1986.  
 XX  
 PF 18-OCT-1985; 85WO-EP00548.  
 XX  
 PR 21-JAN-1985; 85GB-0001473.  
 PR 18-OCT-1984; 84FR-0016013.  
 PR 16-NOV-1984; 84GB-0029099.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PA (INSP ) INST PASTEUR.  
 XX  
 PI Montagnier L, Krust B, Chamaret S, Clavel F, Chermann J-C;  
 PI Barre-Sinoussi F, Alizon M, Sonigo P, Stewart C, Danos O;  
 PI Wain-Hobson S;  
 XX  
 DR WPI: 1986-119166/18.  
 DR N-PSDB; AAN60365.  
 XX  
 PT Purified glyco:protein and peptide(s) - are recognised by sera contg.  
 PT antibodies against lymphadenopathy virus and useful in detecting  
 PT AIDS antibodies or in vaccines  
 XX  
 PS Disclosure; Fig 4; 75pp; English.  
 XX  
 CC The inventors claim a polypeptide which is recognised by sera of  
 CC human origin contg. antibodies against the virus of  
 CC lymphadenopathies (LAV) or acquired immune deficiency syndrome  
 CC (AIDS). Also claimed are various peptides corresp. to the AA  
 CC sequences deducible from proteins encoded by LAV DNA, defined by  
 CC specific residues (e.g. 12-32, 37-46, 49-79, 88-153) in accordance  
 CC with a formula given in the specification.  
 XX  
 SQ Sequence 216 AA;

Query Match 49.1%; Score 1107; DB 7; Length 216;  
 Best Local Similarity 98.1%; Pred. No. 7.9e-97;  
 Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 110 MGKWKSSVVGWPTVREMRRAEPAADGVGAASRDLEKHGATTSNTAATNAACAWLEA 169  
 DB 11 mgkwwkssvvgwptvremrraepaahvgvaaspldkhgaitsntaataacawlea 70  
 QY 170 QEEEEVGFPTPOVPLRPMYTKAAVDLSHFLKEKGLGGLIHSQRQDILDWYHTQGY 229  
 DB 71 qeeevgfptpqvplrmpmtkaavdlshflkekggleglihsqrqdlldwlyhtqgy 130  
 QY 230 FPDQNYTPGPGVRYPLTFGWCYKLYPVPDPKVEEANKGENTSLHPVSLHGMDPEREV 289  
 DB 131 fpdqnytpgpgvrypltfwgcyklypvpdpkveeankgentsllhpvslhgmdperv 190  
 QY 290 LEWRFSRLAFHFAHVELHPEYFKNC 315  
 DB 191 lewrfsrlafhfhvarelhphqyfknc 216

RESULT 21  
 AAW90179  
 ID AAW90179 standard; Protein; 206 AA.  
 XX  
 AC AAW90179;  
 XX  
 DT 14-JUN-1999 (first entry)  
 XX  
 DE HTLV-III E' protein.  
 XX  
 KW AIDS; acquired immunodeficiency syndrome; viral infection; env protein;  
 KW fusion polypeptide; E' protein; gag protein; pol protein; p' protein;  
 KW gp signal peptide; detection; vaccination; etiological agent;  
 KW infection inhibitor; AIDS associated retrovirus; p24; gp41.

OS Human lymphotropic virus type III.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 11 /label= Val, Ile  
 FT Misc-difference 51 /label= Thr, Asn  
 FT Misc-difference 54 /label= Asp, Ala  
 FT Misc-difference 65 /label= Glu, Lys  
 FT Misc-difference 151 /label= Glu, Asp  
 FT Misc-difference 153 /label= Leu, Val  
 XX  
 PN US853978-A.  
 XX  
 PD 29-DEC-1998.  
 XX  
 PF 29-JUL-1994; 94US-0282857.  
 XX  
 PR 08-MAY-1986; 86US-0861016.  
 PR 24-DEC-1984; 84US-0685272.  
 PR 04-DEC-1985; 85US-0805069.  
 PR 02-AUG-1988; 88US-0227568.  
 PR 19-NOV-1992; 92US-0979391.  
 PR 29-SEP-1993; 93US-0129009.  
 PR 29-JUL-1994; 94US-0282857.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Berman PW, Capon DJ, Lasky LA;  
 XX  
 DR WPI: 1999-094894/08.  
 DR N-PSDB; AAV74271.  
 XX  
 PT New AIDS-associated fusion poly:peptide(s) - used for the detection  
 PT of AIDS or to inhibit infection by AIDS associated retrovirus or  
 PT dissemination of such retrovirus in infected individuals  
 XX  
 PS Example 1: Fig 2A-J; 47pp; English.  
 XX  
 CC This invention describes a novel fusion polypeptide which comprises  
 CC (a) a first polypeptide sequence of an AIDS associated E', env, or gag  
 CC polypeptide, that specifically binds complementary antibody and (b) a  
 CC second polypeptide sequence which is not an AIDS associated virus  
 CC polypeptide. Also described are (1) a fusion polypeptide having a  
 CC herpes simplex virus (HSV) gp signal peptide sequence fused in reading  
 CC frame with a polypeptide sequence other than HSV gp, (2) a nucleic acid  
 CC encoding a fusion polypeptide as in (1); (3) an expression vector  
 CC comprising a nucleic acid as in (2); (4) a host comprising a vector as  
 CC in (3). The AIDS-associated fusion polypeptides can be used in the  
 CC detection of and vaccination against viral etiological agents of AIDS.  
 CC They can also be administered as a pharmaceutical agent to inhibit  
 CC infection by AIDS associated retrovirus or dissemination of such  
 CC retrovirus in infected individuals.  
 XX  
 SQ Sequence 206 AA;

Query Match 48.4%; Score 1092; DB 20; Length 206;  
 Best Local Similarity 96.1%; Pred. No. 2e-95;  
 Matches 198; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 110 MGKWKSSVVGWPTVREMRRAEPAADGVGAASRDLEKHGATTSNTAATNAACAWLEA 169  
 DB 1 mgkwwkssvvgwptvremrraepaahvgvaaspldkhgaitsntaataacawlea 60  
 QY 170 QEEEEVGFPTPOVPLRPMYTKAAVDLSHFLKEKGLGGLIHSQRQDILDWYHTQGY 229  
 DB 61 qeeevgfptpqvplrmpmtkaavdlshflkekggleglihsqrqdlldwlyhtqgy 120

QY 230 FPDWQNTGPGVRYPLTFCWCYKLVPEVPDKVVEANKGENTSLHPVSLRGMDPPEREV 289  
Db 121 fpdwqntgpgirylpttgwcyklyvpvpepxxxeeankgentllhpsvhlghmdpperev 180

QY 290 LEWRFSRLAFHHVARELHPEYFKNC 315  
Db 181 lewrfsrlafhhvarelhpeyfknc 206

RESULT 22  
AAE04960  
ID AAE04960 standard; Protein; 216 AA.  
AC AAE04960;  
XX  
DT 10-SEP-2001 (first entry)  
DE HIV-1 jrf1 Nef protein.  
XX  
XX DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV;  
KW cell mediated immune response; cytotoxic T lymphocyte; CTL;  
KW human immunodeficiency virus-1; HIV-1; mutant; mutain.  
XX  
OS Human immunodeficiency virus type 1.  
XX Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 2 /note= "Myristylation site"  
XX  
XX WO200143693-A2.  
XX  
XX 21-JUN-2001.  
XX  
XX 15-DEC-2000; 2000WO-US34162.  
XX  
XX 17-DEC-1999; 99US-0172442.  
XX  
XX (MERI ) MERCK & CO INC.  
XX  
XX Shiver JW, Liang X, Fu T;  
PI  
XX  
XX WPI; 2001-417878/44.  
XX  
XX N-PSDB; AAD09603.  
XX  
XX Novel DNA vaccine useful for inducing cell mediated immune response  
PT against virulent strains of HIV, comprises DNA expression vector, and  
PT DNA containing codon optimized open reading frame encoding Nef protein  
PT  
XX  
XX Claim 5; Page 13; 84pp; English.  
XX  
XX The present invention relates to a DNA vaccine comprising a DNA  
CC expression vector, and a DNA molecule containing a codon optimised open  
CC reading frame encoding a Nef protein or its immunogenic derivative. The  
CC Nef protein or its derivative is expressed and generates an immune  
CC response which provides a substantial level of protection against HIV  
CC infection, upon administration of to a host. The DNA vaccine is useful  
CC for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL)  
CC response against infection or disease caused by virulent strains of HIV,  
CC by administering the DNA vaccine into the tissue of the vertebrate host,  
CC preferably human. It is also useful for lowering transmission rate to  
CC previously uninfected individuals and/or for reducing levels of viral  
CC loads within an infected individual, so as to prolong the asymptomatic  
CC phase of HIV infection. The present sequence is human immunodeficiency  
CC virus-1 (HIV-1) jrf1 Nef protein. The different codon optimised nef  
CC constructs of the invention are used in the exemplification of the  
CC invention.  
XX  
XX Sequence 216 AA;  
SQ

Query Match 44.8%; Score 1011; DB 22; Length 216;

Best Local Similarity 83.8%; Pred. No. le-87;  
Matches 181; Conservative 15; Mismatches 10; Indels 10; Gaps 1;

QY 110 MGKSKSSVVGWPTVRMRRAEPAAD-----GVGAARDLEKHGAITSNTAA 159  
Db 1 mggkwsksrvpgwstvrermraepaadvrrtepaavgvavsrdekhgaitssntaa 60

QY 160 TNAACAWLEAQEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSORQDIL 219  
Db 61 tnadacawleaqedevegfpvrpqvplrpmtkygavdlshflkekggleglihsqkrqdl 120

QY 220 DLMIYHTQGYFPDQWQNTGPGVRYPLTFCWCYKLVPEVPDKVVEANKGENTSLHPVSL 279  
Db 121 dlwyhtqgyfpdwqntgpgirylpttgwcyklyvpvpepxxxeeankgentllhpsmq 180

QY 280 HCMDDPEREVLWRFSRLAFHHVARELHPEYFKNC 315  
Db 181 hgiedpekevlwrfdsrlafhhvarelhpeyykdc 216

RESULT 23  
AAW53113  
ID AAW53113 standard; Protein; 210 AA.  
XX  
AC AAW53113;  
XX  
DT 25-JUN-1998 (first entry)  
XX  
DE Protein 6 contained in a complete ARV-2 nucleotide sequence.  
XX  
KW ARV-2; enhanced promoter; gene expression; cytomegalovirus;  
KW HIV; AIDS.  
XX  
OS Human Immunodeficiency virus type 1.  
XX  
XX US5688688-A.  
XX  
XX 18-NOV-1997.  
XX  
XX 10-AUG-1994; 94US-0288336.  
XX  
XX 24-DEC-1987; 87US-0138894.  
XX  
XX 31-OCT-1984; 84US-0667501.  
XX  
XX 30-JAN-1985; 85US-0696534.  
XX  
XX 06-SEP-1985; 85US-0773447.  
XX  
XX 17-AUG-1992; 92US-0931191.  
XX  
XX 28-JUN-1993; 93US-0083391.  
XX  
XX 17-AUG-1993; 93US-0107377.  
XX  
XX 10-AUG-1994; 94US-0288336.  
XX  
XX (CHIR ) CHIRON CORP.  
XX  
XX Chapman BS, Dina D, Haigwood NL, Luciw PA, Rosenberg S;  
PI Thayer RM;  
XX  
XX WPI; 1998-007982/01.  
XX  
XX Enhanced promoter for gene expression - comprising cytomegalovirus  
PT immediate early promoter plus intron  
XX  
XX Example 1; Fig 4C-P; 99pp; English.  
XX  
XX This sequence represents a protein of unspecified function contained in a  
CC complete nucleotide sequence of ARV-2 derived from partial sequences of a  
CC several ARV clones. The invention provides a method for construction of a  
CC vector for expression of a polypeptide in a mammalian cell, comprising a  
CC polypeptide coding sequence operably linked downstream of an enhanced  
CC promoter. The enhanced promoter comprises the human cytomegalovirus  
CC immediate early region (HCMV IE1) promoter and the first intron proximate  
CC to the 3' end of the HCMV IE1 promoter. The polypeptide can be any of the  
CC HIV recombinant polypeptides and especially HIV gp120. Expression of HIV  
CC gp120 by COS 7 cells transfected with pCMV6a containing the gp120 coding  
CC region, where pCMV6a is a vector containing the above enhanced promoter,  
CC

CC is increased by a factor of 50-100 compared with the use of a vector  
CC containing the SV40 early promoter.

XX Sequence 210 AA;  
SQ Query Match 44.2%; Score 997; DB 19; Length 210;  
Best Local Similarity 85.2%; Pred. No. 2.1e-86;  
Matches 179; Conservative 16; Mismatches 11; Indels 4; Gaps 1;  
QY 110 MGGKWSKSSVVGWPTVYRMR-----RAEPAADGVGAASRDLEKKGAGTSSNTAATNAACA 165  
Db 1 mggkwsksrmggsalrerrmrtaepaadvgaavsdlekghgaitssntaataadca 60  
QY 166 WLEAQEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSQRQDILDLYH 225  
Db 61 wleaqeeevgfpvtpqvlrmpmtkaalidishflkekgleglwsgqrqeldlwyh 120  
QY 226 TQGYFDMQNYTPGCVRYPLTFGWCYKLVPEPDKVEEANKGENTSLLLHPVSLHGMDDP 285  
Db 121 tqgyfwdqnytpggyirpftfgwcfklvpvepkeveanegenllhpsmlhgmada 180  
QY 286 EREVLEWRFDSRLAFHHVARELHPEYFKNC 315  
Db 181 ekevlwrfdsklafhmarelhpeyykdc 210

RESULT 24  
AAAY77299  
ID AAY77299 standard; Protein; 210 AA.  
XX AC AAY77299;  
XX DT 22-MAY-2000 (first entry)  
XX DE HIV-1 (ATCC CRL 8597) ORF #3-encoded protein.  
XX KW HIV-1; immunoassay; antigen; pol fragment; p31; recombinant; antibody;  
XX KW detection.

Human immunodeficiency virus type 1 'ATCC CRL 8597'.

US6013432-A.  
PD 11-JAN-2000.  
XX PF 17-MAY-1995; 95US-0443434.  
XX PR 08-JUL-1993; 93US-0089407.  
XX PR 24-DEC-1987; 87US-0138894.  
XX PR 17-AUG-1992; 92US-0931154.  
XX PR 31-OCT-1984; 84US-0667501.  
XX PR 30-JAN-1985; 85US-0696534.  
XX PR 06-SEP-1985; 85US-0773447.  
XX PA (CHIR ) CHIRON CORP.  
XX PI Luciw PA, Dina D;  
XX DR WPI: 2000-170256/15.  
XX DR N-PSDB; AA290201.

XX Immunoassay for antibodies against human immune deficiency virus, for  
PT diagnosing infection, uses an immunogenic fragment of the pol protein  
PT as antigen -

XX Example 1; Fig 40-P; 99pp; English.

XX The invention relates to the improvement of HIV-1 immunoassays by the  
CC use of an HIV-1 antigen comprising an immunogenic fragment of  
CC recombinant or synthetic HIV-1 pol, which is encoded by an approximately  
CC 9.7 kb sequence between a BstXI restriction site at position 3006 and an  
CC NdeI site at position 5131 of the genome (the proviral DNA sequence is

CC given in AA290201). The immunogenic pol fragment is not immunologically  
CC cross-reactive with human T cell lymphotropic viruses 1 or II. The  
CC invention also encompasses the use of p31 as an antigen. The recombinant  
CC antigens may be produced in Escherichia coli, Saccharomyces cerevisiae or  
CC in mammalian cells. Immunoassays using the recombinant HIV proteins may  
CC be used to diagnose and stage HIV-1 infections. Sequences  
CC AA77294-777299 represent proteins encoded by the genome of HIV-1 (ATCC  
CC CRL 8597).

XX SQ Sequence 210 AA;

Query Match 44.2%; Score 997; DB 21; Length 210;  
Best Local Similarity 85.2%; Pred. No. 2.1e-86;  
Matches 179; Conservative 16; Mismatches 11; Indels 4; Gaps 1;  
QY 110 MGGKWSKSSVVGWPTVYRMR-----RAEPAADGVGAASRDLEKKGAGTSSNTAATNAACA 165  
Db 1 mggkwsksrmggsalrerrmrtaepaadvgaavsdlekghgaitssntaataadca 60  
QY 166 WLEAQEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSQRQDILDLYH 225  
Db 61 wleaqeeevgfpvtpqvlrmpmtkaalidishflkekgleglwsgqrqeldlwyh 120  
QY 226 TQGYFDMQNYTPGCVRYPLTFGWCYKLVPEPDKVEEANKGENTSLLLHPVSLHGMDDP 285  
Db 121 tqgyfwdqnytpggyirpftfgwcfklvpvepkeveanegenllhpsmlhgmada 180  
QY 286 EREVLEWRFDSRLAFHHVARELHPEYFKNC 315  
Db 181 ekevlwrfdsklafhmarelhpeyykdc 210

RESULT 25

AAAE04962  
ID AAE04962 standard; Protein; 217 AA.  
XX AC AAE04962;  
XX DT 10-SEP-2001 (first entry)  
XX DE HIV-1 Jrf1 Nef (G2A, LLAA) mutant protein.  
XX KW DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV;  
XX KW cell mediated immune response; cytotoxic T lymphocyte; CTL; mutin.  
XX KW human immunodeficiency virus-1; HIV-1; Jrf1 Nef; mutant; mutin.  
XX OS Human immunodeficiency virus type 1.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Misc-difference 2 /note= "Wild type myristylation site at Gly2 substituted  
XX FT with Ala"  
XX FT Misc-difference 174, 175 /note= "Wild type dileucine motif (Leu-Leu) substituted  
XX FT with Ala-Ala"

XX WO200143693-A2.

XX PD 21-JUN-2001.

XX PF 15-DEC-2000; 2000WO-US34162.

XX PR 17-DEC-1999; 99US-0172442.

XX PA (MERI ) MERCK & CO INC.

XX PI Shiver JW, Liang X, Fu T;

XX DR WPI: 2001-417878/44.

XX DR N-PSDB; AAD09605.





[illegible]

OS	Chimeric - Human immunodeficiency virus type 1.
OS	Chimeric - Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..26
FT	/label= "Leader peptide"
FT	/note= "Human tissue plasminogen activator (tPA)"
FT	leader sequence"
FT	27..237
FT	Protein
FT	/note= "Mature HIV-1 Nef (6-216aa) protein"
FT	/note= "195..196"
FT	Misc-difference
FT	/note= "Wild type dileucine motif (Leu-Leu) substituted with Ala-Ala"
FT	
FN	WO200143693-A2.
XX	
XX	21-JUN-2001.
PD	
XX	
XX	15-DEC-2000; 2000WO-US34162.
PE	
XX	
PR	17-DEC-1999; 99US-OI72442.
XX	
PA	(MERI ) MERCK & CO INC.
XX	
PI	Shiver JW, Liang X, Fu T;
XX	
DR	WPI; 2001-417878/44.
XX	N-PSDB; AAD09606.
XX	
PT	Novel DNA vaccine useful for inducing cell mediated immune response
PT	against virulent strains of HIV, comprises DNA expression vector' and
PT	DNA containing codon optimized open reading frame encoding Nef protein
PT	
XX	
PS	Claim 29; Page 19; 84pp; English.
XX	
CC	The present invention relates to a DNA vaccine comprising a DNA
CC	expression vector, and a DNA molecule containing a codon optimised open
CC	reading frame encoding a Nef protein or its immunogenic derivative. The
CC	Nef protein or its derivative is expressed and generates an immune
CC	response which provides a substantial level of protection against HIV
CC	infection, upon administration of to a host. The DNA vaccine is useful
CC	for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL)
CC	response against infection or disease caused by virulent strains of HIV,
CC	by administering the DNA vaccine into the tissue of the vertebrate host,
CC	preferably human. It is also useful for lowering transmission rate to
CC	previously uninfected individuals and/or for reducing levels of viral
CC	loads within an infected individual, so as to prolong the asymptomatic
CC	phase of HIV infection. The present sequence is human tissue plasminogen
CC	activator (tPA) leader peptide-human immunodeficiency virus-1 (HIV-1)
CC	jrf1 Nef (LLAA) chimeric mutant protein. The different codon
CC	optimised nef constructs of the invention are used in the exemplification
CC	of the invention.
XX	
SQ	Sequence 237 AA;

RESULT	28	
AAE04963		
ID	AAE04963 standard; Protein; 237 AA.	
XX		
AC	AAE04963;	
XX		
DT	10-SEP-2001 (first entry)	
XX		
DE	Human tPA leader peptide-HIV-1 jrlf Nef (LLAA) mutant protein.	
XX		
KW	DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV;	
KW	cell mediated immune response; cytotoxic T lymphocyte; CTL;	
KW	human immunodeficiency virus-1; HIV-1; human; jrlf nef; opt tpane;	
KW	tissue plasminogen activator; tPA; chimeric protein; mutant; mutein.	
XX		

	Query Match	42.9%	Score 968;	DB 22;	Length 237;
	Best Local Similarity	82.5%	Pred. No. 1.5e-83;		
	Matches 174;	Conservative 15;	Mismatches 12;	Indels 10;	Gaps 1;
Qy	115	SKSSVVGHTVVRNRRRAEPAAD-----GVGAASRLEKHGATTSNTAATNAAC	164		
Db	27	skrsvpgwstvrnmrraepaadvrrtpeaavgvavgsrdlkhgaitssntaatnadc	86		
Qy	165	AWLEAQEEEEGVFPVTPVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORQDILDWIIY	224		
Db	87	awleaqedeegvfvrpvavplrmcykavdlslhflkekgglegllhsqkrqdlldlwy	146		
Qy	225	HTQGYFPDQWQNTYTPGPGVRYPLTFGWCKYKLVPEVPDKVEANKGENTSLLLHPVSLHGMD	284		
Db	147	htqgyfpdwqnytpgpggirfoltfgwcklvpvepekeveanegencaahpmsahgied	206		



Db 2843 fpdwhnycpgpvrzpltfgrcfklvpvpreveeanegedncllhpcqhgmeddhrev 2902  
Qy 290 LEWRPDSRLAFHHVARELHPEYFKNCTSEPYDPR-----LEPWKHFGSQPKTACTNCY 342  
Db 2903 lkwkfdsqlahrarelhpefykdcxhrrdfprglstgafkevws--ggtgsgqpsnaa 2960  
Qy 343 CKKCCFHC 350  
Db 2961 ykqlifac 2968

Search completed: August 26, 2002, 08:12:27  
Job time: 236 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 08:10:39 ; Search time 38.46 Seconds  
(without alignments)  
261.022 Million cell updates/sec

Title: US-09-509-239-17  
Perfect score: 2255  
Sequence: 1 CSHSSNMANTQMKSDKIII.....QSRGDTGPKETSGHHHHH 411

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents.AA.\*

- 1: /cgn2\_6/ptodata/2/1aa/5A-COMB.pap.\*
- 2: /cgn2\_6/ptodata/2/1aa/5B-COMB.pap.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A-COMB.pap.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B-COMB.pap.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS-COMB.pap.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	1138	50.5	239	4	US-08-679-493A-76	Sequence 76, Appl
2	1115	49.4	206	3	US-08-388-353-644	Sequence 644, App
3	1115	49.4	206	3	US-08-488-551B-644	Sequence 644, App
4	971	43.1	206	4	US-08-679-493A-75	Sequence 75, Appl
5	638	28.3	123	4	US-09-124-900-10	Sequence 10, Appl
6	585.5	26.0	278	4	US-09-485-885-21	Sequence 21, Appl
7	579	25.7	383	4	US-09-485-885-23	Sequence 23, Appl
8	576	25.5	220	4	US-09-485-885-8	Sequence 8, Appl
9	575	25.5	220	4	US-09-485-885-1	Sequence 1, Appl
10	572	25.4	227	4	US-09-485-885-16	Sequence 16, Appl
11	572	25.4	371	4	US-09-485-885-6	Sequence 6, Appl
12	569	25.2	227	4	US-09-485-885-19	Sequence 19, Appl
13	564	25.0	273	4	US-09-485-885-4	Sequence 4, Appl
14	498.5	22.1	151	4	US-08-679-493A-74	Sequence 74, Appl
15	486	21.6	86	1	US-08-450-257-1	Sequence 1, Appl
16	486	21.6	86	1	US-08-450-246-1	Sequence 1, Appl
17	486	21.6	86	1	US-08-450-098-1	Sequence 1, Appl
18	486	21.6	86	1	US-08-451-233-1	Sequence 1, Appl
19	486	21.6	86	1	US-08-450-236-1	Sequence 1, Appl
20	486	21.6	86	3	US-07-808-452-1	Sequence 1, Appl
21	486	21.6	86	3	US-09-030-613-19	Sequence 19, Appl
22	486	21.6	86	4	US-09-124-900-6	Sequence 6, Appl
23	486	21.6	86	4	US-09-451-905-19	Sequence 19, Appl
24	486	21.6	86	4	US-08-235-403-1	Sequence 1, Appl
25	486	21.6	86	5	PCT-US92-10770-1	Sequence 1, Appl
26	486	21.6	86	5	PCT-US95-06077-2	Sequence 2, Appl
27	478.5	21.2	266	3	US-08-815-809-5	Sequence 5, Appl

28	478.5	21.2	280	2	US-08-816-155B-43	Sequence 43, Appl
29	478.5	21.2	280	4	US-09-079-587-43	Sequence 43, Appl
30	470	20.8	86	2	US-08-505-210-1	Sequence 1, Appl
31	470	20.8	86	4	US-09-099-333-1	Sequence 1, Appl
32	466	20.7	83	2	US-08-417-210A-96	Sequence 96, Appl
33	455	20.2	82	1	US-08-053-079A-15	Sequence 15, Appl
34	439	19.5	253	2	US-08-659-251-4	Sequence 4, Appl
35	439	19.5	253	4	US-09-256-490-4	Sequence 4, Appl
36	439	19.5	253	5	PCT-US96-11445-4	Sequence 4, Appl
37	409	18.1	72	3	US-09-030-613-17	Sequence 17, Appl
38	409	18.1	72	4	US-09-451-905-17	Sequence 17, Appl
39	385	17.1	72	2	US-08-893-853-1	Sequence 1, Appl
40	385	17.1	72	4	US-09-113-921-1	Sequence 1, Appl
41	372	16.5	122	6	5304466-3	Patent No. 5304466
42	365.5	16.2	312	1	US-08-094-128A-27	Sequence 27, Appl
43	365.5	16.2	312	1	US-08-455-674-27	Sequence 27, Appl
44	365.5	16.2	312	1	US-08-455-992-27	Sequence 27, Appl
45	365.5	16.2	312	1	US-08-455-972-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1  
US-08-679-493A-76  
; Sequence 76, Application US/08679493A  
; Patent No. 6303295  
; GENERAL INFORMATION:  
; APPLICANT: Taylor, Ethan W.  
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
; FILE REFERENCE: 55-95  
; CURRENT APPLICATION NUMBER: US/08/679,493A  
; PRIOR FILING DATE: 1996-07-12  
; PRIOR APPLICATION NUMBER: 60/001203  
; PRIOR FILING DATE: 1995-07-14  
; PRIOR APPLICATION NUMBER: 60/003,112  
; PRIOR FILING DATE: 1995-09-01  
; NUMBER OF SEQ ID NOS: 216  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 76  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)..(239)  
; OTHER INFORMATION: X os selenocysteine.  
US-08-679-493A-76

Query Match	50.5%	Score 1138;	DB 4;	Length 239;
Best Local Similarity	88.7%	Pred. No. 9.6e-107;		
Matches 211;	Conservative 2;	Mismatches 25;	Indels 0;	Gaps 0;
QY	110	MGKSKSVVWCVPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNACAWLEA	169	
Db	1	MGKSKSVVWCVPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNACAWLEA	60	
QY	170	QEEVEGVFPVTVPLRPMYTKAAVDLSHFLKEKGGLEGLIHSORQDILDLMYHTQGY	229	
Db	61	QEEVEGVFPVTVPLRPMYTKAAVDLSHFLKEKGGLEGLIHSORQDILDLMYHTQGY	120	
QY	230	FPDQWNYTPGVPYPLTFGWCYKLVPEPDKVVEEANKGENTSLHPVSLHGMDDPEREV	289	
Db	121	FPDQWNYTPGVPYPLTFGWCYKLVPEPDKVVEEANKGENTSLHPVSLHGMDDPEREV	180	
QY	290	LEWRDSDRLAFHHVARELHPEYFKNCTSEVPDRLEPWHKPGSQKTACTNCKYKCC	347	
Db	181	LEWRDSDRLAFHHVARELHPEYFKNCTSEVPDRLEPWHKPGSQKTACTNCKYKCC	238	

RESULT 2  
US-08-388-353-644

Sequence 644, Application US/08388353  
Patent No. 6010895  
GENERAL INFORMATION:  
APPLICANT: Deacon, Nicholas J.  
APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 644:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 206 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-388-353-644

Query Match 49.4%; Score 1115; DB 3; Length 206;  
Best Local Similarity 98.1%; Pred. No. 1.6e-104;  
Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 110 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169  
Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKHGAITSSNTAANNAACAWLEA 60  
Qy 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDWIYHTQGY 229  
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDWIYHTQGY 120  
Qy 230 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPSVSLHGMDPPEREV 289  
Db 121 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPSVSLHGMDPPEREV 180  
Qy 290 LEWRFDSRLAFHHVARELHPEYFKNC 315  
Db 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 3  
US-08-488-551B-644  
Sequence 644, Application US/08488551B  
Patent No. 6015661  
GENERAL INFORMATION:  
APPLICANT: Nicholas J. Deacon  
APPLICANT: Dale A. McPhee  
APPLICANT: David Cooper

TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 841  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
STREET: 400 GARDEN CITY PLAZA  
CITY: GARDEN CITY  
STATE: NEW YORK  
COUNTRY: U.S.A.  
ZIP: 11530-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,551B  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PM3864 (AU)  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: PM4002 (AU)  
FILING DATE: 21-FEB-1994  
APPLICATION NUMBER: PM0284 (AU)  
FILING DATE: 23-DEC-1994  
APPLICATION NUMBER: US 08/388,353  
FILING DATE: 14-FEB-1995  
APPLICATION NUMBER: PM3021/95  
FILING DATE: 17-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: FRANK S. DIGIGLIO  
REFERENCE/DOCKET NUMBER: 96062  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
INFORMATION FOR SEQ ID NO: 644:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 206 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-551B-644

Query Match 49.4%; Score 1115; DB 3; Length 206;  
Best Local Similarity 98.1%; Pred. No. 1.6e-104;  
Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 110 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169  
Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKHGAITSSNTAANNAACAWLEA 60  
Qy 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDWIYHTQGY 229  
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDWIYHTQGY 120  
Qy 230 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPSVSLHGMDPPEREV 289  
Db 121 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPSVSLHGMDPPEREV 180  
Qy 290 LEWRFDSRLAFHHVARELHPEYFKNC 315  
Db 181 LEWRFDSRLAFHHVARELHPEYFKNC 206  
RESULT 4  
US-08-679-493A-75  
Sequence 75, Application US/08679493A  
Patent No. 6303295  
GENERAL INFORMATION:  
APPLICANT: Taylor, Ethan W.  
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
FILE REFERENCE: 55-95

;; CURRENT APPLICATION NUMBER: US/08/679,493A  
;; CURRENT FILING DATE: 1996-07-12  
;; PRIOR APPLICATION NUMBER: 60/001203  
;; PRIOR FILING DATE: 1993-07-14  
;; PRIOR APPLICATION NUMBER: 60/003,112  
;; PRIOR FILING DATE: 1995-09-01  
;; NUMBER OF SEQ ID NOS: 216  
;; SOFTWARE: Patent in Ver. 2.0  
;; SEQ ID NO 75  
;; LENGTH: 206  
;; TYPE: PRT  
;; ORGANISM: Human immunodeficiency virus type 1  
;; NAME/KEY: VARIANT  
;; LOCATION: (1)..(206)  
;; OTHER INFORMATION: X is selenocysteine.  
US-08-679-493A-75

Query Match 43.1%; Score 971; DB 4; Length 206;  
Best Local Similarity 89.0%; Pred. No. 5.3e-90;  
Matches 186; Conservative 2; Mismatches 15; Indels 6; Gaps 3;  
QY 110 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169  
Db 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60  
QY 170 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLIHSQRDILDLYIHTQGY 226  
Db 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLIHSQRDILDLYIHTQGY 120  
QY 227 QGFPDQWNTPGVRYPLTFGWCYKLVPEPDKEVEANKGENTSLLLHPVSLHGMDDE 286  
Db 119 R-LLPDQWNTPGVRYPLTFGWCYKLVPEPDKEVEANKGENTSLLLHPVSLHGMDDE 177  
QY 287 REVLEWRFDSRLAFHVAHELHPEYKNC 315  
Db 178 REVLEWRFDSRLAFHVAHELHPEYKNC 206

RESULT 5  
US-09-124-900-10  
;; Sequence 10, Application US/09124900  
;; Patent No. 6268484  
;; GENERAL INFORMATION:  
;; APPLICANT: KATINGER, Hermann  
;; APPLICANT: BUCHACHER, Andrea  
;; APPLICANT: ERNST, Wolfgang  
;; APPLICANT: BALLAUN, Claudia  
;; APPLICANT: PURTSCHER, Martin  
;; APPLICANT: TRKOLA, Alexandra  
;; APPLICANT: PREDL, Renate  
;; APPLICANT: SCHMATZ, Christine  
;; APPLICANT: KLIMA, Annelies  
;; APPLICANT: STEINDL, Franz  
;; APPLICANT: MÜSTER, Thomas  
;; TITLE OF INVENTION: HIV-Vaccines  
;; FILE REFERENCE: 1939-112P  
;; CURRENT APPLICATION NUMBER: US/09/124,900  
;; CURRENT FILING DATE: 1998-07-30  
;; PRIOR APPLICATION NUMBER: PCT/EP95/01481  
;; PRIOR FILING DATE: 1995-04-19  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: Patent in version 3.0  
;; SEQ ID NO 10  
;; LENGTH: 123  
;; TYPE: PRT  
;; ORGANISM: Human immunodeficiency virus type 1  
US-09-124-900-10

Query Match 28.3%; Score 638; DB 4; Length 123;  
Best Local Similarity 97.6%; Pred. No. 9.3e-57;

Matches 120; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 110 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169  
Db 1 MGGKWSKSSVVGWPAVVRMRRAEPAADGVGAASRDLEKHGAITSSNTAANADCAWLEA 60  
QY 170 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLIHSQRDILDLYIHTQGY 229  
Db 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLIHSQRDILDLYIHTQGY 120  
QY 230 FPD 232  
Db 121 FPD 123  
RESULT 6  
US-09-485-885-21  
;; Sequence 21, Application US/09485885  
;; Patent No. 6342224  
;; GENERAL INFORMATION:  
;; APPLICANT: Bruck, Claudine  
;; APPLICANT: Cabezon Silva, Teresa  
;; APPLICANT: Delisse, Anne-Marie Eva Fernande  
;; APPLICANT: Gerard, Catherine Marie Ghislaine  
;; APPLICANT: Lombardo-Bencheikh, Angela  
;; TITLE OF INVENTION: Vaccine  
;; FILE REFERENCE: B45107  
;; CURRENT APPLICATION NUMBER: US/09/485,885  
;; CURRENT FILING DATE: 2000-02-18  
;; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
;; PRIOR FILING DATE: 1998-08-17  
;; PRIOR APPLICATION NUMBER: GB 9717953.5  
;; PRIOR FILING DATE: 1997-08-22  
;; NUMBER OF SEQ ID NOS: 23  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 21  
;; LENGTH: 278  
;; TYPE: PRT  
;; ORGANISM: Homo sapien  
US-09-485-885-21

Query Match 26.0%; Score 585.5; DB 4; Length 278;  
Best Local Similarity 36.0%; Pred. No. 6e-51;  
Matches 155; Conservative 26; Mismatches 73; Indels 177; Gaps 12;  
QY 2 SSSSSNNANTQMSDKIIIAHRCASGYLPHTLESKALAFQAQADYLEQDLAMTKDGLRV 61  
Db 4 SSSSSNNANTQMSDKIIIAHRCASGYLPHTLESKALAFQAQADYLEQDLAMTKDGLRV 63  
QY 62 VIHDFLDGLTDVAKFPFHRKDGRIYVDFTLKEIQSLEMTENFETMGKWSKSSVWG 121  
Db 64 VIHDFLDGLTDVAKFPFHRKDGRIYVDFTLKEIQSLEMTENFETMA----- 113  
QY 122 WPTVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATN--AACAW-----LEAQEEEEV 175  
Db 114 -----REFDP-----TRRYPKLPDLCTELNTSLQDIEITCYCKVTELVTEFEF 158  
QY 176 GFPVTPQVPLRPMTYKAADVLSHFLKEKGLIHSQRDILDLYIHTQGYFPDQW 235  
Db 159 AFK-----DLFVY----- 167  
QY 236 YTPGPGVRYPLTFGWCYKLV-----PVEPDKEE-ANKGENTSLLLHPVSLH 280  
Db 168 -----RDSIPHAACHKIDFYSRIRLHRYSDSVYGDTLKLTNTGLYNLLIRLCRCQ 220  
QY 281 GMDPPERVLEWRFDSRLAFHVAHELHPEYKNCISEPVDPRLEKHPGSKPTACTN 340  
Db 221 KPLNPAEKLR--HLNEKRREHNIAGHYRGO----- 248  
QY 341 CYCKKCCFHQCQVFITKALGISYGRKKRRRRRPPGOSQTHQVSLSKQPTSQSRGDDTGP 400  
Db 249 --CHSC-----NRAQERLORRRETQ----- 268

QY 401 KETSGHHHHH 411  
Db 269 -VTSGHHHHH 278

## RESULT 7

US-09-485-885-23  
; Sequence 23, Application US/09485885  
; Patent No. 6342224  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/09/485,885  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 23  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-485-885-23

Query Match 25.78; Score 579; DB 4; Length 383;

Best Local Similarity 34.58; Pred. No. 4.4e-50;

Matches 167; Conservative 21; Mismatches 118; Indels 178; Gaps 11;

QY 2 SSSSNMANTOMKSDKIIIAHAGSGYLPHTLESKALAFQAQADYLEODLMTKDGRLV 61  
Db 4 SSSSNMANTOMKSDKIIIAHAGSGYLPHTLESKALAFQAQADYLEODLMTKDGRLV 63  
QY 62 VIHDFLDGLTDVAKKFPHRHRKDGYYVIDFTLKEIOSLEMTENFETMGG----- 112  
Db 64 VIHDFLDGLTDVAKKFPHRHRKDGYYVIDFTLKEIOSLEMTENFETMARFEDPTRPY 123  
QY 113 -----KWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHKAIT- 154  
Db 124 KLPLDCLTELNTSLODIEITCYVCKTVLETFEFAFKDLFVYVYRDSIPHAACHKCIDFY 183  
QY 155 -----SNTAATNAACAWLEAQEEEEVEGFPVTPQVPLRPMYKAA 193  
Db 184 SPIRELHYSDVSGDTLEKLTNTGLYLLRLCLRCQK-----PLNPAEKLRLHNEK-- 235  
QY 194 VDSLHFLKEKGLEGLIHS---ORQDILDLYHTOGYFFPDWQNYTPGPGVRYPLTFGW 250  
Db 236 ---RRFHNIAHYRQCHSCCNRAQ----- 258  
QY 251 CYKLVPVFPDKEANKGENTSLH-----PVSL---HGMDPPRE 288  
Db 259 -----ERLQRRRETQVMHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEE 306  
QY 289 VLEWRDRLAPHHVARELHEP-YFKNCTSEPVDRLEPWRKPGSQPTACTNCYCKKCC 347  
Db 307 NDE--IDGVNHQHLPARAEQPHRTMLCMCKCKCEARIELVWESSADDLRAQOQLFNLTS 364  
QY 348 FHCQVCFITKALGISYGRKKRRRRPQGSQTHOVSLSKOPTSOSRGDPTGPKETSGHH 407  
Db 365 FVCPWC-----ASQOTSQGH 379  
QY 408 HHHH 411  
Db 380 HHHH 383

## RESULT 8

US-09-485-885-8  
; Sequence 8, Application US/09485885  
; Patent No. 6342224  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/09/485,885  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-485-885-8

Query Match 25.58; Score 576; DB 4; Length 220;

Best Local Similarity 66.58; Pred. No. 3.9e-50;

Matches 123; Conservative 9; Mismatches 27; Indels 26; Gaps 3;

QY 2 SSSSNMANTOMKSDKIIIAHAGSGYLPHTLESKALAFQAQADYLEODLMTKDGRLV 61  
Db 4 SSSSNMANTOMKSDKIIIAHAGSGYLPHTLESKALAFQAQADYLEODLMTKDGRLV 63  
QY 62 VIHDFLDGLTDVAKKFPHRHRKDGYYVIDFTLKEIOSLEMTENFETMGGKWSKSSVVG 121  
Db 64 VIHDFLDGLTDVAKKFPHRHRKDGYYVIDFTLKEIOSLEMTENFETMAMHGD----- 118  
QY 122 WPTVRERMRRAEPAADGVGAASRDLEKHKAITSSNTAATNAACAWLEAQEEEEVEGFPVTP 181  
Db 119 -PTLHMYLDLQP-----ETDLYGYQLNDS-----SEEDIDGPAGQ 157  
QY 182 QVPLR 186  
Db 158 AEPDR 162

## RESULT 9

US-09-485-885-1  
; Sequence 1, Application US/09485885  
; Patent No. 6342224  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/09/485,885  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: Homo sapien

US-09-485-885-1

Query Match 25.5%; Score 575; DB 4; Length 220;  
Best Local Similarity 66.5%; Pred. No. 4.9e-50;  
Matches 123; Conservative 9; Mismatches 27; Indels 26; Gaps 3;

QY 2 SSHSNMANTOMKSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEODLMTKDGRLV 61  
DB 4 SSHSNMANTOMKSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEODLMTKDGRLV 63  
QY 62 VIHDFDLGLTDVAKKFPFHRKRGYVYIDFTLKEIQSLEMTENFETMGKWSKSSVVG 121  
DB 64 VIHDFDLGLTDVAKKFPFHRKRGYVYIDFTLKEIQSLEMTENFETMAHMGDT----- 118  
QY 122 WPTVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEAOEEVEEVPFVTP 181  
DB 119 -PTLHEYMLDLP-----ETDLYCYELNDS-----SEEDIDGPAGQ 157  
QY 182 QVPLR 186  
DB 158 AEPDR 162

## RESULT 10

US-09-485-885-16  
; Sequence 16, Application US/09485885  
; Patent No. 6342224

## GENERAL INFORMATION:

; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine

; FILE REFERENCE: B45107

; CURRENT APPLICATION NUMBER: US/09/485,885

; CURRENT FILING DATE: 2000-02-18

; PRIOR APPLICATION NUMBER: PCT/EP98/05285

; PRIOR FILING DATE: 1998-08-17

; PRIOR APPLICATION NUMBER: GB 9717953.5

; PRIOR FILING DATE: 1997-08-22

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 16

; LENGTH: 227

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-485-885-16

Query Match 25.4%; Score 572; DB 4; Length 227;  
Best Local Similarity 36.5%; Pred. No. 1e-49;  
Matches 150; Conservative 14; Mismatches 59; Indels 188; Gaps 10;

QY 2 SSHSNMANTOMKSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEODLMTKDGRLV 61  
DB 4 SSHSNMANTOMKSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEODLMTKDGRLV 63  
QY 62 VIHDFDLGLTDVAKKFPFHRKRGYVYIDFTLKEIQSLEMTENFETMGKWSKSSVVG 121  
DB 64 VIHDFDLGLTDVAKKFPFHRKRGYVYIDFTLKEIQSLEMTENFETM----- 112  
QY 122 WPTVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEAOEEVEEVPFVTP 181  
DB 113 -----AMHGPKATLQDIVLH-----LEPONE----- 133  
QY 182 QVPLRMTYKAAVDLSHFLKEKGLSLSORRQDILDLIWYHGTGYPDQWNTYPPG 241  
DB 134 -IP-----VDL-----LCHQLSDS----- 147  
QY 242 VRYPLTFGWCYKLVVPEPKVEEANKGENTSLHHPVSLHGMDDPEREVLWRPDSLAPH 301

DB 148 -----EENDEIDEVN-----HQ-----H 161  
QY 302 HVARELHPE-YFNKCTSEPVDPLEPKHGPSQPKTACTNCKYCKKCFHCQVCFITKALG 360  
DB 162 LPARAEPRQHTMLCMCCCEARIELWESSADDLRAFOQLFNTLSFVCPWC----- 214  
QY 361 ISVGRKKRRORRRPPGSGQTHQVSLSKOPTSQSRGDPGPKETSGHHHHH 411  
DB 215 -----ASQOTSQHSHHHH 227

## RESULT 11

US-09-485-885-6  
; Sequence 6, Application US/09485885  
; Patent No. 6342224

## GENERAL INFORMATION:

; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine

; FILE REFERENCE: B45107

; CURRENT APPLICATION NUMBER: US/09/485,885

; CURRENT FILING DATE: 2000-02-18

; PRIOR APPLICATION NUMBER: PCT/EP98/05285

; PRIOR FILING DATE: 1998-08-17

; PRIOR APPLICATION NUMBER: GB 9717953.5

; PRIOR FILING DATE: 1997-08-22

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 6

; LENGTH: 371

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-485-885-6

Query Match 25.4%; Score 572; DB 4; Length 371;  
Best Local Similarity 34.5%; Pred. No. 2.1e-49;  
Matches 164; Conservative 27; Mismatches 112; Indels 172; Gaps 14;

QY 2 SSHSNMANTOMKSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEODLMTKDGRLV 61  
DB 4 SSHSNMANTOMKSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEODLMTKDGRLV 63  
QY 62 VIHDFDLGLTDVAKKFPFHRKRGYVYIDFTLKEIQSLEMTENFETMGKWSKSSVVG 121  
DB 64 VIHDFDLGLTDVAKKFPFHRKRGYVYIDFTLKEIQSLEMTENFETM-----AM 114  
QY 122 WPTVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEAOEEVEEVPFVTP 181  
DB 115 FQDQPRPRKLPOLCTELOTTIHI-----ILECVYCKQ----- 149  
QY 182 QVPLRMTYKAAVDLSHFLKEKGLSLSORRQDILDLIWYHGTG-----YF 230  
DB 150 --LLREVIDFA-----FRDLCIVIRGDNVPYAVCDKCLKFY 183  
QY 231 PQWNTYTPGVRGYPLTFGWCYKLVVPEPKVEEANKGENTSLHHPVSLHGMDDPEREVL 290  
DB 184 SKTSEYR-----HYCYSYLTLE--QYKPKCLDLLIRINCQKPLCPKEK-- 228  
QY 291 EWRFDRLAFHHVARELHPEYFNKCTSEPVDPRL-----PWKHP-----GSQPKTACTNC 341  
DB 229 QRHLDDKQRFHNRGRWTRGCMSCCRSSRRRTQMLHMGDTPTLHEYMLDLPETDLYC 288  
QY 342 Y-----CKKCCFHCQVC-----FIT 356  
DB 289 YEOLNDSSEEDIDGPAGOAEPDRAHYNIIVTFCCCKDSTLRLCVQSTHVIDIFLTLDM 348  
QY 357 KALGISYGRKKRRQRRPPGSGQTHQVSLSKOPTSQSRGDPGPKETSGHHHHH 411  
DB 349 GTLGIVC-----PICSQ-----KFTSGHHHHH 371



```
RESULT 12
US-09-485-885-19
; Sequence 19, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fermande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485, 885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-19

Query Match      25.2%; Score 569; DB 4; Length 227;
Best Local Similarity 36.3%; Pred. No. 2,1e-49;
Matches 149; Conservative 15; Mismatches 59; Indels 188; Gaps 9;

QY 2 SSSSNMANTQKSDKIIIAHNGASGYLPENTLESKALAFQAQADYLEODLMTKDGRLV 61
DB 4 SSSSNMANTQKSDKIIIAHNGASGYLPENTLESKALAFQAQADYLEODLMTKDGRLV 63
QY 62 VINDHFLDGLTDVAKKFPRIHRRKDGRIYVIDFTLKEIQSLKTEMTENFTNGKWKSSVYG 121
DB 64 VINDHFLDGLTDVAKKFPRIHRRKDGRIYVIDFTLKEIQSLKTEMTENFTNGKWKSSVYG 112
QY 122 WPTVERMRAPADGVGAASRDLEKNGALITSSNTAATNACAMLEAEDEEVEGPRVTP 181
DB 113 -----AMHGRKATLDIVLA-----LEPONE----- 133
QY 182 QVLRPMYTKAANDLSHFLKEKGLGEGLIHSORRODILDLWYHTOGYPRDMQNTYPRG 241
DB 134 -IP-----VDLL-----GHQQLSDSEENDEID-----G 156
QY 242 VKRPLTFGCYKLVPRVDKVEANKGENTSLIHVSLHGMDDREVELMWRDRLAHN 301
DB 157 VNHQ-----H 161
QY 302 HVARELHPRE-YFNKCTSEVPDRLEPMKHNRSOPKTACTNCKSCSPHOCVFITKALG 360
DB 162 LPARRAEPOHNYMLWCSCSEARIELVESSADLRAFOOLFNTLSFVCRWC----- 214
QY 361 ISYGRKKRRORRRPQSGTQHOVSLSKOPTSQRGDPRTPKETSGHNNH 411
DB 215 -----ASQQTSGHNNH 227

RESULT 13
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fermande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine

FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485, 885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match      25.0%; Score 564; DB 4; Length 273;
Best Local Similarity 35.9%; Pred. No. 8,6e-49;
Matches 151; Conservative 24; Mismatches 84; Indels 162; Gaps 12;

QY 2 SSSSNMANTQKSDKIIIAHNGASGYLPENTLESKALAFQAQADYLEODLMTKDGRLV 61
DB 4 SSSSNMANTQKSDKIIIAHNGASGYLPENTLESKALAFQAQADYLEODLMTKDGRLV 63
QY 62 VINDHFLDGLTDVAKKFPRIHRRKDGRIYVIDFTLKEIQSLKTEMTENFTNGKWKSSVYG 121
DB 64 VINDHFLDGLTDVAKKFPRIHRRKDGRIYVIDFTLKEIQSLKTEMTENFTNGKWKSSVYG 114
QY 122 WPTVERMRAPADGVGAASRDLEKNGALITSSNTAATNACAMLEAEDEEVEGPRVTP 181
DB 115 FDDPOERPKKLQOLTELDTTHDI-----ILECVICKOO----- 149
QY 182 QVLRPMYTKAANDLSHFLKEKGLGEGLIHSORRODILDLWYHTOG-----YF 230
DB 150 --LIREYVDF-----FRDLCTIVYRDGNPVAVCDKCLKFY 183
QY 231 PDMQNTYPRGVRYPPLTFGCYKLVPRVDKVEANKGENTSLIHVSLHGMDDREVEL 290
DB 184 SKISER-----HYCYSYLTGLE--QYKPKLDDLIRINOKPLCPREK-- 228
QY 291 EWRFDRLAHNVARELHPREYFNKCTSEVPDRLEPMKHNRSOPKTACTNCKSCSPHNC 350
DB 229 QHNLDKKORFHNIRG-----W-----TGCMSC----- 253
QY 351 QVCFITKALGISYGRKKRRORRRPQSGTQHOVSLSKOPTSQRGDPRTPKETSGHNNH 410
DB 254 -----RSSRTRE-----TOLTSGHNNH 272
QY 411 H 411
DB 273 H 273

RESULT 14
US-08-679-493A-74
; Sequence 74, Application US/08679493A
; Patent No. 6303295
; GENERAL INFORMATION:
; APPLICANT: Taylor, Ethan W.
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
; FILE REFERENCE: 55-95
; CURRENT APPLICATION NUMBER: US/08/679,493A
; CURRENT FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 60/001203
; PRIOR FILING DATE: 1995-07-14
; PRIOR APPLICATION NUMBER: 60/003,112
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 74
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
```

FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1), (151)  
OTHER INFORMATION: X is selenocysteine.  
US-08-679-493A-74

Query Match 22.1%; Score 498.5; DB 4; Length 151;  
Best Local Similarity 73.0%; Pred. No. 1.5e-42;  
Matches 103; Conservative 4; Mismatches 7; Indels 27; Gaps 3;  
QY 110 MGKWKSSVGVPTVRRMRRAEPAADGGAASRDLEKHGAISSNTAATNAACAWLEA 169  
DB 1 MGKWKSSVGVPTVRRMRRAEPAADGGAASRDLEKHGAISSNTAATNAACAWLEA 60  
QY 170 QEEVEGVFTVQVPLRPMTYAAVDLSHFLKEKGG----- 205  
DB 61 QEEVEGVFTVQVPLRPMTYAAVDLSHFLKEKGGTGRANSLPTKTRYPXSVLDLPHRL 120  
QY 206 LEG--IHSORRODI-LDLWI 223  
DB 121 LPXLAELHTRARGGISTDLWM 141

RESULT 15

US-08-450-257-1  
Sequence 1, Application US/08450257  
Patent No. 5652122  
GENERAL INFORMATION:  
APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOUM, James G.  
APPLICANT: FAWELL, Stephen E.  
APPLICANT: PEPINSKY, R. B.  
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,257  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLSCULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: human immunodeficiency virus  
STRAIN: type 1  
US-08-450-257-1

Query Match 21.6%; Score 486; DB 1; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.2e-41;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 EPVDPRLEPKHGPSQPKTACTNCKYCKCFHCQVCFITKALGISYGRKKRRRRPPQG 377  
DB 2 EPVDPRLEPKHGPSQPKTACTNCKYCKCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
QY 378 SOTHQVSLSKQPTSQSRGDPGPK 402  
DB 62 SOTHQVSLSKQPTSQSRGDPGPK 86

RESULT 16

US-08-450-246-1  
Sequence 1, Application US/08450246  
Patent No. 5670617  
GENERAL INFORMATION:  
APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOUM, James G.  
APPLICANT: FAWELL, Stephen E.  
APPLICANT: PEPINSKY, R. B.  
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,246  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE: human immunodeficiency virus  
STRAIN: type 1  
US-08-450-246-1

Query Match 21.6%; Score 486; DB 1; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.2e-41;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 318 EPVDPRLPEPKHGPSQPKTACTNCTCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 377  
DB 2 EPVDPRLPEPKHGPSQPKTACTNCTCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
QY 378 SOTHQVSLSKOPTSQSRGDPGPK 402  
DB 62 SOTHQVSLSKOPTSQSRGDPGPK 86

RESULT 17  
US-08-450-098-1  
Sequence 1, Application US/08450098  
Patent No. 5674980  
GENERAL INFORMATION:  
APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOUM, James G.  
APPLICANT: FAWELL, Stephen E.  
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450.098  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE: human immunodeficiency virus  
STRAIN: type 1  
US-08-450-098-1  
Query Match 21.6%; Score 486; DB 1; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.2e-41;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 318 EPVDPRLPEPKHGPSQPKTACTNCTCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 377  
DB 2 EPVDPRLPEPKHGPSQPKTACTNCTCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
QY 378 SOTHQVSLSKOPTSQSRGDPGPK 402  
DB 62 SOTHQVSLSKOPTSQSRGDPGPK 86

RESULT 18  
US-08-451-233-1  
Sequence 1, Application US/08451233  
Patent No. 5747641  
GENERAL INFORMATION:  
APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOUM, James G.  
APPLICANT: FAWELL, Stephen E.  
APPLICANT: PEPINSKY, R. B.  
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451.233  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662

```

; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: human immunodeficiency virus
; STRAIN: type 1
; US-08-451-233-1

Query Match          21.6%; Score 486; DB 1; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-41;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 EPVDRLPEPKHPGQPKTACTNCYKCCFHCQVCFITKALGISYGRKKRRRRPPQG 377
Db 2 EPVDRLPEPKHPGQPKTACTNCYKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61
QY 378 SOTHQVSLSKQPTSQSRGDPGPK 402
Db 62 SOTHQVSLSKQPTSQSRGDPGPK 86

RESULT 19
US-08-450-236-1
; Sequence 1, Application US/08450236
; Patent No. 5804604
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPIISKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,236
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993

; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: human immunodeficiency virus
; STRAIN: type 1
; US-08-450-236-1

Query Match          21.6%; Score 486; DB 1; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-41;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 EPVDRLPEPKHPGQPKTACTNCYKCCFHCQVCFITKALGISYGRKKRRRRPPQG 377
Db 2 EPVDRLPEPKHPGQPKTACTNCYKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61
QY 378 SOTHQVSLSKQPTSQSRGDPGPK 402
Db 62 SOTHQVSLSKQPTSQSRGDPGPK 86

RESULT 20
US-07-808-452-1
; Sequence 1, Application US/07808452
; Patent No. 6063612
; GENERAL INFORMATION:
; APPLICANT: Jayasena, Sumedha D.
; APPLICANT: Johnston, Brian H.
; TITLE OF INVENTION: Antiviral Reagents Based on
; TITLE OF INVENTION: RNA-Binding Proteins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/808,452
; FILING DATE: 19911213
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8255-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 1:
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SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: the sequence of the TAT protein of  
INDIVIDUAL ISOLATE: HIV-1  
US-07-808-452-1

Query Match 21.6%; Score 486; DB 3; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.2e-41;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 EPVDPRLPFWKHGSPQKPTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPOG 377  
|||||

Db 2 EPVDPRLPFWKHGSPQKPTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPOG 61  
|||||

QY 378 SOTHQVSLSKQPTSSRGDPTGPK 402  
|||||

Db 62 SOTHQVSLSKQPTSSRGDPTGPK 86  
|||||

RESULT 21  
US-09-030-613-19  
Sequence 19, Application US/09030613  
Patent No. 6083706  
GENERAL INFORMATION:  
APPLICANT: FlorKiewicz, Robert Z.  
APPLICANT: Baird, J. Andrew  
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030.613  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6083706tendrup Ph.D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 760100.418C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-030-613-19

Query Match 21.6%; Score 486; DB 3; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.2e-41;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 EPVDPRLPFWKHGSPQKPTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPOG 377  
|||||

Db 2 EPVDPRLPFWKHGSPQKPTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPOG 61  
QY 378 SOTHQVSLSKQPTSSRGDPTGPK 402  
|||||

Db 62 SOTHQVSLSKQPTSSRGDPTGPK 86  
|||||

RESULT 22  
US-09-124-900-6  
Sequence 6, Application US/09124900  
Patent No. 6268484  
GENERAL INFORMATION:  
APPLICANT: KATINGER, Hermann  
APPLICANT: BUCHACHER, Andrea  
APPLICANT: ERNST, Wolfgang  
APPLICANT: BALLAUN, Claudia  
APPLICANT: PUTSCHER, Martin  
APPLICANT: TRKOLA, Alexandra  
APPLICANT: PREDL, Renate  
APPLICANT: SCHWATZ, Christine  
APPLICANT: KLIMA, Annelies  
APPLICANT: STEINDL, Franz  
APPLICANT: MUSTER, Thomas  
TITLE OF INVENTION: HIV-Vaccines  
FILE REFERENCE: 1939-112P  
CURRENT APPLICATION NUMBER: US/09/124.900  
CURRENT FILING DATE: 1998-07-30  
PRIOR APPLICATION NUMBER: PCT/EP95/01481  
PRIOR FILING DATE: 1995-04-19  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6  
LENGTH: 86  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-124-900-6

Query Match 21.6%; Score 486; DB 4; Length 85;  
Best Local Similarity 100.0%; Pred. No. 1.2e-41;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 EPVDPRLPFWKHGSPQKPTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPOG 377  
|||||

Db 2 EPVDPRLPFWKHGSPQKPTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPOG 61  
|||||

QY 378 SOTHQVSLSKQPTSSRGDPTGPK 402  
|||||

Db 62 SOTHQVSLSKQPTSSRGDPTGPK 86  
|||||

RESULT 23  
US-09-451-905-19  
Sequence 19, Application US/09451905  
Patent No. 6306613  
GENERAL INFORMATION:  
APPLICANT: Robert Z. FlorKiewicz  
APPLICANT: Andrew Baird  
APPLICANT: Dale E. Warnock  
TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT  
TITLE OF INVENTION: AND METHODS FOR IDENTIFYING AND USING THE SAME  
FILE REFERENCE: 200124.402C4  
CURRENT APPLICATION NUMBER: US/09/451.905  
CURRENT FILING DATE: 1999-12-01  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 19  
LENGTH: 86  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-451-905-19

Query Match 21.6%; Score 486; DB 4; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.2e-41;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 EPVDPRLPEPKHGPSQPKTACTNCKYCKKCCFHQCVCFITKALGISYGRKKRRRRPPQG 377  
|||||  
Db 2 EPVDPRLPEPKHGPSQPKTACTNCKYCKKCCFHQCVCFITKALGISYGRKKRRRRPPQG 61  
|||||

QY 378 SOTHQVSLSKQPTSQSRGDPGPK 402  
|||||  
Db 62 SOTHQVSLSKQPTSQSRGDPGPK 86  
|||||

RESULT 24  
US-08-235-403-1  
; Sequence 1, Application US/08235403  
; Patent No. 6316003  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: PABO, Carl  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: FAWELL, Stephen E.  
; APPLICANT: PEPINSKY, R. B.  
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/235,403  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/7934,375  
; FILING DATE: 21-AUG-1992  
; APPLICATION NUMBER: US/07098,766  
; FILING DATE: 28-JUL-1993  
; APPLICATION NUMBER: PCT/US93/07833  
; FILING DATE: 19-AUG-1993  
; APPLICATION NUMBER: US/07454,450  
; FILING DATE: 21-DEC-1989  
; APPLICATION NUMBER: US/07636,662  
; FILING DATE: 02-JAN-1991  
; APPLICATION NUMBER: US/08/158,015  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B170 CIP 2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 86 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: human immunodeficiency virus  
; STRAIN: type 1  
US-08-235-403-1

Query Match 21.6%; Score 486; DB 4; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.2e-41;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 EPVDPRLPEPKHGPSQPKTACTNCKYCKKCCFHQCVCFITKALGISYGRKKRRRRPPQG 377  
|||||  
Db 2 EPVDPRLPEPKHGPSQPKTACTNCKYCKKCCFHQCVCFITKALGISYGRKKRRRRPPQG 61  
|||||

QY 378 SOTHQVSLSKQPTSQSRGDPGPK 402  
|||||  
Db 62 SOTHQVSLSKQPTSQSRGDPGPK 86  
|||||

RESULT 25  
PCT-US92-10770-1  
; Sequence 1, Application PC/TUS9210770  
; GENERAL INFORMATION:  
; APPLICANT: Jayasena, Slumedha D.  
; APPLICANT: Johnston, Brian H.  
; TITLE OF INVENTION: Antiviral Reagents Based on  
; TITLE OF INVENTION: RNA-Binding Proteins  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SRI International  
; STREET: 333 Ravenswood Avenue  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/10770  
; FILING DATE: 19921211  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/808,452  
; FILING DATE: 13-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fabian, Gary R.  
; REGISTRATION NUMBER: 33,875  
; REFERENCE/DOCKET NUMBER: P-2962  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 859-4550  
; TELEFAX: (415) 859-3880  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 86 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: the sequence of the TAT protein of  
; INDIVIDUAL ISOLATE: HIV-1  
PCT-US92-10770-1

Query Match 21.6%; Score 486; DB 5; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.2e-41;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 EPVDPRLPEPKHGPSQPKTACTNCKYCKKCCFHQCVCFITKALGISYGRKKRRRRPPQG 377  
|||||  
Db 2 EPVDPRLPEPKHGPSQPKTACTNCKYCKKCCFHQCVCFITKALGISYGRKKRRRRPPQG 61  
|||||

QY 378 SOTHQVSLSKQPTSQSRGDPGPK 402  
|||||

Db 62 SOTHVSLSKQPTSQSRGDPGPK 86

RESULT 26  
PCT-US95-06077-2  
Sequence 2, Application PC/TUS9506077  
GENERAL INFORMATION:  
APPLICANT: Immunobiology Research, Institute Inc.  
TITLE OF INVENTION: Vaccine Interdiction of Extracellular  
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus  
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar  
TITLE OF INVENTION: Intercellular Transactivating Strategies  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr, PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/06077  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/247,991  
FILING DATE: 23-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: IRI44PCT  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-06077-2

Query Match 21.6%; Score 486; DB 5; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.2e-41;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 EPVDPLEPKHPGSPKACTNCKYCKCFHCQVCFITKALGISYGRKKRRRRPPQG 377  
|||||  
Db 2 EPVDPLEPKHPGSPKACTNCKYCKCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
|||||

QY 378 SOTHVSLSKQPTSQSRGDPGPK 402  
Db 62 SOTHVSLSKQPTSQSRGDPGPK 86

RESULT 27  
US-08-815-809-5  
Sequence 5, Application US/08815809  
Patent No. 6004777  
GENERAL INFORMATION:  
APPLICANT: TARTAGLIA, James  
APPLICANT: GOEBEL, Scott J.  
APPLICANT: COX, William I.  
APPLICANT: GETTIG, Russell R.  
APPLICANT: PINCUS, Steven E.  
APPLICANT: PAOLETTI, Enzo  
APPLICANT: JACOBS, Bertram L.

; TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND METHODS OF  
; TITLE OF INVENTION: MAKING AND USES THEREOF  
; FILE REFERENCE: 454310-3010  
; CURRENT APPLICATION NUMBER: US/08/815,809  
; CURRENT FILING DATE: 1997-03-12  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 266  
; TYPE: PRT  
; ORGANISM: Vaccinia virus  
US-08-815-809-5

Query Match 21.2%; Score 478.5; DB 3; Length 266;  
Best Local Similarity 77.3%; Pred. No. 3.5e-40;  
Matches 92; Conservative 4; Mismatches 6; Indels 17; Gaps 4;

QY 175 VGFPTVPOVPLRPMYKAAVDLSHFLKKGGLGTHSRRQDILDLYHTQGYFPDQW 234  
Db 136 VGFPTVPOVPLRPMYKAAVDLSHFLKKGGLGTHSRRQDILDLYHTQGYFPDQW 195  
QY 235 NYTPGPGVRYPLTFGWCYKLVPEPKVEANKGENTSLLLHPVSLH-GMDDPEREYLEW 292  
Db 196 NYTPGPGVRYPLTFGWCYKLVPM-----IETV-----PVKLPKGMGDP--KVQW 238

RESULT 28  
US-08-816-155B-43  
Sequence 43, Application US/08816155B  
Patent No. 5990091  
GENERAL INFORMATION:  
APPLICANT: TARTAGLIA, JAMES  
APPLICANT: COX, WILLIAM I.  
APPLICANT: GETTIG, RUSSELL R.  
APPLICANT: MARTINEZ, HECTOR  
APPLICANT: PAOLETTI, ENZO  
APPLICANT: PINCUS, STEVEN E.  
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND  
TITLE OF INVENTION: METHODS OF MAKING AND USES THEREOF  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10151  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,155B  
FILING DATE: 12-MAR-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: KOWALSKI, THOMAS J.  
REGISTRATION NUMBER: 32,147  
REFERENCE/DOCKET NUMBER: 454310-2990  
TELEPHONE: 212-588-0800  
TELEFAX: 212-588-0500  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 280 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: amino acid  
US-08-816-155B-43

Query Match 21.2%; Score 478.5; DB 2; Length 280;  
Best Local Similarity 77.3%; Pred. No. 3.7e-40;  
Matches 92; Conservative 4; Mismatches 6; Indels 17; Gaps 4;

QY 175 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLIHSQRQDILDLIWIHTQGYFFPDWQ 234  
|||||  
DB 150 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLIHSQRQDILDLIWIHTQGYFFPDWQ 209  
|||||

QY 235 NYTPGPGVRYPLTFGWCYKLVPEPDKVEANKGENTSLLLHPVSLH-GMDDPEREVLW 292  
|||||  
DB 210 NYTPGPGVRYPLTFGWCYKLVPEPDKVEANKGENTSLLLHPVSLH-GMDDPEREVLW 252  
|||||

RESULT 29  
US-09-079-587-43  
; Sequence 43, Application US/09079587  
; Patent No. 6130066  
; GENERAL INFORMATION:  
; APPLICANT: TARTAGLIA, JAMES  
; APPLICANT: COX, WILLIAM I.  
; APPLICANT: GETTIG, RUSSELL R.  
; APPLICANT: MARTINEZ, HECTOR  
; APPLICANT: PAOLETTI, ENZO  
; APPLICANT: PINCUS, STEVEN E.  
; TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND  
; TITLE OF INVENTION: METHODS OF MAKING AND USES THEREOF  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FROMMER LAWRENCE & HAUG LLP  
; STREET: 745 FIFTH AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10151  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,587  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/816,155  
; FILING DATE: 12-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOHALSKI, THOMAS J.  
; REGISTRATION NUMBER: 32,147  
; REFERENCE/DOCKET NUMBER: 454310-2990  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-588-0800  
; TELEFAX: 212-588-0500  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 280 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: n/a  
; TOPOLOGY: linear  
; MOLECULE TYPE: amino acid  
US-09-079-587-43

Query Match 21.2%; Score 478.5; DB 4; Length 280;  
Best Local Similarity 77.3%; Pred. No. 3.7e-40;  
Matches 92; Conservative 4; Mismatches 6; Indels 17; Gaps 4;

QY 175 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLIHSQRQDILDLIWIHTQGYFFPDWQ 234  
|||||  
DB 150 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLIHSQRQDILDLIWIHTQGYFFPDWQ 209  
|||||

QY 235 NYTPGPGVRYPLTFGWCYKLVPEPDKVEANKGENTSLLLHPVSLH-GMDDPEREVLW 292  
|||||

DB 210 NYTPGPGVRYPLTFGWCYKLVPEPDKVEANKGENTSLLLHPVSLH-GMDDPEREVLW 252  
|||||

RESULT 30  
US-08-505-210-1  
; Sequence 1, Application US/08505210  
; Patent No. 5981258  
; GENERAL INFORMATION:  
; APPLICANT: MEHTALI, Majid  
; APPLICANT: GUSS, Tania  
; TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS  
; TITLE OF INVENTION: OF VIRAL PROTEINS FOR OBTAINING AN ANTIVIRAL EFFECT  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
; STREET: 1737 King Street, Suite 500  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22314-2756  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/505,210  
; FILING DATE: 14-AUG-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,248  
; FILING DATE: 21-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR94/01457  
; FILING DATE: 13-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Radio, Susan M.  
; REGISTRATION NUMBER: 40,373  
; REFERENCE/DOCKET NUMBER: 017753-066  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 86 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Human immunodeficiency virus type 1  
; STRAIN: Lai  
; INDIVIDUAL ISOLATE: sequence of the TAT protein of HIV-1  
US-08-505-210-1

Query Match 20.8%; Score 470; DB 2; Length 86;  
Best Local Similarity 96.5%; Pred. No. 4.8e-40;  
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 318 EPVDPRLPEPKHPSQPKTACTNCKYKCCFHCQVCFITKALGTSYGRKKRRRRPPQG 377  
|||||

DB 2 EPVDPRLPEPKHPSQPKTACTNCKYKCCFHCQVCFITKALGTSYGRKKRRRRPPQG 61  
|||||

QY 378 SQTHQVSLSKOPTSQSRGDPDTPGKE 402  
|||||

DB 62 SQTHQVSLSKOPTSQSRGDPDTPGKE 86  
|||||



Mon Aug 26 09:05:50 2002

us-09-509-239-17.rai

Page 14

Search completed: August 26, 2002, 08:10:40  
Job time: 129 sec

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: August 26, 2002, 08:13:21 ; Search time 50.45 Seconds  
(without alignments)  
782.809 Million cell updates/sec

Title: US-09-509-239-17

Perfect score: 2255

Sequence: 1 CSSHSSNANTQMSKDKIII.....QSRGDPCTPKETSGHHHHH 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5.

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR71:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1130	50.1	206	1 ASLJFV	nef protein - huma
2	1115	49.4	205	2 S43467	nef protein - huma
3	1115	49.4	206	2 S03244	nef protein (clone
4	1114	49.4	206	1 ASLJVL	nef protein - huma
5	1108	49.1	206	1 ASLJ12	nef protein - huma
6	1097	48.6	206	2 JC3400	nef protein (clone
7	1096	48.6	206	2 S03245	nef protein - huma
8	1081.5	48.0	205	1 ASLJH3	nef protein - huma
9	1019	45.2	204	2 S24985	nef protein - huma
10	1019	45.2	204	2 S24985	nef protein - huma
11	1019	45.2	204	1 ASLJBR	nef protein - huma
12	1007	44.7	206	2 S25937	nef protein - huma
13	997	44.2	210	1 ASLJ02	nef protein - huma
14	991.5	44.0	214	1 I44J01	nef protein - huma
15	987	43.8	182	2 S03247	nef protein (clone
16	987	43.8	204	2 S03246	nef protein (clone
17	911	40.4	212	1 QQLJZR	nef protein - huma
18	903.5	40.1	207	1 QQLJND	nef protein - huma
19	837	37.1	205	1 B44963	nef protein - huma
20	834.5	37.0	209	2 T01673	nef protein - huma
21	832	36.9	205	1 ASLJIK	nef protein - huma
22	578.5	25.7	364	2 S59931	glycerophosphodies
23	578.5	25.7	364	2 S59932	glycerophosphodies
24	578.5	25.7	364	2 A43576	glycerophosphodies
25	578.5	25.7	364	2 S59934	glycerophosphodies
26	572.5	25.4	364	2 S59933	glycerophosphodies
27	562.5	24.9	364	2 G64086	glycerophosphodies
28	556.5	24.7	364	2 S59936	glycerophosphodies
29	486	21.6	86	2 S33982	trans-activating t

30	478	21.2	95	1 TNLJ12	trans-activating t
31	470	20.8	86	2 A25700	trans-activating t
32	443	19.6	226	2 S46353	nef protein - simi
33	439.5	19.5	97	2 S54385	nef protein - huma
34	437	19.4	101	2 T09446	tat protein - huma
35	434	19.2	101	1 E44001	trans-activating t
36	429.5	19.0	309	2 S07993	nef protein - simi
37	426.5	18.9	259	2 T11567	nef protein - simi
38	421.5	18.7	255	2 S53099	nef protein - huma
39	421	18.7	257	2 S12160	nef protein - huma
40	413	18.3	260	1 ASLJJCZ	nef protein - huma
41	411.5	18.2	263	2 T11556	nef protein - simi
42	411	18.2	86	2 JC5591	transactivator pro
43	409	18.1	250	2 S54851	nef protein - simi
44	408	18.1	86	2 S54381	tat protein - huma
45	405	18.0	86	1 TNLJZR	trans-activating t

## ALIGNMENTS

RESULT 1

ASLJFV

nef protein - human immunodeficiency virus type 1 (isolate LAV-la)

N:Alternate names: 3'-orf protein; orf-F protein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: Host Homo sapiens (man)

C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999

C:Accession: A04008; S14609

R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Allison, M.

Cell 40, 9-17, 1985

A:Title: Nucleotide sequence of the AIDS virus, LAV.

A:Reference number: A90866; MUID:85099333

A:Accession: A04008

A:Molecule type: DNA

A:Residues: 1-206 &lt;NA&gt;

A:Cross-references: GB:K03013; NID:g326417; PIDN:AAB59752.1; PID:g326425

R:Experimental source: isolate LAV-la

R:Ciccarelli, R.B.

Submitted to the EMBL Data Library, March 1991

A:Reference number: S14607

A:Accession: S14609

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-206 &lt;CIC&gt;

A:Cross-references: EMBL:X58780; NID:g60113; PIDN:CAA41585.1; PID:g60114

C:Genetics:

A:Gene: nef; 3'-orf; orf-F

C:Superfamily: AIDS nef protein

C:Keywords: AIDS; immunodeficiency; phosphoprotein

Query Match 50.1%; Score 1130; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.2e-80; Mismatches 0; Indels 0; Gaps 0;  
Matches 206; Conservative 0;

QY 110 MGKSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGAITSSNTAATNAACAWLEA 169

Db 1 MGCKSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGAITSSNTAATNAACAWLEA 60

QY 170 QEEEVGFPVTPQVLRPMYTKAAVDLSHFLKEKGGLEGLIHSORRODILDLWIYHTQGY 229

Db 61 QEEEVGFPVTPQVLRPMYTKAAVDLSHFLKEKGGLEGLIHSORRODILDLWIYHTQGY 120

QY 230 FPDQNTYTPGVRYPITFGWCYKLVPEPDKVEEANKGENTSLHHPVSLHGMDPPREV 289

Db 121 FPDQNTYTPGVRYPITFGWCYKLVPEPDKVEEANKGENTSLHHPVSLHGMDPPREV 180

QY 290 LEWRFSRLAFHFAHVELHPEYFNC 315

Db 181 LEWRFSRLAFHFAHVELHPEYFNC 206

```
RESULT 2
S43467
nef protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C:Accession: S43467
R:Freund, J.; Kellner, R.; Houthaeve, T.; Kalbitzer, H.R.
Eur. J. Biochem. 221, 811-819, 1994
A:Title: Stability and proteolytic domains of Nef protein from human immunodeficiency vi
A:Reference number: S43467; MUID:94229079
A:Accession: S43467
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-205 <PRE>
C:Superfamily: AIDS nef protein

Query Match 49.4%; Score 1115; DB 2; Length 205;
Best Local Similarity 99.0%; Pred. No. 1.7e-79;
Matches 203; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 111 GKGWSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGATSSNTAATNAACAWLEA 170
|||||
Db 1 GKGWSSVVGWPAVRMRRAEPAADGVGAASRDLEKHGATSSNTAATNAACAWLEA 60
|||||

QY 171 EEEVGFVPTQVPLRPMTYKAAVDLSHFLKKGGLHSGRRQDILDLWIYHTQGYF 230
|||||
Db 61 EEEVGFVPTQVPLRPMTYKAAVDLSHFLKKGGLHSGRRQDILDLWIYHTQGYF 120
|||||

QY 231 PDQNTPTGPGVRYPLTFGCYKLVPEPDKVEANKGNTSLLHPVSLHGMDPDERVL 290
|||||
Db 121 PDQNTPTGPGVRYPLTFGCYKLVPEPDKVEANKGNTSLLHPVSLHGMDPDERVL 180
|||||

QY 291 EWRFDLSRLAFHHVARELHPEYFKNC 315
|||||
Db 181 EWRFDLSRLAFHHVARELHPEYFKNC 205
|||||

RESULT 3
S03244
nef protein (clone HXB2) - human immunodeficiency virus type 1
N:Alternate names: 3'-orf protein
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
C:Accession: S03244
R:Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettawa
Nucleic Acids Res. 13, 8219-8229, 1985
A:Title: Polymorphism of the 3' open reading frame of the virus associated with the acqu
A:Reference number: S03244; MUID:86067228
A:Accession: S03244
A:Molecule type: DNA
A:Residues: 1-206 <RAT>
A:Cross-references: EMBL:X03187
A:Note: the in-frame stop codon at residue 124, shown as 'X', may be suppressed
C:Genetics:
A:Gene: nef; 3'-orf; orf-F
C:Superfamily: AIDS nef protein

Query Match 49.4%; Score 1115; DB 2; Length 206;
Best Local Similarity 98.5%; Pred. No. 1.7e-79;
Matches 203; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 110 MGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGATSSNTAATNAACAWLEA 169
|||||
Db 1 MGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGATSSNTAATNAACAWLEA 60
|||||

QY 170 QEEVGFVPTQVPLRPMTYKAAVDLSHFLKKGGLHSGRRQDILDLWIYHTQGY 229
|||||
Db 61 QEEVGFVPTQVPLRPMTYKAAVDLSHFLKKGGLHSGRRQDILDLWIYHTQGY 120
|||||

QY 230 FPDQNTPTGPGVRYPLTFGCYKLVPEPDKVEANKGNTSLLHPVSLHGMDPDERV 289
|||||
Db 121 FPDQNTPTGPGVRYPLTFGCYKLVPEPDKVEANKGNTSLLHPVSLHGMDPDERV 180
|||||

Query Match 49.1%; Score 1108; DB 1; Length 206;
Best Local Similarity 97.1%; Pred. No. 6e-79;
```

```
Db 121 FPDQNTPTGPGVRYPLTFGCYKLVPEPDKVEANKGNTSLLHPVSLHGMDPDERV 180
QY 290 LEWRFDLSRLAFHHVARELHPEYFKNC 315
|||||
Db 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206
|||||

RESULT 4
ASLJVL
nef protein - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: 3'-orf protein; orf-F protein
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A04007
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy ret
A:Reference number: A93355; MUID:85111157
A:Accession: A04007
A:Molecule type: DNA
A:Residues: 1-206 <MUE>
A:Cross-references: GB:K02083; NID:9555008; PIDN:AAB59874.1; PID:9328560
C:Genetics:
A:Gene: nef; 3'-orf; orf-F
C:Superfamily: AIDS nef protein
C:Keywords: AIDS; immunodeficiency

Query Match 49.4%; Score 1114; DB 1; Length 206;
Best Local Similarity 97.6%; Pred. No. 2.1e-79;
Matches 201; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 110 MGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGATSSNTAATNAACAWLEA 169
|||||
Db 1 MGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKHGATSSNTAATNAACAWLEA 60
|||||

QY 170 QEEVGFVPTQVPLRPMTYKAAVDLSHFLKKGGLHSGRRQDILDLWIYHTQGY 229
|||||
Db 61 QEEVGFVPTQVPLRPMTYKAAVDLSHFLKKGGLHSGRRQDILDLWIYHTQGY 120
|||||

QY 230 FPDQNTPTGPGVRYPLTFGCYKLVPEPDKVEANKGNTSLLHPVSLHGMDPDERV 289
|||||
Db 121 FPDQNTPTGPGVRYPLTFGCYKLVPEPDKVEANKGNTSLLHPVSLHGMDPDERV 180
|||||

QY 290 LEWRFDLSRLAFHHVARELHPEYFKNC 315
|||||
Db 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206
|||||

RESULT 5
ASLJ12
nef protein - human immunodeficiency virus type 1 (isolate HTLV-III, 12)
N:Alternate names: 3'-orf protein; orf-F protein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C:Accession: A04006
R:Arya, S.K.; Gallo, R.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986
A:Title: Three novel genes of human T-lymphotropic virus type III: immune reactivit
A:Reference number: A94093; MUID:86177573
A:Accession: A04006
A:Molecule type: DNA
A:Residues: 1-206 <ARY>
A:Cross-references: EMBL:M11840; NID:9328453; PIDN:AAA45001.1; PID:9328458
C:Genetics:
A:Gene: nef; 3'-orf; orf-F
C:Superfamily: AIDS nef protein
C:Keywords: AIDS; immunodeficiency

Query Match 49.1%; Score 1108; DB 1; Length 206;
Best Local Similarity 97.1%; Pred. No. 6e-79;
```

Matches 200; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 110 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 169  
 Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDLIWIHTQGY 229  
 Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDLIWIHTQGY 120

QY 230 FPDQNTYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 289  
 Db 121 FPDQNTYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180

QY 290 LEWRDLSRLAFHHVARELHPEYFKNC 315  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

RESULT 6  
 JC5400  
 nef protein - Human immunodeficiency virus type 1, HIV-1  
 C:Species: Human immunodeficiency virus type 1, HIV-1  
 C:Date: 07-Jul-1997 #sequence\_revision 18-Jul-1997 #text\_change 31-Oct-1997  
 C:Accession: JC5400  
 R:Macreadie, I.G.; Lowe, M.G.; Curtin, C.C.; Hewish, D.; Azad, A.A.  
 Biochem. Biophys. Res. Commun. 232, 707-711, 1997  
 A:Title: Cytotoxicity resulting from addition of HIV-1 Nef N-terminal peptides to yeast  
 A:Reference number: JC5400; MUID:97271389  
 A:Molecule type: protein  
 A:Residues: 1-206 <MAC>  
 C:Comment: The amino-terminal part possesses membrane-perturbing and fusogenic activities.  
 C:Superfamily: AIDS nef protein  
 F:2-206/Product: nef protein #status predicted <MAT>

Query Match 48.6%; Score 1097; DB 2; Length 206;  
 Best Local Similarity 97.1%; Pred. No. 4.3e-78;  
 Matches 200; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 110 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 169  
 Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDLIWIHTQGY 229  
 Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDLIWIHTQGY 120

QY 230 FPDQNTYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 289  
 Db 121 FPDQNTYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180

QY 290 LEWRDLSRLAFHHVARELHPEYFKNC 315  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

RESULT 7  
 S03245  
 nef protein (clone HXB3) - human immunodeficiency virus type 1  
 N:Alternate names: 3'-orf protein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 20-Sep-1999  
 C:Accession: S03245  
 R:Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettawa  
 Nucleic Acids Res. 13, 8219-8229, 1985  
 A:Title: Polymorphism of the 3' open reading frame of the virus associated with the acqu  
 A:Reference number: S03244; MUID:86067228  
 A:Accession: S03245  
 A:Molecule type: DNA  
 A:Residues: 1-206 <RAT>

A:Cross-references: EMBL:X03188; NID:g61556; PIDN:CAA26947.1; PID:g61557  
 C:Genetics:  
 A:Gene: nef; 3'-orf; Orf-F  
 C:Superfamily: AIDS nef protein

Query Match 48.6%; Score 1096; DB 2; Length 206;  
 Best Local Similarity 96.6%; Pred. No. 5.2e-78;  
 Matches 199; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 110 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 169  
 Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDLIWIHTQGY 229  
 Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDLIWIHTQGY 120

QY 230 FPDQNTYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 289  
 Db 121 FPDQNTYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180

QY 290 LEWRDLSRLAFHHVARELHPEYFKNC 315  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

RESULT 8  
 S33986  
 nef protein - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Sep-1999  
 C:Accession: S33986  
 R:Carlini, F.  
 submitted to the EMBL Data Library, November 1991  
 A:Reference number: S33979  
 A:Accession: S33986  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-206 <CAR>  
 A:Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77629.1; PID:g60200  
 C:Superfamily: AIDS nef protein

Query Match 48.6%; Score 1096; DB 2; Length 206;  
 Best Local Similarity 96.6%; Pred. No. 5.2e-78;  
 Matches 199; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 110 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 169  
 Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDLIWIHTQGY 229  
 Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDLIWIHTQGY 120

QY 230 FPDQNTYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 289  
 Db 121 FPDQNTYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180

QY 290 LEWRDLSRLAFHHVARELHPEYFKNC 315  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

RESULT 9  
 ASLJH3  
 nef protein - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)  
 N:Alternate names: 3'-orf protein; Orf-F protein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 31-Jan-1997  
 C:Accession: A04005



A:Reference number: S25937; MUID:91156044

A:Accession: S25937

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: nucleic acid

A:Residues: 1-206 <GUO>

A:Cross-references: EMBL:X57465; NID:g60217; PIDN:CAA40702.1; PID:g60218

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1991

C:Superfamily: AIDS nef protein

Query Match 44.7%; Score 1007; DB 2; Length 206;

Best Local Similarity 85.9%; Pred. No. 4.4e-71;

Matches 177; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

QY 110 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGAGTSSNTAATNAACAWLEA 169

DB 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGAGTSSNTAATNAACAWLEA 60

QY 170 QEEVEVGFPPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRODILDWYHTQGY 229

DB 61 QEEVEVGFPPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRODILDWYHTQGY 120

QY 230 FPDWNTYTPGVRYPYPLTFGWCYKLVVPVEPKVEANKGENTSLHPVSLHGMDPPEV 289

DB 121 FPDWNTYTPGVRYPYPLTFGWCYKLVVPVEPKVEANKGENTSLHPVSLHGMDPPEV 180

QY 290 LEWRFDSRLAFHHVARELHPYFKN 315

DB 181 LEWRFDSRLAFHHVARELHPYFKN 206

RESULT 13

ASLQ02

nef protein - human immunodeficiency virus type 1 (isolate ARV-2)

N:Alternate names: 3'-orf protein; Orf-F protein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 17-May-1995 #sequence\_revision 17-May-1995 #text\_change 16-Jul-1999

C:Accession: A04009

R:Sanchez-Rescador, R.; Power, M.D.; Barr, P.J.; Stelmier, K.S.; Stempien, M.M.; Brown-SH

Science 227, 484-492, 1985

A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).

A:Reference number: A04003; MUID:85090453

A:Accession: A04009

A:Molecule type: DNA

A:Residues: 1-210 <SAN>

A:Cross-references: GB:X02007; NID:g328658; PIDN:AAB59883.1; PID:g328667

C:Genetics:

A:Gene: nef; 3'-orf; Orf-F

C:Superfamily: AIDS nef protein

C:Keywords: AIDS; immunodeficiency

Query Match 44.2%; Score 997; DB 1; Length 210;

Best Local Similarity 85.2%; Pred. No. 2.7e-70;

Matches 179; Conservative 16; Mismatches 11; Indels 4; Gaps 1;

QY 110 MGGKWSKSSVVGWPTVRMR-----RAEPAADGVGAASRDLEKKGAGTSSNTAATNAACA 165

DB 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGAGTSSNTAATNAACA 60

QY 166 WLEAQEEVEVGFPPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRODILDWYH 225

DB 61 WLEAQEEVEVGFPPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRODILDWYH 120

QY 226 TQGYFPDQNTYTPGVRYPYPLTFGWCYKLVVPVEPKVEANKGENTSLHPVSLHGMDP 285

DB 121 TQGYFPDQNTYTPGVRYPYPLTFGWCYKLVVPVEPKVEANKGENTSLHPVSLHGMDP 180

QY 286 BREVLWFDSRLAFHHVARELHPYFKN 315

DB 181 EKEVLWRFDSRLAFHHVARELHPYFKN 210

RESULT 14

I44001

nef protein - human immunodeficiency virus type 1 (strain YU-2)

N:Alternate names: 3'-orf protein; Orf-F protein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 23-Feb-1997

C:Accession: I44001

R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M

J. Virol. 66, 6587-6600, 1992

A:Title: Complete nucleotide sequence, genome organization, and biological properties

A:Reference number: A44001; MUID:93021387

A:Accession: I44001

A:Molecule type: DNA

A:Residues: 1-214 <LIY>

A:Cross-references: GB:M93258

C:Genetics:

A:Gene: nef; 3'-orf; Orf-F

C:Superfamily: AIDS nef protein

C:Keywords: AIDS; immunodeficiency

Query Match 44.0%; Score 991.5; DB 1; Length 214;

Best Local Similarity 84.2%; Pred. No. 7.5e-70;

Matches 181; Conservative 12; Mismatches 11; Indels 11; Gaps 2;

QY 110 MGGKWSKSSVVGWPTVR-----ERMRAEPAADGVGAASRDLEKKGAGTSSNTAA 159

DB 1 MGGKWSKSSVVGWPTVRERMRAEPAADGVGAASRDLEKKGAGTSSNTAA 60

QY 160 TNAACAWLEAQEEVEVGFPPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRODIL 219

DB 61 TNAACAWLEAQEEVEVGFPPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRODIL 120

QY 220 DLWYHTQGYFPDQNTYTPGVRYPYPLTFGWCYKLVVPVEPKVEANKGENTSLHPVSL 279

DB 121 DLWYHTQGYFPDQNTYTPG-GTRWPLTFGWCYKLVVPVEPKVEANKGENTSLHPVSL 179

QY 280 HGMDPPEVLEWRFDSRLAFHHVARELHPYFKN 314

DB 180 HGMDPPEVLEWRFDSRLAFHHVARELHPYFKN 214

RESULT 15

S03247

nef protein (clone C15) - human immunodeficiency virus type 1 (fragment)

N:Alternate names: 3'-orf protein

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 20-Jun-2000

C:Accession: S03247

R:Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pett

Nucleic Acids Res. 13, 8219-8229, 1985

A:Title: Polymorphism of the 3' open reading frame of the virus associated with the a

A:Reference number: S03244; MUID:86067228

A:Accession: S03247

A:Molecule type: mRNA

A:Residues: 1-182 <RAT>

A:Cross-references: EMBL:X03189; NID:g61552; PIDN:CAA26948.1; PID:g1335562

C:Genetics:

A:Gene: nef; 3'-orf; Orf-F

C:Superfamily: AIDS nef protein

Query Match 43.8%; Score 987; DB 2; Length 182;

Best Local Similarity 98.4%; Pred. No. 1.4e-69;

Matches 179; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 134 PAADGVGAASRDLEKKGAGTSSNTAATNAACAWLEAQEEVEVGFPPVTPQVPLRPMTYKAA 193

DB 1 PAADGVGAASRDLEKKGAGTSSNTAATNAACAWLEAQEEVEVGFPPVTPQVPLRPMTYKAA 60

QY 194 VDSLHFLKEKGGLEGLIHSORRODILDWYHTQGYFPDQNTYTPGVRYPYPLTFGWCYK 253

Db 61 VDSLHFLKEKGLSLHSQRQDILDLYHTQGYFPDQWNTYTPGVRPLTFGWCYK 120  
Qy 254 LVPVEPKVEANKGENTSLHHPVSLHGMDDPEREVLEWRFDSRLAFHHVARELHPEYFK 313  
Db 121 LVPVEPKVEANKGENTSLHHPVSLHGMDDPEREVLEWRFDSRLAFHHVARELHPEYFK 180  
Qy 314 NC 315  
Db 181 NC 182

## RESULT 16

S03246  
nef protein (clone HAT3) - human immunodeficiency virus type 1  
N:Alternate names: 3'-orf protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 20-Sep-1999  
C:Accession: S03246  
R:Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettawa  
Nucleic Acids Res. 13, 8219-8229, 1985  
A:Title: Polymorphism of the 3' open reading frame of the virus associated with the acqu  
A:Reference number: S03244; MUID:8606728  
A:Accession: S03246  
A:Molecule type: DNA  
A:Residues: 1-204 <RAT>  
A:Cross-references: EMBL:X03190; NID:961550; PIDN:CAA26949.1; PID:961551  
C:Note: the authors translated the codon AGT for residue 11 as Gly  
C:Genetics:  
A:Gene: nef; 3'-orf; Orf-F  
C:Superfamily: AIDS nef protein

Query Match 43.8%; Score 987; DB 2; Length 204;  
Best Local Similarity 84.5%; Pred. No. 1.6e-69;  
Matches 174; Conservative 16; Mismatches 14; Indels 2; Gaps 1;

Qy 110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169  
Db 1 MGGKWSKSKMGWPAVRERMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 58  
Qy 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDILDLYHTQGY 229  
Db 59 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDILDLYHTQGY 118  
Qy 230 FPDQWNTYTPGVRPLTFGWCYKLVPEPKVEANKGENTSLHHPVSLHGMDDPEREV 289  
Db 119 FPDQWNTYTPGVRPLTFGWCYKLVPEPKVEANKGENTSLHHPVSLHGMDDPEREV 178  
Qy 290 LEWRFDSRLAFHHVARELHPEYFKNC 315  
Db 179 LVWKFDSRLAFHHVARELHPEYFKDC 204

## RESULT 17

QOLJZR  
nef protein - human immunodeficiency virus Zr-6  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: human immunodeficiency virus Zr-6  
C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999  
C:Accession: F26192  
R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu  
Gene 52, 71-82, 1987  
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleot  
A:Reference number: A26192; MUID:87248097  
A:Accession: F26192  
A:Molecule type: DNA  
A:Residues: 1-212 <SRI>  
A:Cross-references: GB:K03458; GB:M16322; NID:9329398; PIDN:AAA45381.1; PID:g329404  
C:Genetics:  
A:Gene: nef; 3'-orf; Orf-F  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; immunodeficiency

Query Match 40.4%; Score 911; DB 1; Length 212;  
Best Local Similarity 77.4%; Pred. No. 1.4e-63;  
Matches 164; Conservative 23; Mismatches 19; Indels 6; Gaps 2;

Qy 110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAISSNTAATNAAC 164  
Db 1 MGGKWSKSSVVGWPAVRERMRRAEPAADGVGAASRDLEKHGAISSNTAATNAAC 60  
Qy 165 AWLEAQEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDILDLY 223  
Db 61 AWLEAQEESEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDILDLY 120  
Qy 224 YHTQGYFPDQWNTYTPGVRPLTFGWCYKLVPEPKVEANKGENTSLHHPVSLHGM 283  
Db 121 YHTQGYFPDQWNTYTPGVRPLTFGWCYKLVPEPKVEANKGENTSLHHPVSLHGM 180  
Qy 284 DPEREVLEWRFDSRLAFHHVARELHPEYFKNC 315  
Db 181 DPEREVLEWRFDSRLAFHHVARELHPEYFKDC 212

## RESULT 18

QOLJND  
nef protein - human immunodeficiency virus type 1 (isolate NDK)  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999  
C:Accession: JQ0068  
R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe,  
Gene 81, 275-284, 1989  
A:Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human im  
A:Reference number: JQ0065; MUID:90034200  
A:Accession: JQ0068  
A:Molecule type: DNA  
A:Residues: 1-207 <SPT>  
A:Cross-references: GB:M27323; NID:g328154; PIDN:AAA44874.1; PID:g328163  
C:Genetics:  
A:Gene: nef  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; immunodeficiency

Query Match 40.1%; Score 903.5; DB 1; Length 207;  
Best Local Similarity 77.3%; Pred. No. 5.1e-63;  
Matches 160; Conservative 25; Mismatches 21; Indels 1; Gaps 1;

Qy 110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169  
Db 1 MGGKWSKSSVVGWPAVRERMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60  
Qy 170 QEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDILDLYHTQGY 228  
Db 61 QEESEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDILDLYHTQGY 120  
Qy 229 YFPDQWNTYTPGVRPLTFGWCYKLVPEPKVEANKGENTSLHHPVSLHGMDDPERE 288  
Db 121 YFPDQWNTYTPGVRPLTFGWCYKLVPEPKVEANKGENTSLHHPVSLHGMDDPERE 180  
Qy 289 VLEWRFDSRLAFHHVARELHPEYFKNC 315  
Db 181 VLMWRFSRLAFHHVARELHPEYFKDC 207

## RESULT 19

B44963  
nef protein - human immunodeficiency virus type 1 (isolate Z321)  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 28-May-1999

C:Accession: B44963  
R:Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J.  
AIDS Res. Hum. Retroviruses 5, 121-129, 1989  
A:Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nu  
C:Reference number: A44963; MUID:85228766

A:Accession: B44963  
A:Molecule type: DNA  
A:Residues: 1-205 <SRT>  
A:Cross-references: GB:M15896; NID:g329392; PIDN:AAB53951.1; PID:g329397

C:Genetics:  
A:Gene: nef; 3'-orf; orf-F  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; immunodeficiency

Query Match 37.1%; Score 837; DB 1; Length 205;  
Best Local Similarity 73.2%; Pred. No. 7.6e-58;  
Matches 153; Conservative 23; Mismatches 25; Indels 8; Gaps 3;

Qy 110 MGGKSKSVVGVVPRVRRMRR---AEPADGVGAASRDLEKHGAITSNTAATNAACAW 166

Db 1 MGNKWSK---GWPAVRIRIQTPAPPAAEGVGAASQDLAKHGAISSNTATNPNPCAW 56

Qy 167 LEAQEE-EVGFPPVTPQVPLRPMYKAAVDLSHFLKKGGLGLIHSORQDILDWIYH 225

Db 57 LEAQEESEVGFPPVTPQVPLRPMYKAAVDLSHFLKKGGLGLIHSORQDILDWIYH 116

Qy 226 TQGYFPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHVPVSLHGMDDP 285

Db 117 TQGYFPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHVPVSLHGMDDP 176

Qy 286 EREVLEWFDLSRLAFHHVARELHPEYFKN 314

Db 177 EREVLEWFDLSRLAFHHVARELHPEYFKN 205

RESULT 20

nef protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 21-Jul-2000

C:Accession: T01673

R:Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.

Cell 46, 63-74, 1986

A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol

A:Reference number: 214389; MUID:86245056

A:Accession: T01673

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-209 <ALI>

A:Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28017.1; PID:g60235

C:Superfamily: AIDS nef protein

Query Match 37.0%; Score 834.5; DB 2; Length 209;

Best Local Similarity 70.1%; Pred. No. 1.2e-57;

Matches 148; Conservative 26; Mismatches 30; Indels 7; Gaps 2;

Qy 110 MGGKSKSVVGVVPRVRRMRRAEPAADGVG----AASRDLEKHGAITSNTAATNAAC 164

Db 1 MGGKSKSVVGVVPRVRRMRRAEPAADGVG----AASRDLEKHGAITSNTAATNAAC 60

Qy 165 AWLEAQEESEVGFPPVTPQVPLRPMYKAAVDLSHFLKKGGLGLIHSORQDILDWIY 224

Db 61 E--PPEEESEVGFPPVTPQVPLRPMYKGAFDLSHFLKKGGLGLVWSPKREIIDLWY 118

Qy 225 HQQGYFPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHVPVSLHGMDD 284

Db 119 HQQGYFPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHVPVSLHGMDD 178

Qy 285 PEREVLEWFDLSRLAFHHVARELHPEYFKN 315

Db 179 AEREVLKWKFDSSSLARHRAHQHPEYKDC 209

RESULT 21

ASLJK

nef protein - simian immunodeficiency virus SIVcpz

N:Alternate names: 3'-orf protein; orf-F protein

C:Species: simian immunodeficiency virus SIVcpz

A:Note: host Pan troglodytes (chimpanzee)

C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999

C:Accession: S09991

R:Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.

Nature 345, 356-359, 1990

A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.

A:Reference number: S09983; MUID:90259077

A:Accession: S09991

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-205 <HUE>

A:Cross-references: EMBL:X52154; NID:g58866; PIDN:CAA36408.1; PID:g58877

C:Genetics:

A:Gene: nef

C:Superfamily: AIDS nef protein

C:Keywords: AIDS; immunodeficiency

Query Match 36.9%; Score 832; DB 1; Length 205;

Best Local Similarity 70.2%; Pred. No. 1.9e-57;

Matches 144; Conservative 27; Mismatches 34; Indels 0; Gaps 0;

Qy 110 MGGKSKSVVGVVPRVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 169

Db 1 MGTKWSKSLVGVPEVRRIRREAPTAAGVGVEGSKDLRHGAITSNTPETNOTLAWLEE 60

Qy 170 QEESEVGFPPVTPQVPLRPMYKAAVDLSHFLKKGGLGLIHSORQDILDWIYHTQGY 229

Db 61 MDNEVGFPPVTPQVPLRPMYKAAVDLSHFLKKGGLGLIHSORQDILDWIYHTQGF 120

Qy 230 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHVPVSLHGMDDPPEV 289

Db 121 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHVPVSLHGMDDPPEV 180

Qy 290 LEWRFDSRLAFHHVARELHPEYFKN 314

Db 181 LVWRFDSRLAFHHVARELHPEYFKN 205

RESULT 22

S59931

glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenzae (strai

N:Alternate names: Igd-binding protein; protein D

C:Species: Haemophilus influenzae

A:Variety: strain 3639

C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999

C:Accession: S59931; S47333

R:Song, X.M.; Forsgren, A.; Janson, H.

Infect. Immun. 63, 696-699, 1995

A:Title: The gene encoding protein D (hpd) is highly conserved among Haemophilus Infl

A:Reference number: S59931; MUID:95122210

A:Accession: S59931

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-364 <SON>

A:Cross-references: EMBL:Z35656; NID:g525213; PIDN:CAA84715.1; PID:g525214

A:Experimental source: strain 3639

C:Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen

Query Match 25.7%; Score 578.5; DB 2; Length 364;

Best Local Similarity 47.1%; Pred. No. 2.1e-37;

Matches 145; Conservative 19; Mismatches 71; Indels 73; Gaps 11;

Qy 1 CSSHSSNMANTOMKSKIIIAHRGAGSYLPEHTLESKALFAQQADYLSQDLAMTKDGR 60

Db 1 CSSHSSNMANTOMKSKIIIAHRGAGSYLPEHTLESKALFAQQADYLSQDLAMTKDGR 60



Db 19 CSSHSSNNANTOMKSDKIIIAHRCASGYLPEHTLESKALAFQAQADYLEQDLAMTKDGL 78  
Qy 61 VVIHDFLDGLTDVAKKPPHRRKGRYVYIDFTLKEIQSLEMTENFETMGK----- 113  
Db 79 VVIHDFLDGLTDVAKKPPHRRKGRYVYIDFTLKEIQSLEMTENFETMGKQAQVYPN 138  
Qy 114 ----W-----SKSSVVG-WPTVVRMRRAEPAADGVGAASRDLE 147  
Db 139 RFLWKSHFRHTFEDEIEFTQGLEKSTGKKGVIYPEIKAPWFHHQNGKDIAAETLKV 198  
Qy 148 KHGAITSSNTAATNAACAWLEAEVEEFGFVPTQVPLRPMTYKAAVDLSHFLKEKGGL 207  
Db 199 KYGDKKTD-----MVYLQTFDFNELKRIKTELLPQMGMDLK-LVQLIAYTDWK---- 246  
Qy 208 GLIHSRRQDILDLYHTQGYFPDQW-----NYTPGPGVRYPLTFGWCYKLV 257  
Db 247 ----ETQEKDPKGYW-----NYNDWMFKPGAMAEVVKYADGVGP-----GW-YMLV 291  
Qy 258 E---PDKV 262  
Db 292 EESKPDNI 299

RESULT 23  
S59932  
glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenzae (strain 3  
N:Alternate names: immunoglobulin D-binding protein; protein D  
C:Species: Haemophilus influenzae  
A:Variety: strain 3640  
C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999  
A:Accession: S59932; S47334  
R:Song, X.M.; Forsgren, A.; Janson, H.  
Infect. Immun. 63, 696-699, 1995  
A:Title: The gene encoding protein D (hpd) is highly conserved among Haemophilus influen  
A:Reference number: S59931; MUID:95122210  
A:Accession: S59932  
A:Molecule type: DNA  
A:Residues: 1-364 <SON>  
A:Cross-references: EMBL:235657; NID:9525215; PIDN:CAA84716.1; PID:9525216  
A:Experimental source: strain 3640  
C:Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen

Query Match 25.7%; Score 578.5; DB 2; Length 364;  
Best Local Similarity 47.1%; Pred. No. 2.1e-37;  
Matches 145; Conservative 19; Mismatches 71; Indels 73; Gaps 11;

Qy 1 CSSHSSNNANTOMKSDKIIIAHRCASGYLPEHTLESKALAFQAQADYLEQDLAMTKDGL 60  
Db 19 CSSHSSNNANTOMKSDKIIIAHRCASGYLPEHTLESKALAFQAQADYLEQDLAMTKDGL 78  
Qy 61 VVIHDFLDGLTDVAKKPPHRRKGRYVYIDFTLKEIQSLEMTENFETMGK----- 113  
Db 79 VVIHDFLDGLTDVAKKPPHRRKGRYVYIDFTLKEIQSLEMTENFETMGKQAQVYPN 138  
Qy 114 ----W-----SKSSVVG-WPTVVRMRRAEPAADGVGAASRDLE 147  
Db 139 RFLWKSHFRHTFEDEIEFTQGLEKSTGKKGVIYPEIKAPWFHHQNGKDIAAETLKV 198  
Qy 148 KHGAITSSNTAATNAACAWLEAEVEEFGFVPTQVPLRPMTYKAAVDLSHFLKEKGGL 207  
Db 199 KYGDKKTD-----MVYLQTFDFNELKRIKTELLPQMGMDLK-LVQLIAYTDWK---- 246  
Qy 208 GLIHSRRQDILDLYHTQGYFPDQW-----NYTPGPGVRYPLTFGWCYKLV 257  
Db 247 ----ETQEKDPKGYW-----NYNDWMFKPGAMAEVVKYADGVGP-----GW-YMLV 291  
Qy 258 E---PDKV 262  
Db 292 EESKPDNI 299

RESULT 24

A43576  
glycerophosphodiester phosphodiesterase (EC 3.1.4.46) precursor - Haemophilus influe  
N:Alternate names: immunoglobulin D-binding protein; protein D  
C:Species: Haemophilus influenzae  
A:Variety: isolate 772  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 08-Oct-1999  
A:Accession: A43576  
R:Janson, H.; Heden, L.O.; Grubb, A.; Ruan, M.; Forsgren, A.  
Infect. Immun. 59, 119-125, 1991  
A:Title: Protein D, an immunoglobulin D-binding protein of Haemophilus influenzae: c  
A:Reference number: A43576; MUID:91099948  
A:Accession: A43576  
A:Molecule type: DNA  
A:Residues: 1-364 <JAN>  
A:Cross-references: GB:M37487; NID:9148970; PIDN:AAA2498.1; PID:9148971  
A:Experimental source: isolate 772  
C:Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-364/Product: glycerophosphodiester phosphodiesterase #status predicted <MAT>

Query Match 25.7%; Score 578.5; DB 2; Length 364;  
Best Local Similarity 47.1%; Pred. No. 2.1e-37;  
Matches 145; Conservative 19; Mismatches 71; Indels 73; Gaps 11;

Qy 1 CSSHSSNNANTOMKSDKIIIAHRCASGYLPEHTLESKALAFQAQADYLEQDLAMTKDGL 60  
Db 19 CSSHSSNNANTOMKSDKIIIAHRCASGYLPEHTLESKALAFQAQADYLEQDLAMTKDGL 78  
Qy 61 VVIHDFLDGLTDVAKKPPHRRKGRYVYIDFTLKEIQSLEMTENFETMGK----- 113  
Db 79 VVIHDFLDGLTDVAKKPPHRRKGRYVYIDFTLKEIQSLEMTENFETMGKQAQVYPN 138  
Qy 114 ----W-----SKSSVVG-WPTVVRMRRAEPAADGVGAASRDLE 147  
Db 139 RFLWKSHFRHTFEDEIEFTQGLEKSTGKKGVIYPEIKAPWFHHQNGKDIAAETLKV 198  
Qy 148 KHGAITSSNTAATNAACAWLEAEVEEFGFVPTQVPLRPMTYKAAVDLSHFLKEKGGL 207  
Db 199 KYGDKKTD-----MVYLQTFDFNELKRIKTELLPQMGMDLK-LVQLIAYTDWK---- 246  
Qy 208 GLIHSRRQDILDLYHTQGYFPDQW-----NYTPGPGVRYPLTFGWCYKLV 257  
Db 247 ----ETQEKDPKGYW-----NYNDWMFKPGAMAEVVKYADGVGP-----GW-YMLV 291  
Qy 258 E---PDKV 262  
Db 292 EESKPDNI 299

RESULT 25

S59934  
glycerophosphodiester phosphodiesterase (EC 3.1.4.46) precursor - Haemophilus influe  
N:Alternate names: immunoglobulin D-binding protein; protein D  
C:Species: Haemophilus influenzae  
A:Variety: strain Eagan; strain HK695  
C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999  
A:Accession: S59934; S59935; S47336; S47337  
R:Song, X.M.; Forsgren, A.; Janson, H.  
Infect. Immun. 63, 696-699, 1995  
A:Title: The gene encoding protein D (hpd) is highly conserved among Haemophilus inf  
A:Reference number: S59931; MUID:95122210  
A:Accession: S59934  
A:Molecule type: DNA  
A:Residues: 1-364 <SON>  
A:Cross-references: EMBL:235659; NID:9525219; PIDN:CAA84718.1; PID:9525220  
A:Experimental source: strain Eagan  
A:Accession: S59935  
A:Molecule type: DNA  
A:Residues: 1-364 <SON>  
A:Cross-references: EMBL:235660; NID:9525221; PIDN:CAA84719.1; PID:9525222  
A:Experimental source: strain HK695  
C:Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen

F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-364/Product: protein D #status predicted <MAT>

Query Match 25.7%; Score 578.5; DB 2; Length 364;  
Best Local Similarity 47.1%; Pred. No. 2.1e-37;  
Matches 145; Conservative 19; Mismatches 71; Indels 73; Gaps 11;

Qy 1 CSSHSSNNANTOMKSDKIIIAHAGSGYLPHTLESKALAFQAQADYLEQDLAMTKDGR 60  
Db 19 CSSHSSNNANTOMKSDKIIIAHAGSGYLPHTLESKALAFQAQADYLEQDLAMTKDGR 78  
Qy 61 VVIHDFLDGLTDVAKFPFHRKDGRIYVDFTLKEIQSLEMTENFETMGK----- 113  
Db 79 VVIHDFLDGLTDVAKFPFHRKDGRIYVDFTLKEIQSLEMTENFETMGKQAQVYPN 138  
Qy 114 ----W-----SKSSVVG-WPTVRMRRAEPAADGVGAASRDLE 147  
Db 139 RPLWKSHFRHTFEDEIEFTQGLEKSTGKKGVIPEIKAPWFHONGKDIAETLKV 198  
Qy 148 KHGATSSNTAATNAACAWLEAQEEVEGFPVTPQVPLRPMTYKAAYDLSHFLKEKGG 207  
Db 199 KYGYDKKTD-----MVYLOTFDFNELKRIKTELLPQMGMDLK-LVQLIAYTDW 246  
Qy 208 GLIHSQRQDILDLIWYHTQGYFPDQW-----NYTPGPGVRYPLTFGWCYK 257  
Db 247 ----ETQEKDPKGYW-----NYNDMMFKPGAMAEVVKYADGVG-----GW-YMLV 291  
Qy 258 E---PDV 262  
Db 292 EESKPDNI 299

RESULT 26  
S59933  
glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenzae (strain 6  
N:Alternate names: immunoglobulin D-binding protein; protein D  
C:Species: Haemophilus influenzae  
A:Variety: strain 6-7626  
C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999  
C:Accession: S59933; S47335  
R:Song, X.M.; Forsgren, A.; Janson, H.  
Infect. Immun. 63, 696-699, 1995  
A:Title: The gene encoding protein D (hpd) is highly conserved among Haemophilus influen  
A:Reference number: S59931; MUID:95122210  
A:Accession: S59933  
A:Molecule type: DNA  
A:Residues: 1-364 <SON>  
A:Cross-references: EMBL:235658; NID:9525217; PIDN:CAA84717.1; PID:9525218  
A:Experimental source: strain 6-7626  
C:Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen

Query Match 25.4%; Score 572.5; DB 2; Length 364;  
Best Local Similarity 46.8%; Pred. No. 6.1e-37;  
Matches 144; Conservative 19; Mismatches 77; Indels 73; Gaps 11;

Qy 1 CSSHSSNNANTOMKSDKIIIAHAGSGYLPHTLESKALAFQAQADYLEQDLAMTKDGR 60  
Db 19 CSSHSSNNANTOMKSDKIIIAHAGSGYLPHTLESKALAFQAQADYLEQDLAMTKDGR 78  
Qy 61 VVIHDFLDGLTDVAKFPFHRKDGRIYVDFTLKEIQSLEMTENFETMGK----- 113  
Db 79 VVIHDFLDGLTDVAKFPFHRKDGRIYVDFTLKEIQSLEMTENFETMGKQAQVYPN 138  
Qy 114 ----W-----SKSSVVG-WPTVRMRRAEPAADGVGAASRDLE 147  
Db 139 RPLWKSHFRHTFEDEIEFTQGLEKSTGKKGVIPEIKAPWFHONGKDIAETLKV 198  
Qy 148 KHGATSSNTAATNAACAWLEAQEEVEGFPVTPQVPLRPMTYKAAYDLSHFLKEKGG 207  
Db 199 KYGYDKKTD-----MVYLOTFDFNELKRIKTELLPQMGMDLK-LVQLIAYTDW 246

Qy 208 GLIHSQRQDILDLIWYHTQGYFPDQW-----NYTPGPGVRYPLTFGWCYK 257  
Db 247 ----ETQEKDPKGYW-----NYNDMMFKPGAMAEVVKYADGVG-----GW-YMLV 291  
Qy 258 E---PDV 262  
Db 292 EESKPDNI 299

## RESULT 27

G64086  
glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenzae (stra.  
N:Alternate names: Igd-binding protein; protein D  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 21-Jul-2000  
C:Accession: G64086  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: G64086  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-364 <TIGR>  
A:Cross-references: GB:U32751; GB:L42023; NID:93212200; PIDN:AAC22348.1; PID:gl573690  
A:Experimental source: strain Rd KW20  
C:Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen

Query Match 24.9%; Score 562.5; DB 2; Length 364;  
Best Local Similarity 46.1%; Pred. No. 3.7e-36;  
Matches 142; Conservative 21; Mismatches 72; Indels 73; Gaps 11;

Qy 1 CSSHSSNNANTOMKSDKIIIAHAGSGYLPHTLESKALAFQAQADYLEQDLAMTKDGR 60  
Db 19 CSSHSSNNANTOMKSDKIIIAHAGSGYLPHTLESKALAFQAQADYLEQDLAMTKDGR 78  
Qy 61 VVIHDFLDGLTDVAKFPFHRKDGRIYVDFTLKEIQSLEMTENFETMGK----- 113  
Db 79 VVIHDFLDGLTDVAKFPFHRKDGRIYVDFTLKEIQSLEMTENFETMGKQAQVYPN 138  
Qy 114 ----W-----SKSSVVG-WPTVRMRRAEPAADGVGAASRDLE 147  
Db 139 RPLWKSHFRHTFEDEIEFTQGLEKSTGKKGVIPEIKAPWFHONGKDIAETLKV 198  
Qy 148 KHGATSSNTAATNAACAWLEAQEEVEGFPVTPQVPLRPMTYKAAYDLSHFLKEKGG 207  
Db 199 KYGYDKKTD-----MVYLOTFDFNELKRIKTELLPQMGMDLK-LVQLIAYTDW 246  
Qy 208 GLIHSQRQDILDLIWYHTQGYFPDQW-----NYTPGPGVRYPLTFGWCYK 257  
Db 247 ----ETQEKDPKGYW-----NYNDMMFKPGAMAEVVKYADGVG-----GW-YMLV 291  
Qy 258 E---PDV 262  
Db 292 EESKPDNI 299

## RESULT 28

S59936  
glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenzae (stra  
N:Alternate names: Igd-binding protein; protein D  
C:Species: Haemophilus influenzae  
A:Variety: strain NCTC 8468  
C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999  
C:Accession: S59936; S47338  
R:Song, X.M.; Forsgren, A.; Janson, H.  
Infect. Immun. 63, 696-699, 1995  
A:Title: The gene encoding protein D (hpd) is highly conserved among Haemophilus infl  
A:Reference number: S59931; MUID:95122210

A:Accession: S59936  
A:Molecule type: DNA  
A:Residues: 1-364 <SON>  
A:Cross-references: EMBL:235661; NID:g525223; PIDN:CAA84720.1; PID:g525224  
A:Experimental source: strain NCTC 8468  
C:Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen

Query Match 24.78; Score 556.5; DB 2; Length 364;  
Best Local Similarity 45.8%; Pred. No. 1.1e-35;  
Matches 141; Conservative 20; Mismatches 74; Indels 73; Gaps 11;  
  
Qy 1 CSSHSSNANTQMSDKIIIAHAGSGYLPEHTLESKALFAQAQADYLEODLAMTKDGL 60  
Db 19 CSSHSSNANTQMSKHIIIAHAGSGYLPEHTLESKALFAQAQADYLEODLAMTKDGL 78  
Qy 61 VYIHDFLDGLTDVAKKPPHRRKGRYYVIDFTLKEIQSLEMTENFETMGK----- 113  
Db 79 VYIHDFLDGLTDVAKKPPHRRKGRYYVIDFTLKEIQSLEMTENFETMGKQAQVYPN 138  
Qy 114 ----W-----SKSSVVG-WPTVRRMRRAEPAADGVAASRDLE 147  
Db 139 RPPLWKSHFRHTFDETEFTQGLEKSTGKKVGIPEIKAPWFHHONGKDIAETLKLK 198  
Qy 148 KHGAISSNTAATNAACAWEAEVEEYGFVTPQVPLRPMTYKAAVDLSHLFKKGGLE 207  
Db 199 KYGYDKTD-----MYVLQTFDFNELKRIKTELLPQMGHDLK-LVOLIAYTDWK---- 246  
Qy 208 GLIHSQRQDILDLYITQGYFDDWQ-----NYTPGPGVRYPLTFTGWCYKLVVP 257  
Db 247 ----ETQEKDPKGYWV----NYNYDMFKPGAMAEVWYADGVP-----GW-YMLVYNK 291  
Qy 258 E---PDKV 262  
Db 292 EESKPDNI 299

## RESULT 29

S33982

trans-activating transcription regulator - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 06-Oct-1994 #sequence\_revision 23-Feb-1996 #text\_change 20-Sep-1999  
C:Accession: S33982; S26385; S19864

submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33982

A:Molecule type: DNA

A:Residues: 1-86 <CAR>

A:Cross-references: EMBL:211530; NID:g60192; PIDN:CAA77625.1; PID:g60196

R:Siderovski, D.P.; Matsuyama, T.; Frigerio, E.; Chui, S.; Min, X.; Erfle, H.; Summer-Sm

Nucleic Acids Res. 20, 5111-5320, 1992

A:Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activator c

A:Reference number: S26385; MUID:93065196

A:Accession: S26385

A:Molecule type: nucleic acid

A:Residues: 1-86 <SID>

A:Cross-references: EMBL:X64650; NID:g60144; PIDN:CAA45921.1; PID:g60145

C:Genetics:

A:Gene: tat

A:Introns: 72/2

C:Superfamily: AIDS trans-activating transcription regulator

C:Keywords: AIDS; immunodeficiency

Query Match 21.6%; Score 486; DB 2; Length 86;  
Best Local Similarity 100.0%; Pred. No. 5.6e-31;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 318 EPVDPRLPEPWKHPGSGPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRRPQ 377

Db 2 EPVDPRLPEPWKHPGSGPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRRPQ 61

Qy 378 SOTHQVSLSKOPTSQSRGDPGPK 402  
Db 62 SOTHQVSLSKOPTSQSRGDPGPK 86

## RESULT 30

TNLJ12

trans-activating transcription regulator - human immunodeficiency virus type 1 (isol  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: Host Homo sapiens (man)  
C:Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 02-Jul-1998  
C:Accession: A04017

R:Atya, S.K.; Gallo, R.C.

Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986

A:Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity

A:Reference number: A94093; MUID:86177573

A:Accession: A04017

A:Molecule type: DNA

A:Residues: 1-95 <ARY>

C:Genetics:

A:Gene: tat

C:Superfamily: AIDS trans-activating transcription regulator

C:Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 21.2%; Score 478; DB 1; Length 95;  
Best Local Similarity 98.8%; Pred. No. 2.7e-30;  
Matches 84; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 318 EPVDPRLPEPWKHPGSGPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRRPQ 377

Db 11 EPVDPRLPEPWKHPGSGPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRRPQ 70

Qy 378 SOTHQVSLSKOPTSQSRGDPGPK 402

Db 71 SOTHQVSLSKOPTSQSRGDPGPK 95

Search completed: August 26, 2002, 08:13:22

Job time: 291 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 08:15:41 ; Search time 40.39 Seconds  
(without alignments)  
394.002 Million cell updates/sec

Title: US-09-509-239-17

Perfect score: 2255

Sequence: 1 CSSHSSNMANTQMKSDKIII.....QSRDPTGPKETSCHHHHHH 411

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1130	50.1	206	1 NEF_HV1BR	P03406 human immun
2	1114	49.4	206	1 NEF_HV1PV	P03405 human immun
3	1111	49.3	206	1 NEF_HV1LW	O70627 human immun
4	1108	49.1	206	1 NEF_HV112	P04324 human immun
5	1088.5	48.3	205	1 NEF_HV1B8	P05855 human immun
6	1019	45.2	218	1 NEF_HV1B8	P12479 human immun
7	1005.5	44.6	205	1 NEF_HV1B3	P19545 human immun
8	997.5	44.2	211	1 NEF_HV1OY	P20886 human immun
9	997	44.2	210	1 NEF_HV1A2	P03407 human immun
10	994	44.1	208	1 NEF_HV1RH	P05858 human immun
11	991.5	44.0	214	1 NEF_HV1Y2	P35959 human immun
12	981	43.5	216	1 NEF_HV1JR	P20867 human immun
13	974	43.2	208	1 NEF_HV1S1	P19546 human immun
14	927.5	41.1	206	1 NEF_HV1EL	P04604 human immun
15	911	40.4	212	1 NEF_HV1Z6	P04602 human immun
16	903.5	40.1	207	1 NEF_HV1ND	P18801 human immun
17	872	38.7	205	1 NEF_HV1U4	P24741 human immun
18	842	37.3	182	1 NEF_HV1MN	P05856 human immun
19	837	37.1	205	1 NEF_HV1ZH	P05859 human immun
20	834.5	37.0	209	1 NEF_HV1MA	P04603 human immun
21	832	36.9	205	1 NEF_HV1C2	P17664 chimpanzee
22	819	36.3	239	1 NEF_HV1SC	P05857 human immun
23	645	28.6	123	1 NEF_HV1H2	P04601 human immun
24	638	28.3	123	1 NEF_HV1B1	P03404 human immun
25	562.5	24.9	364	1 GLPQ_HAEIN	Q06282 haemophilus
26	486	21.6	86	1 TAT_HV1B1	P04606 human immun
27	481	21.3	86	1 TAT_HV1PV	P04607 human immun
28	478	21.2	86	1 TAT_HV112	P04326 human immun
29	470	20.8	86	1 TAT_HV1BR	P04610 human immun
30	461	20.4	102	1 TAT_HV1H2	P05908 human immun
31	454	20.1	86	1 TAT_HV1H2	P04608 human immun
32	446	19.8	101	1 TAT_HV1JR	P20879 human immun
33	439.5	19.5	97	1 NEF_HV1Z2	P12478 human immun

34	439	19.5	253	1 NEF_HV2KR	O74127 human immun
35	437	19.4	101	1 TAT_HV1SC	P05906 human immun
36	435	19.3	101	1 TAT_HV1C4	P05907 human immun
37	435	19.3	101	1 TAT_HV1S1	P19553 human immun
38	434	19.2	101	1 TAT_HV1Y2	P35965 human immun
39	431	19.1	101	1 TAT_HV1MN	P05905 human immun
40	431	19.1	101	1 TAT_HV1S3	P19552 human immun
41	429.5	19.0	309	1 NEF_HV1S4	P12482 simian immun
42	426.5	18.9	261	1 NEF_HV1SVP	P19501 simian immun
43	421	18.7	257	1 NEF_HV2D1	P17753 human immun
44	419	18.6	101	1 TAT_HV1A2	P04614 human immun
45	419	18.6	101	1 TAT_HV1OY	P20893 human immun

## ALIGNMENTS

RESULT 1					
NEF_HV1BR					
ID	NEF_HV1BR	STANDARD:	PRT:	206 AA.	
AC	P03406;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Negative factor (F-protein) (27 kDa protein) (3'ORF).				
GN	NEF.				
OS	Human immunodeficiency virus type 1 (BRU isolate) (HIV-1), and				
OC	Human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).				
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11686, 11698;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-ISOLATE BRU;				
RX	MEDLINE=85099333; PubMed=2981635;				
RA	Wain-Hobson S., Sonigo P., Danos O., Cole S., Alison M.;				
RT	"Nucleotide sequence of the AIDS virus, LAV.";				
RL	Cell 40:9-17(1985).				
RN	[2]				
RP	SEQUENCE FROM N.A. (CLONE PNL4-3).				
RC	STRAIN-ISOLATE NEW YORK-5;				
RA	Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;				
RN	[3]				
RP	Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.				
RX	MEDLINE=88039140; PubMed=3118220;				
RA	Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,				
RA	Montagnier L., Lecocq J.-P.;				
RT	"Hiv F/3' orf encodes a phosphorylated GTP-binding protein resembling				
RT	an oncogene product.";				
RL	Nature 330:266-269(1987).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 54-205 IN COMPLEX WITH NEF.				
RX	MEDLINE=96279837; PubMed=8681387;				
RA	Lee C.H., Sakela K., Mirza U.A., Chait B.T., Kuriyan J.;				
RT	"Crystal structure of the conserved core of HIV-1 Nef complexed with				
RL	a Src family SH3 domain.";				
CC	Cell 85:931-942(1996).				
CC	!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING				
CC	ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.				
CC	-----				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL; K02013; AAB59752.1; -				
DR	EMBL; M19921; AAA44993.1; -				
DR	EMBL; A04321; CAA00353.1; -				
DR	PIR; A04008; ASLJFV				
DR	PDB; 1EFN; 11-JAN-97.				

DR HIV; K02013; NEFSBRU.  
DR HIV; M19921; NEFSN143.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS; Myristate; GTP-binding; Phosphorylation; 3D-structure.  
FT LIPID 2 MYRISTATE.  
FT MOD\_RES 15 15 PHOSPHORYLATION (BY PKC).  
FT VARIANT 11 11 V-> I (IN CLONE PNLA-3).  
FT VARIANT 15 15 T-> A (IN CLONE PNLA-3).  
FT VARIANT 33 33 A-> V (IN CLONE PNLA-3).  
FT VARIANT 51 51 T-> N (IN CLONE PNLA-3).  
SQ SEQUENCE 206 AA; 23342 MW; 77453FC80B6004F2 CRC64;

Query Match 50.1%; Score 1130; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. le-86;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 110 MGGKWSKSSVVGWPTVRERMRAEPAADVGGAASRDLEKHGAITSNTAATNAACAWLEA 169  
DB 1 MGGKWSKSSVVGWPTVRERMRAEPAADVGGAASRDLEKHGAITSNTAATNAACAWLEA 60  
QY 170 QEEVEGVPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGSLHSQRQDILDWIYHTQGY 229  
DB 61 QEEVEGVPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGSLHSQRQDILDWIYHTQGY 120  
QY 230 FPDQNYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEREV 289  
DB 121 FPDQNYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEREV 180  
QY 290 LEWRFDSRLAFHHVARELHPEYFKNC 315  
DB 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 2  
NEF\_HV1PV  
ID NEF\_HV1PV STANDARD; PRT; 206 AA.  
AC P03405.  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
GN NEF.  
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.  
OX NCBI\_TaxID=11700;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85111157; PubMed=2982104;  
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,  
RA Capon D.J.;  
RT "Nucleic acid structure and expression of the human  
RT AIDS/lymphadenopathy retrovirus.";  
RL Nature 313:450-458(1985).  
RN [2]  
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.  
RX MEDLINE=88039140; PubMed=3118220;  
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,  
RA Montagnier L., Lecocq J.-P.;  
RT "Hiv F3' orf encodes a phosphorylated GTP-binding protein resembling  
RT an oncogene product.";  
RL Nature 330:266-269(1987).  
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
CC  
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CC EMBL; K02083; AAB59874.1; -;  
DR EMBL; X01762; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A04007; ASLJVL.  
DR HSP; P03406; 1EFN.  
DR HIV; K02083; NEFSPV22.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS; Myristate; GTP-binding.  
FT LIPID 2 MYRISTATE.  
SQ SEQUENCE 206 AA; 23352 MW; EDE64281A17C6735 CRC64;

Query Match 49.4%; Score 1114; DB 1; Length 206;  
Best Local Similarity 97.6%; Pred. No. 2.le-85;  
Matches 201; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 110 MGGKWSKSSVVGWPTVRERMRAEPAADVGGAASRDLEKHGAITSNTAATNAACAWLEA 169  
DB 1 MGGKWSKSSVVGWPAVRERMRAEPAADVGGAASRDLEKHGAITSNTAATNAACAWLEA 60  
QY 170 QEEVEGVPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGSLHSQRQDILDWIYHTQGY 229  
DB 61 QEEVEGVPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGSLHSQRQDILDWIYHTQGY 120  
QY 230 FPDQNYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEREV 289  
DB 121 FPDQNYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEREV 180  
QY 290 LEWRFDSRLAFHHVARELHPEYFKNC 315  
DB 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 3  
NEF\_HV1LV  
ID NEF\_HV1LV STANDARD; PRT; 206 AA.  
AC Q70627;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
GN NEF.  
OS Human immunodeficiency virus type 1 (WI2.3 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.  
OX NCBI\_TaxID=82834;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95127297; PubMed=7826699;  
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,  
RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker  
RT infected with HIV type 1 (HTLV type IIIB).";  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [2]  
RP STRUCTURE BY NMR OF 56-206.  
RX MEDLINE=97337445; PubMed=9194185;  
RA Grzesiek S., Bax A., Hu J.S., Kaufman J., Palmer I., Stahl S.J.,  
RA Tjandra N., Wingfield P.T.;  
RT "Refined solution structure and backbone dynamics of HIV-1 Nef.";  
RL Protein Sci. 6:1248-1263(1997).  
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
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DR PDB: 2NEF; 07-JUL-97.
DR InterPro: IPR001558; F-protein.
DR Pfam: PF00469; F-protein; 1.
KW AIDS; Myristate; GTP-binding; 3D-structure.
FT LIPID 2 MYRISTATE.
SQ SEQUENCE 206 AA; 23414 MW; ED81F68F6B61278E CRC64;

Query Match 49.3%; Score 1111; DB 1; Length 206;
Best Local Similarity 97.1%; Pred. No. 3.8e-85;
Matches 200; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 110 MGKSKSVGWGPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
DB 1 MGKSKSVGWGPTVRRMRRAEPAADGVGAASQDLEKHGAITSSNTAATNADCAWLEA 60
QY 170 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGLIHSQRQDILDWYHTQGY 229
DB 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGLIHSQRQDILDWYHTQGY 120
QY 230 FPDWQNTGPGVRYPLTFCWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPERV 289
DB 121 FPDWQNTGPGVRYPLTFCWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPERV 180
QY 290 LEWRFDRLAFHVAHRELHPEYFKNC 315
DB 181 LEWRFDRLAFHVAHRELHPEYFKNC 206

RESULT 4
NEF_HV112 STANDARD; PRT; 206 AA.
AC P04324;
DT 20-MAR-1987 (Rel. 04, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (clone 12) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11679;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177573; PubMed=3008154;
RA Arya S.K., Gallo R.C.;
RT "Three novel genes of human T-lymphotropic virus type III: Immune
RT reactivity of their products with sera from acquired immune
RT deficiency syndrome patients."
RT Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
RL [2]
RN POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
RP MEDLINE=88039140; PubMed=3118220;
RX Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
RA Montagnier L., Lecocq J.-P.;
RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
RT an oncogene product."
RL Nature 330:266-269(1987).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC
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CC
CC EMBL; M11840; AAA45001.1;
DR PIR; A04006; ASLJ12.
DR HSP; P03406; LEFN.
DR HIV; M11840; NEFSPV12.
DR InterPro; IPR001558; F-protein.

DR PDB: 2NEF; 07-JUL-97.
DR InterPro: IPR001558; F-protein; 1.
DR Pfam: PF00469; F-protein; 1.
KW AIDS; Myristate; GTP-binding; 3D-structure.
FT LIPID 2 MYRISTATE.
SQ SEQUENCE 206 AA; 23414 MW; ED81F68F6B61278E CRC64;

Query Match 49.1%; Score 1108; DB 1; Length 206;
Best Local Similarity 97.1%; Pred. No. 6.7e-85;
Matches 200; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 110 MGKSKSVGWGPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
DB 1 MGKSKSVGWGPTVRRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
QY 170 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGLIHSQRQDILDWYHTQGY 229
DB 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGLIHSQRQDILDWYHTQGY 120
QY 230 FPDWQNTGPGVRYPLTFCWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPERV 289
DB 121 FPDWQNTGPGVRYPLTFCWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPERV 180
QY 290 LEWRFDRLAFHVAHRELHPEYFKNC 315
DB 181 LEWRFDRLAFHVAHRELHPEYFKNC 206

RESULT 5
NEF_HV1B8 STANDARD; PRT; 205 AA.
AC P05855;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11684;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85111123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Ghayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III."
RL Nature 313:277-284(1985).
RN [2]
RN POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
RP MEDLINE=88039140; PubMed=3118220;
RX Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
RA Montagnier L., Lecocq J.-P.;
RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
RT an oncogene product."
RL Nature 330:266-269(1987).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC
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CC
CC EMBL; K02011; -; NOT_ANNOTATED_CDS.
DR HSP; P03406; LEFN.
DR HIV; K02011; NEFSB8.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
```

Matches 185; Conservative 12; Mismatches 7; Indels 16; Gaps 2

QY 110 MGKWSKSSVVGWPTVRRMR-----RAEPAADGVGAASRDLEKKGAISS 155  
 Ddb 1 MGKWSK--MAGWSTVRRMRRAEPARERMRRAEPAADGVGAASRDLEKKGAISS 58

QY 156 NTAATNAACAWLEAQEEVEEYGFPTVQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRR 215  
 Ddb 59 NTAATNADCAWLEAQEEVEEYGFVVKPOVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQOR 118

QY 216 QDILDWYHTQGYFFDMQNYTGPGVRYPLTGTWCVKLVPVDPDKVEEANKGENTSLLH 275  
 Ddb 119 QDILDWYHTQGYFFDMQNYTGPGVRYPLTGTWCVKLVPVDPDKVEEANKGENTSLLH 178

QY 276 PVSIGHGMDPEREVLWRFDSDRLAFHHVARELHPEYKNC 315  
 Ddb 179 PMSHGMDPEREVLWRFDSDRLAFHHMARELHPEYKNC 218

RESULT 7  
 ID NEF\_HV153 STANDARD; PRT; 205 AA.  
 AC P19545;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
 GN NEF.  
 OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).  
 OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 RN NCBI\_TaxID=11690;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90317906; PubMed=2370688;  
 RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;  
 RT "Human immunodeficiency virus type 1 cellular host range,  
 RT replication, and cytopathicity are linked to the envelope region of  
 RT the viral genome.";  
 RL J. Virol. 64:4016-4020(1990).  
 CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
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 CC -----  
 CC EMBL: M38427; AAA45068.1; -  
 DR HSP: P03406; 1EFN  
 DR HIV: M38427; NEFSF33.  
 DR InterPro: IPR001558; F-protein.  
 DR Pfam: PF00469; F-protein; 1.  
 DR AIDS: Myristate; GTP-binding.  
 DR LIPID 2  
 FT MYRISTATE (BY SIMILARITY).  
 SQ SEQUENCE 205 AA; 23318 MW; FFB419A1C5DFC9F3 CRC64;

Query Match 44.6%; Score 1005.5; DB 1; Length 205;  
 Best Local Similarity 86.4%; Pred. No. 2.le-76;  
 Matches 178; Conservative 19; Mismatches 8; Indels 1; Gaps 1;

QY 110 MGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNACAWLEA 169  
 Ddb 1 MGKWSKSK--MGWPAVRERMRKRAEPAADGVGAASRDLEKKGALTSSNTAATNADCAWLEA 59

QY 170 QEEVEEYGFPTVQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRDLDLWIYHTQGY 229  
 Ddb 60 QEEVEEYGFVVKPOVPLRPMTYKAAVDLSHFLKEKGGLEGVLVSOKRDLDLWIYHTQGY 119

QY 230 FPDQNYTGPGVRYPLTGTWCVKLVPVDPDKVEEANKGENTSLLHPPVSLHGMDPDREV 289

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Db 120 FPDQNTTGGVRRPLTGGWCKLVPEPEKVEEANGENSLHHPMSLHGNEDEPEKV 179
QY 290 LEWRFSRLAFHVAHELHPEYFKNC 315
Db 180 LVKFDKSLAFHVAHELHPEYFKNC 205

RESULT 8
NEF_HV10Y
ID NEF_HV10Y STANDARD; PRT: 211 AA.
AC P20886;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11699;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90148544; PubMed=2559749;
RA Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.;
RT "A highly defective HIV-1 strain isolated from a healthy Gabonese
RT individual presenting an atypical western blot.";
RL AIDS 3:707-715(1989).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -!- MISCELLANEOUS: THE OYI ISOLATE WAS TAKEN FROM THE BLOOD OF A
CC HEALTHY GABONESE INDIVIDUAL.
CC -----
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CC -----
DR EMBL: M26727; AA83398.1;
DR HSP: P03406; IEFN.
DR HIV: M26727; NEF80YI.
DR InterPro: IPR001558; F-protein.
DR Pfam: PF00469; F-protein; 1.
KW AIDS; Myristate; GTP-binding.
FT LIPID 2 2 MYRISTATE.
SQ SEQUENCE 211 AA; 24067 MW; 64D846EEC55DAB8C CRC64;

Query Match 44.2%; Score 997.5; DB 1; Length 211;
Best Local Similarity 82.9%; Pred. No. 1e-75;
Matches 175; Conservative 22; Mismatches 9; Indels 5; Gaps 1;

QY 110 MGGKWSKSSVVGWPTVRRMRRA-----EPAADGVGAASRDLEKKGAISSNTAATNAAC 164
Db 1 MGGKWSKSMKGWPTIRERMKRAELQPPPEAEGVGAASRDLEKKGAISSNTAATNADC 60

QY 165 AMLAQEEVEEFGPVPQVPLRPMTYKAAVDLSHFLEKKGLEGLIHSQRQDILDWY 224
Db 61 AMLAQEEVEEFGPVPQVPLRPMTYKGAIDLSHFLEKKGLEGLIYSQKQDILDWY 120

QY 225 HTQGYFPDQNTTGGVRRPLTGGWCKLVPEPEKVEEANGENSLHHPMSLHGMD 284
Db 121 HTQGYFPDQNTTGGVRRPLTGGWCKLVPEPEKVEEANGENSLHHPMSLHGMD 180

QY 285 PEREVLWRFDSRLAFHVAHELHPEYFKNC 315
Db 181 PEKVLWRFDSRLAFHVAHELHPEYFKNC 211

RESULT 9
NEF_HV1A2
```

```
ID NEF_HV1A2 STANDARD; PRT: 210 AA.
AC P03407;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85090453; PubMed=2578227;
RA Sanchez-Pescador R., Power M.D., Barr P.J., Stelmer K.S.,
RA Stenplen M.W., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
RA Levy J.A., Dina D., Luciw P.A.;
RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
RT (ARV-2).";
RL Science 227:484-492(1985).
RN [2]
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
RX MEDLINE=88039140; PubMed=3118220;
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
RA Montagnier L., Lecocq J.-P.;
RT "HIV F3' orf encodes a phosphorylated GTP-binding protein resembling
RT an oncogene product.";
RL Nature 330:268-269(1987).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -----
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CC -----
DR EMBL: K02007; AA59893.1;
DR PIR: A04009; ASLJO2.
DR HSP: P03406; IEFN.
DR HIV: K02007; NEF8SF2.
DR InterPro: IPR001558; F-protein.
DR Pfam: PF00469; F-protein; 1.
KW AIDS; Myristate; GTP-binding.
FT LIPID 2 2 MYRISTATE.
SQ SEQUENCE 210 AA; 24042 MW; ED25233F8A17DAB CRC64;

Query Match 44.2%; Score 997; DB 1; Length 210;
Best Local Similarity 85.2%; Pred. No. 1e-75;
Matches 179; Conservative 16; Mismatches 11; Indels 4; Gaps 1;

QY 110 MGGKWSKSSVVGWPTVRRMR-----RAEPAADGVGAASRDLEKKGAISSNTAATNAACA 165
Db 1 MGGKWSKSMKGWSAIRERMRRAEPAEPAADGVGAASRDLEKKGAISSNTAATNADCA 60

QY 166 WLEAQEEVEEFGPVPQVPLRPMTYKAAVDLSHFLEKKGLEGLIHSQRQDILDWY 225
Db 61 WLEAQEEVEEFGPVPQVPLRPMTYKAAVDLSHFLEKKGLEGLIHSQRQDILDWY 120

QY 226 TQGYFPDQNTTGGVRRPLTGGWCKLVPEPEKVEEANGENSLHHPMSLHGMD 285
Db 121 TQGYFPDQNTTGGVRRPLTGGWCKLVPEPEKVEEANGENSLHHPMSLHGMD 180

QY 286 PEREVLWRFDSRLAFHVAHELHPEYFKNC 315
Db 181 PEREVLWRFDSRLAFHVAHELHPEYFKNC 210

RESULT 10
NEF_HV1RH
ID NEF_HV1RH STANDARD; PRT: 208 AA.
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AC P05858;
DT 01-NOV-1998 (Rel. 09, Created)
DT 01-NOV-1998 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11701;
RN [1]
RP SEQUENCE FROM N.A.
RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S.,
RA Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
RA Wong-Staal F.;
RL Submitted (XXX-1987) to the HIV data bank.
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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CC -----
DR EMBL; M17451; AAA45058.1; -
DR HSP; P03406; IEFN.
DR HIV; M17451; NEFSRF.
DR InterPro: IPR001558; F-protein.
DR Pfam: PF00469; F-protein; 1.
DR AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 208 AA; 23532 MW; 8F836FE980F084C CRC64;
-----
Query Match 44.1%; Score 994; DB 1; Length 208;
Best Local Similarity 84.6%; Pred. No. 2e-75;
Matches 176; Conservative 16; Mismatches 14; Indels 2; Gaps 1;
QY 110 MGGKWSKSVVGVPTVRERMRRAEPAADGVGAASRDLEKHGAITSNTAAATNAACAWLEA 169
DB 1 MGGKWSKSMGWPVAVREMRQAEPAADGVGAASRDLEKHGITSNTAANAACWLEA 60
QY 170 Q--EEEVGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLGLIHSORRQDIL 227
DB 61 QDEDEEVGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLGLVFSQKRODILDLVYHTQ 120
QY 228 GYFPDMQNTPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPER 287
DB 121 GYFPDMQNTPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPER 180
QY 288 EYLEWRFDSRLAFHHVARELHPEYFKN 315
DB 181 EYLVNKFDSRLAFHHVARELHPEYKDC 208
RESULT 11
NEF_HV1Y2
ID NEF_HV1Y2 STANDARD; PRT; 214 AA.
AC P35559;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=36377;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
RA MEDLINE=93021387; PubMed=1404605;
RA
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RA Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological
RT properties of human immunodeficiency virus type 1 in vivo: evidence
RT for limited defectiveness and complementation.";
RL J. Virol. 66:6587-6600(1992).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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CC -----
DR EMBL; M93258; -; NOT_ANNOTATED_CDS.
DR PIR; I44001; I44001.
DR HSP; P03406; IEFN.
DR InterPro: IPR001558; F-protein.
DR Pfam: PF00469; F-protein; 1.
DR AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 214 AA; 24532 MW; E188D43D7B084D04 CRC64;
-----
Query Match 44.0%; Score 991.5; DB 1; Length 214;
Best Local Similarity 84.2%; Pred. No. 3.3e-75;
Matches 181; Conservative 12; Mismatches 11; Indels 11; Gaps 2;
QY 110 MGGKWSKSVVGVPTVR-----ERMRAEPAADGVGAASRDLEKHGAITSNTAA 159
DB 1 MGGKWSKSMAGVPTVRERMRRAEPAEARMRAEPAADGVGAASRDLEKHGAITSNTAA 60
QY 160 TNAACAWLEAQEEVEVGFVTPQVPLRPMTYKAAVDLSHFLKKEGGLGLIHSORRQDIL 219
DB 61 TNAACAWLEAQEEVEVGFVTPQVPLRPMTYKAAVDLSHFLKKEGGLGLIHSORRQDIL 120
QY 220 DLWYHTQGYFPDMQNTPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSL 279
DB 121 DLWYHTQGYFPDMQNTPG-CTRWPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSL 179
QY 280 HCMDDPEREVLWRFDSRLAFHHVARELHPEYFKN 314
DB 180 HCMDDPEREVLWRFDSRLAFHHVARELHPEYFKN 214
RESULT 12
NEF_HV1JR
ID NEF_HV1JR STANDARD; PRT; 216 AA.
AC P20867;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (JRCF isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen I.S.Y.;
RL Submitted (DEC-1988) to the HIV data bank.
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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CC -----
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CC EMBL; M38429; AAB03750.1; -
DR HSSP; P03406; IEFN
DR HIV; M38429; NEFSJRCFSF.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 216 AA; 24567 MW; D163FFA8C71529DC CRC64;

Query Match 43.5%; Score 981; DB 1; Length 216;
Best Local Similarity 81.9%; Pred. No. 2.5e-74;
Matches 177; Conservative 15; Mismatches 14; Indels 10; Gaps 1;

Qy 110 MGGKWSKSVVGVPTVRMRRAEPAAD-----GVGAASRDLEKHGAITSNTAA 159
Dy 1 MGGKWSKSHVPGWSTVRMRRAEPAATDRVQTEPAAGVGVASRDLEKHGAITSNTAA 60
Qy 160 TNAACAWLEAOEVEEGFPVTPVPLRPMYKAAVDLSHFLKEKGLGLHSQRQDIL 219
Dy 61 TNADCAWLEAVEDEVGFPVTPVPLRPMYKAAIDLSHFLKEKGLGLHSQRQDIL 120
Qy 220 DLWIYHTQGYFPDMQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHHPVSL 279
Dy 121 DLWIYHTQGYFPDMQNYTAGCVRFPLTFGWCYKLVPEPKVEANKGENTSLHHPVSL 180
Qy 280 HQMDPPEVLEWRDPSRLAFHHVARELHPEYFKNC 315
Dy 181 HQMDPPEVLEWRDPSRLAFHHVARELHPEYFKNC 216

RESULT 13
NEF_HV1S1
ID NEF_HV1S1 STANDARD; PRT; 208 AA.
AC P19546;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL J. Virol. 64:4390-4398(1990).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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CC
CC EMBL; M65024; AAA5073.1; -
DR HSSP; P03406; IEFN.
DR HIV; M38428; NEFSF162.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 208 AA; 23684 MW; AUB1007D14E4E32 CRC64;

Query Match 43.2%; Score 974; DB 1; Length 208;
Best Local Similarity 79.1%; Pred. No. 6.4e-70;
Matches 163; Conservative 24; Mismatches 18; Indels 1; Gaps 1;
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Best Local Similarity 84.2%; Pred. No. 9e-74;
Matches 176; Conservative 16; Mismatches 13; Indels 4; Gaps 2;

Qy 110 MGGKWSKSVVGVPTVRMRMR---AEPADGVGAASRDLEKHGAITSNTAATAACAW 166
Dy 1 MGGKWSK-RMSGWSAVRMRMRRAEPAEPAAGVGVASRDLEKHGAITSNTAANAADCAW 59
Qy 167 LEAOEVEEGFPVTPVPLRPMYKAAVDLSHFLKEKGLGLHSQRQDILDLWIYHT 226
Dy 60 LEAOEVEDVGFPVTPVPLRPMYKAAVDLSHFLKEKGLGLHSQRQDILDLWIYHT 119
Qy 227 QGYFPDMQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHHPVSLHGMDDPE 286
Dy 120 QGYFPDMQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHHPVSLHGMDDPE 179
Qy 287 REVLEWRDPSRLAFHHVARELHPEYFKNC 315
Dy 180 KEVLWRDPSRLAFHHVARELHPEYFKNC 208

RESULT 14
NEF_HV1E1
ID NEF_HV1E1 STANDARD; PRT; 206 AA.
AC P04604;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86245056; PubMed=2424612;
RA Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
RT of two isolates from African patients.";
RL Cell 46:63-74(1986).
RN [2]
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
RX MEDLINE=88039140; PubMed=3118220;
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
RA Montagnier L., Lecocq J.-P.;
RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
RT an oncogene product.";
RL Nature 330:266-269(1987).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC
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CC
CC EMBL; K03454; AAA44330.1; -
DR EMBL; A07108; CAA00617.1; -
DR HSSP; P03406; IEFN.
DR HIV; K03454; NEFSLI.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 206 AA; 23612 MW; 4CFF9F18AEAB503C CRC64;
```

Query Match 41.1%; Score 927.5; DB 1; Length 206;  
Best Local Similarity 79.1%; Pred. No. 6.4e-70;  
Matches 163; Conservative 24; Mismatches 18; Indels 1; Gaps 1;



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QY 229 YFPDQNTPGVGYRPLTFGWCYKLVPEVDKVEEANKGENTSLHPVSLHGDDPERE 288
DB 121 IFPDQNTPGGIRYPLTFGWCYKLVPEVDKVEEANKGENTSLHPVSLHGDDPERE 180
QY 289 VLEWRDPSRLAFHVAHELHPEYFKNC 315
DB 181 VLMWRNSRLALEKHARELHPEYFKDC 207

RESULT 17
NEF_HV104
ID NEF_HV104 STANDARD; PRT; 205 AA.
AC P24741;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (strain Ugandan / isolate U455)
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11703;
RN [1]
RP MEDLINE=91090981; PubMed=2265025;
RX Oram J.D., Downing R.G., Roff M., Clegg J.C.S., Serwadda D.,
RA Carswell J.W.;
RT "Nucleotide sequence of a Ugandan HIV-1 provirus reveals genetic
diversity from other HIV-1 isolates.";
RL AIDS Res. Hum. Retroviruses 6:1073-1078(1990).
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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CC -----
DR EMBL; M62320; AAA75023.1; -
DR HSP; P03406; 1EFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; Myristate; Gtp-binding.
FT LIPID 2
SQ SEQUENCE 205 AA; 23253 MW; 869AB03B6E7893C4 CRC64;

Query Match 38.7%; Score 872; DB 1; Length 205;
Best Local Similarity 75.1%; Pred. No. 2.6e-65;
Matches 154; Conservative 24; Mismatches 27; Indels 0; Gaps 0;

QY 110 MGGKWSKSSVVGWPTVTRERMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 169
DB 1 MGGKWSKSRVWENPEVRKMRMTEPAAGKGVGAASRDLEKHGAITSNTAATNAACAWLEA 60
QY 170 QEEVEVGFPPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDILDWIYHTQGY 229
DB 61 QEEGDVGFPPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDILDWIYHTQGF 120
QY 230 FPDQNTPGVGYRPLTFGWCYKLVPEVDKVEEANKGENTSLHPVSLHGDDPERE 289
DB 121 FPDQNTPGGIRYPLTFGWCYKLVPEVDKVEEANKGENTSLHPVSLHGDDPERE 180
QY 290 LEWRDPSRLAFHVAHELHPEYFKNC 314
DB 181 LMKFPDSTALKHAYELHPEYFKD 205

RESULT 18
NEF_HV1MN

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ID NEF_HV1MN STANDARD; PRT; 182 AA.
AC P05856;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11696;
RN [1]
RP MEDLINE=88219542; PubMed=3369091;
RX Gurgo C., Guo H.-G., Franchini G., Aldovini A., Colliatti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988).
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
PATIENT IN 1984.
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CC -----
DR EMBL; M17449; AAA44858.1; -
DR HSP; P03406; 1EFN.
DR HIV; M17449; NEFSMN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; Myristate; Gtp-binding.
FT LIPID 2
SQ SEQUENCE 182 AA; 20632 MW; 2C5B5A6E3EF13B26 CRC64;

Query Match 37.3%; Score 842; DB 1; Length 182;
Best Local Similarity 87.4%; Pred. No. 6.8e-63;
Matches 153; Conservative 11; Mismatches 7; Indels 4; Gaps 2;

QY 110 MGGKWSKSSVVGWPTVTRERMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAW 166
DB 1 MGGKWSK-RVGTGPTVTRERMRRAEPAELAADGVGAASRDLEKHGAITSNTAATNAACAW 59
QY 167 LEAQEEVEVGFPPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDILDWIYHT 226
DB 60 LEAQEEVEVGFPPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDILDWIYHT 119
QY 227 QGYFPDQNTPGVGYRPLTFGWCYKLVPEVDKVEEANKGENTSLHPVSLHG 281
DB 120 QGYFPDQNTPGGIRYPLTFGWCYKLVPEVDKVEEANKGENTSLHPVSLHG 174

RESULT 19
NEF_HV12H
ID NEF_HV12H STANDARD; PRT; 205 AA.
AC P05859;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (Zaire H2321 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11692;
RN [1]
RP MEDLINE=89228766; PubMed=2713163;
RX Srinivasan A., York D., Butler D. Jr., Jannoun-Nasr R., Getchell J.,

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RA McCormick J., Ou C.Y., Myers G., Smith T., Chen E.;  
RT "Molecular characterization of HIV-1 isolated from a serum collected  
RT in 1976: nucleotide sequence comparison to recent isolates and  
RT generation of hybrid HIV-1";  
RL AIDS Res. Hum. Retroviruses 5:121-129(1989).  
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL: M15896; AAB53951.1; -;  
DR PIR: B44963;  
DR HSP: P03406; IEFN.  
DR HIV: M15896; NEFSZ321.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
DR AIDS; Myristate; GTP-binding.  
KW AIDS; Myristate; GTP-binding.  
FT Lipid 2  
SQ SEQUENCE 205 AA; 23306 MW; EA55B18AF412A9D0 CRC64;  
-----  
Query Match 37.1%; Score 837; DB 1; Length 205;  
Best Local Similarity 73.2%; Pred. No. 2.1e-62;  
Matches 153; Conservative 23; Mismatches 25; Indels 8; Gaps 3;  
QY 110 MGGKWSKSSVVGWTVTRMR---AEPADGVGAASRDLEKKGAISSNTAATNAACAW 166  
DB 1 MGNKWSK----GWPAVRERIRQTPPPAAEGVGAASQDLAKHGAISSNTATNPPDCAW 56  
QY 167 LEAQEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKKGGLGTHSRRQDILDLYH 225  
DB 57 LEAQEESEVGFPVTPQVPLRPMTYKAAVDLSHFLKKGGLGTHSRRQDILDLYH 116  
QY 226 TQGFPPDMONTGPGVRYPTFGWCYKLVPEPDKVEANKGENTSLLLHPVSLHGMDDP 285  
DB 117 TQGFPPDMONTGPGVRYPTFGWCYKLVPEPDKVEANKGENTSLLLHPVSLHGMDDP 176  
QY 286 EREVLEWRFDSPALPHVARELHPEYFKN 314  
DB 177 EREVLEWRFDSPALPHVARELHPEYFKN 205  
-----  
RESULT 20  
NEF_HV1MA  
ID NEF_HV1MA STANDARD; PRT; 209 AA.  
AC P04603;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
GN NEF.  
OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI_TaxID=11697;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86245056; PubMed=2424612;  
RA Allison M., Wain-Hobson S., Montagnier L., Sonigo P.;  
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis  
RT of two isolates from African patients.";  
RL Cell 46:63-74(1986).  
RN [2]  
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.  
RX MEDLINE=88039140; PubMed=3118220;  
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,  
RA Montagnier L., Lecocq J.-P.;  
RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
```

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RT an oncogene product.";  
RL Nature 330:266-269(1987).  
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
CC -----  
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CC -----  
DR EMBL: X04415; CAA28017.1; -;  
DR EMBL: A07116; CAA00624.1; -;  
DR HSP: P03406; IEFN.  
DR HIV: K03456; NEFSMAL.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; Myristate; GTP-binding.  
FT Lipid 2  
SQ SEQUENCE 209 AA; 23644 MW; D0B30A2442C8CC44 CRC64;  
-----  
Query Match 37.0%; Score 834.5; DB 1; Length 209;  
Best Local Similarity 70.1%; Pred. No. 3.4e-62;  
Matches 148; Conservative 26; Mismatches 30; Indels 7; Gaps 2;  
QY 110 MGGKWSKSSVVGWTVTRMRRAEPAADGVG-----AASRDLEKKGAISSNTAATNAAC 164  
DB 1 MGGKWSKSSIVGPKIRIRIRPTETGCGAVSQDVLKCGAAASSPAANNASC 60  
QY 165 AWLEAQEESEVGFPVTPQVPLRPMTYKAAVDLSHFLKKGGLGTHSRRQDILDLYH 224  
DB 61 E--PPEEESEVGFPVTPQVPLRPMTYKAAVDLSHFLKKGGLGTHSRRQDILDLYH 118  
QY 225 HTQGYFPDMONTGPGVRYPTFGWCYKLVPEPDKVEANKGENTSLLLHPVSLHGMDD 284  
DB 119 HTQGYFPDMONTGPGVRYPTFGWCYKLVPEPDKVEANKGENTSLLLHPVSLHGMDD 178  
QY 285 PEREVLWRFDSPALPHVARELHPEYFKN 315  
DB 179 AEREVLKWKFDSSALPHVARELHPEYFKN 209  
-----  
RESULT 21  
NEF_SIVCZ  
ID NEF_SIVCZ STANDARD; PRT; 205 AA.  
AC P17664;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
GN NEF.  
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI_TaxID=11723;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90259077; PubMed=2188136;  
RA Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;  
RT "Genetic organization of a chimpanzee lentivirus related to HIV-1.";  
RL Nature 345:356-359(1990).  
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
CC -----  
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CC -----
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CC EMBL: X52154; CAA36408.1; -
DR PIR: S09991; ASLJIK.
DR HSP: P03406; 1EFN.
DR HIV: X52154; NEFSCP2.
DR InterPro: IPR001558; F-protein.
DR Pfam: PF00469; F-protein; 1.
DR KW: Myristate; GTP-binding.
DR AIDS: Myristate; GTP-binding.
DR LIPID 2
FT SEQUENCE 205 AA; 23850 MW; 21E0A3EC99F1811F CRC64;
SQ

Query Match 36.9%; Score 832; DB 1; Length 205;
Best Local Similarity 70.2%; Pred. No. 5.3e-62;
Matches 144; Conservative 27; Mismatches 34; Indels 0; Gaps 0;

QY 110 MGGKWSKSSVVGWPTVRMRRAEPAADVGGAARDLEKKGGLHSHFLEKGGGLHSORRQDILDWIYHTQGY 169
Db 1 MGTKWSKSSLVGWPEVRRIEAPTAAGVGGEVSKOLERHCAITSRNPTETNQTALWLEE 60
QY 170 QEEVEVGFPTVPQPLRPMTYKAAVDLSHFLKKEKGGGLHSHFLEKGGGLHSORRQDILDWIYHTQGY 229
Db 61 MDNEEVGFPPVPRQVPTPRMTYKAAFDLSHFLKKEKGGGLHSHFLEKGGGLHSORRQDILDWIYHTQGF 120
QY 230 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVPEAKNGENTSLHPVSLHGMDDPEREV 289
Db 121 FPDQNTYTPGCTRPPLCFGWCYKLVPEEQVEQANEGDNCLLHPICQHGMEDEKVEV 180
QY 290 LEWRFDLSRLAFHVAHELHPEYFKN 314
Db 181 LVWRFDLSRLARHIAREQHPYKYD 205

RESULT 22
NEF_HV1SC
ID NEF_HV1SC STANDARD; PRT; 239 AA.
AC P05857;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgu C., Guo H.-G., Franchini G., Aldovini A., Colliatti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988).
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
CC 1984 IN SOUTHERN CALIFORNIA.
CC
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Query Match 36.3%; Score 819; DB 1; Length 239;
Best Local Similarity 75.5%; Pred. No. 7.8e-61;
Matches 157; Conservative 31; Mismatches 31; Indels 4; Gaps 2;

QY 110 MGGKWSKSSVVGWPTVRMRRAEPAADVGGAARDLEKKGGLHSHFLEKGGGLHSORRQDILDWIYHTQGY 169
Db 1 MGGKWSKRSVVGWPTVRMRMRKTEPAADVGGAARDLEKKGGLHSHFLEKGGGLHSORRQDILDWIYHTQGY 60
QY 170 QEEVEVGFPTVPQPLRPMTYKAAVDLSHFLKKEKGGGLHSHFLEKGGGLHSORRQDILDWIYHTQGY 229
Db 61 QEEVEVGFPPVPRQVPLRPMTYKAAVDLSHFLKKEKGGGLHSHFLEKGGGLHSORRQDILDWIYHTQGY 118
QY 230 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVPEAKNGENTSLHPVSLHGMDDPER 287
Db 119 ATSLIGRTHHOGQSDIPLCFGWCYKLVPEKPEKEEANEENEGENNSLLHPMSLHGMDDPER 178
QY 288 EVLEWRDLSRLAFHVAHELHPEYFKN 315
Db 179 EVLEWRDLSRLAFHVAHELHPEYFKN 206

RESULT 23
NEF_HV1H2
ID NEF_HV1H2 STANDARD; PRT; 123 AA.
AC P04601; O09780;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
RT virus.";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]
RP REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
RX MEDLINE=88039140; PubMed=3118220;
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
RA Montagnier L., Lecocq J.-P.;
RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
RT an oncogene product".
RL Nature 330:266-269(1987).
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -1- MISCELLANEOUS: IN THIS ISOLATE A MUTATION IN POSITION 124 ADDS A
CC STOP CODON AND THE PROTEIN IS MUCH SHORTER THAN IN OTHER ISOLATES
CC (210 AA).
CC
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Infect. Immun. 61:4546-4552(1993).

[4]

SEQUENCE FROM N.A.

STRAIN=EAGAN, 3639, 3640, NCTC 8468, 6-7636, AND HK695;

MEDLINE=95122210; PubMed=7822043;

Song X.-M., Forsgren A., Janson H.;

"The gene encoding protein D (hpd) is highly conserved among Haemophilus influenzae type B and nontypeable strains.";

Infect. Immun. 63:696-699(1995).

[5]

CHARACTERIZATION.

STRAIN-NTHI 772;

MEDLINE=92192801; PubMed=1548059;

Janson H., Heden L.-O., Forsgren A.;

"Protein D, the immunoglobulin D-binding protein of Haemophilus influenzae, is a lipoprotein.";

Infect. Immun. 60:1336-1342(1992).

-I- FUNCTION: GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE HYDROLIZES DEACETYLATED PHOSPHOLIPIDS TO G3P AND THE CORRESPONDING ALCOHOLS. HAS A SPECIFIC AFFINITY FOR HUMAN IMMUNOGLOBULIN D MYELOMA PROTEIN.

-I- CATALYTIC ACTIVITY: A glycerophosphodiester + H(2)O = an alcohol + sn-glycerol 3-phosphate.

-I- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor.

-I- PTM: CONTAINS BOTH ESTER- AND AMIDE-LINKED FATTY ACIDS.

-I- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAINS NTHI 772 AND RD / KW20.

-I- SIMILARITY: TO E. COLI AND B. SUBTILIS GLPO.

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EMBL: U32751; AAC22348.1; -

EMBL: M37487; AAA24998.1; -

EMBL: L12445; AAA24999.1; -

EMBL: Z35656; CAA84715.1; -

EMBL: Z35657; CAA84716.1; -

EMBL: Z35658; CAA84717.1; -

EMBL: Z35659; CAA84718.1; -

EMBL: Z35660; CAA84719.1; -

EMBL: Z35661; CAA84720.1; -

TIGR: H10689; -

InterPro: IPR0041129; GDDP.

Pfam: PF03009; GDDP; 1.

PROSITE: PS00013; PROKAR\_LIPOPROTEIN; 1.

Glycosyl metabolism; Hydrolase; Signal; Lipoprotein; Outer membrane; Complete proteome.

FT SIGNAL 1 18

FT CHAIN 19 364

FT

FT LIPID 19 19 GLYCEROPHOSPHORYL DIESTER

FT VARIANT 13 13 PHOSPHODIESTERASE.

FT VARIANT 15 16 N-ACYL DIGLYCERIDE.

FT VARIANT 25 25 A -> T (IN STRAIN NCTC 8468).

FT VARIANT 28 28 L -> V (IN STRAIN NCTC 8468).

FT VARIANT 34 34 N -> S (IN STRAIN NCTC 8468).

FT VARIANT 34 34 N -> K (IN STRAIN 6-7626).

FT VARIANT 62 62 D -> H (IN STRAIN NCTC 8468).

FT VARIANT 62 62 H -> Q (IN STRAINS EAGAN; 3639; 3640; 6-7626; HK695; MINNA).

FT VARIANT 63 63 S -> A (IN STRAINS EAGAN; 3639; 3640; NCTC 8468; 6-7626; HK695; MINNA).

FT VARIANT 98 98 Y -> H (IN STRAINS EAGAN; 3639; 3640; NCTC 8468; 6-7626; HK695; MINNA).

FT VARIANT 99 99 R -> H (IN STRAIN NCTC 8468).

FT VARIANT 144 144 K -> Q (IN STRAIN 6-7626).

FT VARIANT 168 168 K -> R (IN STRAIN 6-7626).

FT VARIANT 191 191 T -> A (IN STRAINS EAGAN; 3639; 3640; NCTC 8468; 6-7626; HK695; MINNA).





Best Local Similarity 98.8%; Pred. No. 4.1e-33;  
Matches 84; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 318 EPVDPRLPEPKHPSQPKTACTNCYCKCCFHCQVCFITKALGISYGRKKRRRRPPQG 377  
|||||  
Db 2 EPVDPRLPEPKHPSQPKTACTNCYCKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
|||||  
QY 378 SOTHQVSLSKQPTSQSRGDPGPK 402  
|||||  
Db 62 SOTHQVSLSKQPTSQSRGDPGPK 86  
|||||

## RESULT 29

TAT\_HV1BR  
ID TAT\_HV1BR STANDARD: PRT: 86 AA.  
AC PO4610;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE TAT protein (Transactivating regulatory protein).  
GN TAT.  
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11686;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85099333; PubMed=2981635;  
RA Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;  
RT "Nucleotide sequence of the AIDS virus, LAV.#";  
RL Cell 40:9-17(1985).  
RN [2]  
RP SEQUENCE FROM N.A. (CLONE PNL4-3).  
RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;  
RL Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE  
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND  
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR  
CC PROMOTER.  
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.  
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CC -----  
DR EMBL; K02013; AAB59745.1; -  
DR EMBL; M19921; AAB44985.1; -  
DR HIV; K02013; TAT5BRU.  
DR HIV; M19921; TAT5NL43.  
DR InterPro; IPR001831; HIV\_Tat.  
DR Pfam; PF00539; Tat; 1.  
DR PRINTS; PR00055; HIVTATDOMAIN.  
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;  
KW AIDS.  
FT VARIANT 24 24 T -> N (IN CLONE PNL4-3).  
FT VARIANT 39 39 T -> M (IN CLONE PNL4-3).  
FT VARIANT 58 61 PPQG -> AHON (IN CLONE PNL4-3).  
FT VARIANT 67 67 V -> A (IN CLONE PNL4-3).  
FT VARIANT 77 77 P -> S (IN CLONE PNL4-3).  
SEQUENCE 86 AA; 9769 MW; 9B1BA915FAF8A14 CRC64;

Query Match 20.8%; Score 470; DB 1; Length 86;  
Best Local Similarity 96.5%; Pred. No. 1.9e-32;  
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 318 EPVDPRLPEPKHPSQPKTACTNCYCKCCFHCQVCFITKALGISYGRKKRRRRPPQG 377  
|||||  
Db 2 EPVDPRLPEPKHPSQPKTACTNCYCKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
|||||

QY 378 SOTHQVSLSKQPTSQSRGDPGPK 402  
|||||  
Db 62 SOTHQVSLSKQPTSQSRGDPGPK 86  
|||||

## RESULT 30

TAT\_HV1RH  
ID TAT\_HV1RH STANDARD: PRT: 102 AA.  
AC PO5908;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE TAT protein (Transactivating regulatory protein).  
GN TAT.  
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11701;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86218077; PubMed=2423250;  
RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S.,  
RA Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,  
RA Wong-Staal F.;  
RT "Identification and characterization of conserved and variable  
RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of  
RT AIDS.";  
RL Cell 45:637-648(1986).  
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE  
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND  
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR  
CC PROMOTER.  
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.  
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CC -----  
DR EMBL; M17451; AAB45050.1; -  
DR HIV; M17451; TAT5RF.  
DR InterPro; IPR001831; HIV\_Tat.  
DR Pfam; PF00539; Tat; 1.  
DR PRINTS; PR00055; HIVTATDOMAIN.  
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;  
KW AIDS.  
SEQUENCE 102 AA; 11538 MW; 3EACFB843C5195BD CRC64;

Query Match 20.4%; Score 461; DB 1; Length 102;  
Best Local Similarity 91.9%; Pred. No. 1.3e-31;  
Matches 79; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 318 EPVDPRLPEPKHPSQPKTACTNCYCKCCFHCQVCFITKALGISYGRKKRRRRPPQG 377  
|||||  
Db 2 EPVDPRLPEPKHPSQPKTACTNCYCKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
|||||  
QY 378 SOTHQVSLSKQPTSQSRGDPGPK 403  
|||||  
Db 62 SOTHQVSLSKQPTSQSRGDPGPK 87  
|||||

Search completed: August 26, 2002, 08:15:42  
Job time: 346 sec

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OM protein - protein search, using sw model

Run on: August 26, 2002, 08:14:55 ; Search time 86.53 Seconds  
(without alignments)  
821.691 Million cell updates/sec

Title: US-09-509-239-17  
Perfect score: 2255  
Sequence: 1 CSHSSNMANTOMKSDKIII.....QSRGDTGPKTSGHHHHH 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_19.\*

1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriaph.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1129	50.1	206	15 Q9WM24	Q9wm24 human immun
2	1124	49.8	206	15 Q9WLM4	Q9wlm4 human immun
3	1119	49.6	206	15 Q40177	Q40177 human immun
4	1115	49.4	206	15 Q90V07	Q90v07 human immun
5	1108	49.1	206	15 Q9PXW9	Q9pxw9 human immun
6	1105	49.0	206	15 Q9PXM16	Q9pml6 human immun
7	1104	49.0	206	15 Q9WM30	Q9wm30 human immun
8	1101	48.8	206	15 Q9PXW8	Q9pxw8 human immun
9	1096	48.6	206	15 Q90179	Q90179 human immun
10	1096	48.6	206	15 Q85588	Q85588 aids-associ
11	1096	48.6	206	15 Q78244	Q78244 human immun
12	1092	48.4	206	15 Q9WLM7	Q9wlm7 human immun
13	1090	48.3	206	15 Q74905	Q74905 human immun
14	1087	48.2	206	15 Q89561	Q89561 human immun
15	1085	48.1	206	15 Q74913	Q74913 human immun
16	1080	47.9	206	15 Q74917	Q74917 human immun

#### ALIGNMENTS

RESULT 1

Q9WM24 ID Q9WM24 PRELIMINARY; PRT; 206 AA.  
AC Q9WM24;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_taxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=12-IT;  
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,  
RA Johansson B., Vahine A., Sonnerborg A.;  
RT "HIV-1 nef mutations and clinical long-term non progression: a  
RT molecular epidemiology study";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4 (T4) ANTIGEN.  
DR EMBL; AF011480; AAD01458.1; -  
DR HSSP; P03406; 1EFN.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23328 MW; FCC69458158F1A03 CRC64;

Query Match 50.1%; Score 1129; DB 15; Length 206;

Best Local Similarity 99.5%; Pred. No. 2.7e-83;

Matches 205; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 110 MGGKWSKSVVGWPTVREMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 169

DB 1 MGGKWSKSVVGWPTVREMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60

QY 170 QBEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSQRQDILDLIWYHTQGY 229

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|||||
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDLYVHTQGY 120
QY 230 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLLHPVSLHGMDPPEV 289
Db 121 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLLHPVSLHGMDPPEV 180
QY 290 LEWRFDLSLAFHHVARELHPEYFKNC 315
Db 181 LEWRFDLSLAFHHVARELHPEYFKNC 206

RESULT 2
Q9WLM4 PRELIMINARY: PRT; 206 AA.
AC Q9WLM4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21-SW;
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,
RA Johanson B., Vahine A., Sonnerborg A.;
RT "HIV-1 nef mutations and clinical long-term non progression: a
RT molecular epidemiology study.";
RL Submitted (Feb-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4 (T4) ANTIGEN.
DR EMBL; AF047087; AA02461.1; -
DR HSSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23341 MW; FCD22B1CEB655BB9 CRC64;

Query Match 49.8%; Score 1124; DB 15; Length 206;
Best Local Similarity 99.0%; Pred. No. 6.9e-83;
Matches 204; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 169
Db 1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60
QY 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDLYVHTQGY 229
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDLYVHTQGY 120
QY 230 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLLHPVSLHGMDPPEV 289
Db 121 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLLHPVSLHGMDPPEV 180
QY 290 LEWRFDLSLAFHHVARELHPEYFKNC 315
Db 181 LEWRFDLSLAFHHVARELHPEYFKNC 206

Query Match 49.8%; Score 1119; DB 15; Length 206;
Best Local Similarity 98.5%; Pred. No. 1.7e-82;
Matches 203; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 169
Db 1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60
QY 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDLYVHTQGY 229
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDLYVHTQGY 120
QY 230 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLLHPVSLHGMDPPEV 289
Db 121 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLLHPVSLHGMDPPEV 180
QY 290 LEWRFDLSLAFHHVARELHPEYFKNC 315
Db 181 LEWRFDLSLAFHHVARELHPEYFKNC 206

RESULT 4
Q9WVU7 PRELIMINARY: PRT; 206 AA.
AC Q9WVU7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEF PROTEIN.
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NL4-3;
RX MEDLINE=96036482; PubMed=7483282;
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
RA Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes
RT from primary virus cultures using the polymerase chain reaction.";
RL Virology 213:80-86(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NL4-3;
RX MEDLINE=86281827; PubMed=3016298;
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
RA Martin M.A.;
RT "Production of acquired immunodeficiency syndrome-associated
RT retrovirus in human and nonhuman cells transfected with an infectious
RT molecular clone.";
RL J. Virol. 59:284-291(1986).
DR EMBL; U26942; AAB60579.1; -
SQ SEQUENCE 206 AA; 23367 MW; 65AF3B6184DC2FE7 CRC64;
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Query Match 49.4%; Score 1115; DB 15; Length 206;  
Best Local Similarity 98.1%; Pred. No. 3.7e-82;  
Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 110 MGKSKSVVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169  
DB 1 MGKSKSVVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60

QY 170 QEEVEGFPVTPQVPLRPMYTYKAADLSHFLKEKGLGIIHSQRQDILDLMWYHTQY 229  
DB 61 QEEVEGFPVTPQVPLRPMYTYKAADLSHFLKEKGLGIIHSQRQDILDLMWYHTQY 120

QY 230 FPDWQNTPGVRYPLTFCWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPEREV 289  
DB 121 FPDWQNTPGVRYPLTFCWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPEREV 180

QY 290 LEWRDLSRLAFHFAHVAHELPEYFKNC 315  
DB 181 LEWRDLSRLAFHFAHVAHELPEYFKNC 206

RESULT 5  
Q9PXW9 PRELIMINARY; PRT; 206 AA.  
AC Q9PXW9;  
DT 01-MAY-2000 (TremBLrel. 13, Created)  
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RC STRAIN-7-IT;  
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,  
Johansson B., Vahine A., Sonnerborg A.;  
RT "HIV-1 nef mutations and clinical long-term non progression: a  
molecular epidemiology study";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL: AF011494; AAD01472.1;  
DR HSP; P03406; IEFN.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23454 MW; 65D5DDE4FB748072 CRC64;

Query Match 49.1%; Score 1108; DB 15; Length 206;  
Best Local Similarity 97.1%; Pred. No. 1.3e-81;  
Matches 200; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 110 MGKSKSVVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169  
DB 1 MGKSKSVVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60

QY 170 QEEVEGFPVTPQVPLRPMYTYKAADLSHFLKEKGLGIIHSQRQDILDLMWYHTQY 229  
DB 61 QEEVEGFPVTPQVPLRPMYTYKAADLSHFLKEKGLGIIHSQRQDILDLMWYHTQY 120

QY 230 FPDWQNTPGVRYPLTFCWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPEREV 289  
DB 121 FPDWQNTPGVRYPLTFCWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPEREV 180

QY 290 LEWRDLSRLAFHFAHVAHELPEYFKNC 315  
DB 181 LEWRDLSRLAFHFAHVAHELPEYFKNC 206

Query Match 49.1%; Score 1108; DB 15; Length 206;  
Best Local Similarity 97.1%; Pred. No. 1.3e-81;  
Matches 200; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 110 MGKSKSVVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169  
DB 1 MGKSKSVVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60

QY 170 QEEVEGFPVTPQVPLRPMYTYKAADLSHFLKEKGLGIIHSQRQDILDLMWYHTQY 229  
DB 61 QEEVEGFPVTPQVPLRPMYTYKAADLSHFLKEKGLGIIHSQRQDILDLMWYHTQY 120

QY 230 FPDWQNTPGVRYPLTFCWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPEREV 289  
DB 121 FPDWQNTPGVRYPLTFCWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPEREV 180

QY 290 LEWRDLSRLAFHFAHVAHELPEYFKNC 315  
DB 181 LEWRDLSRLAFHFAHVAHELPEYFKNC 206

## RESULT 6

Q9WM16 PRELIMINARY; PRT; 206 AA.  
AC Q9WM16;  
DT 01-NOV-1999 (TremBLrel. 12, Created)  
DT 01-NOV-1999 (TremBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RC STRAIN-7-IT;  
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,  
Johansson B., Vahine A., Sonnerborg A.;  
RT "HIV-1 nef mutations and clinical long-term non progression: a  
molecular epidemiology study";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL: AF011494; AAD01472.1;  
DR HSP; P03406; IEFN.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23333 MW; 2EBF2A6A3ECAF5EA CRC64;

Query Match 49.0%; Score 1105; DB 15; Length 206;  
Best Local Similarity 97.1%; Pred. No. 2.3e-81;  
Matches 200; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 110 MGKSKSVVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169  
DB 1 MGKSKSVVGVGPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60

QY 170 QEEVEGFPVTPQVPLRPMYTYKAADLSHFLKEKGLGIIHSQRQDILDLMWYHTQY 229  
DB 61 QEEVEGFPVTPQVPLRPMYTYKAADLSHFLKEKGLGIIHSQRQDILDLMWYHTQY 120

QY 230 FPDWQNTPGVRYPLTFCWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPEREV 289  
DB 121 FPDWQNTPGVRYPLTFCWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPEREV 180

QY 290 LEWRDLSRLAFHFAHVAHELPEYFKNC 315  
DB 181 LEWRDLSRLAFHFAHVAHELPEYFKNC 206

## RESULT 7

Q9WM30 PRELIMINARY; PRT; 206 AA.  
AC Q9WM30;  
DT 01-NOV-1999 (TremBLrel. 12, Created)  
DT 01-NOV-1999 (TremBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RC STRAIN-8-IT;  
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,  
Johansson B., Vahine A., Sonnerborg A.;  
RT "HIV-1 nef mutations and clinical long-term non progression: a  
molecular epidemiology study";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

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DR EMBL; AF011469; AAD01447.1; -.
DR HSSP; P03406; 1EFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS: GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23345 MW; 0ED69927C2E03BB6 CRC64;

Query Match 49.0%; Score 1104; DB 15; Length 206;
Best Local Similarity 97.1%; Pred. No. 2.8e-81;
Matches 200; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 110 MGGKSKSVGVGPTVVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
Db 1 MGGKSKSVGVGPTVVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60

Qy 170 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKKEGGLGLHSQRQDILDWIYHTQGY 229
Db 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKKEGGLGLHSQRQDILDWIYHTQGY 120

Qy 230 FPDQNTYTPGQVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPDERV 289
Db 121 FPDQNTYTPGQVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPDERV 180

Qy 290 LEWRDLSRLAFHHVARELHPEYFKN 315
Db 181 LEWRDLSRLAFHHVARELHPEYFKN 206

RESULT 8
Q9PXW8 PRELIMINARY; PRT; 206 AA.
AC Q9PXW8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93152025; PubMed=1301062;
RA Kohleisen B., Neumann M., Herrmann R., Brack-Werner R., Krohn K.J.,
RT "Cellular localization of Nef expressed in persistently HIV-1-infected
RT low-producer astrocytes."
RL AIDS 6:1427-1436(1992).
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(74) ANTIGEN.
DR HSSP; P03406; 1EFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS: GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23439 MW; 8478CF194D39D5B9 CRC64;

Query Match 48.8%; Score 1101; DB 15; Length 206;
Best Local Similarity 96.1%; Pred. No. 4.9e-81;
Matches 198; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 110 MGGKSKSVGVGPTVVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
Db 1 MGGKSKSVGVGPTVVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60

Qy 170 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKKEGGLGLHSQRQDILDWIYHTQGY 229
Db 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKKEGGLGLHSQRQDILDWIYHTQGY 120

Qy 230 FPDQNTYTPGQVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPDERV 289
Db 121 FPDQNTYTPGQVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPDERV 180
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Qy 290 LEWRDLSRLAFHHVARELHPEYFKN 315
Db 181 LEWRDLSRLAFHHVARELHPEYFKN 206

RESULT 9
Q90179 PRELIMINARY; PRT; 206 AA.
AC Q90179;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95074930; PubMed=7983770;
RA Fang H., Pincus S.H.;
RT "Unique insertion sequence and pattern of CD4 expression in variants
RT selected with immunotoxins from human immunodeficiency virus type 1-
RT infected T cells."
RL J. Virol. 69:75-81(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Fang H., Pincus S.H.;
RT "Spontaneous activation of human immunodeficiency virus type 1 in an
RT immunotoxin-resistant variant T cell line."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(74) ANTIGEN.
DR EMBL; AF070521; AAC28453.1; -.
DR HSSP; P03406; 1EFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS: GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23334 MW; 3E2B9C4017FDC68 CRC64;

Query Match 48.6%; Score 1096; DB 15; Length 206;
Best Local Similarity 95.6%; Pred. No. 1.2e-80;
Matches 197; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 110 MGGKSKSVGVGPTVVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
Db 1 MGGKSKSVGVGPTVVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60

Qy 170 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKKEGGLGLHSQRQDILDWIYHTQGY 229
Db 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKKEGGLGLHSQRQDILDWIYHTQGY 120

Qy 230 FPDQNTYTPGQVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPDERV 289
Db 121 FPDQNTYTPGQVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPDERV 180

Qy 290 LEWRDLSRLAFHHVARELHPEYFKN 315
Db 181 LEWRDLSRLAFHHVARELHPEYFKN 206

RESULT 10
Q85588 PRELIMINARY; PRT; 206 AA.
AC Q85588;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Aids-associated retrovirus.
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OC Viruses; Retroviral viruses; Retroviridae.
OX NCBI_TaxID=11966;
RN [1]
RX SEQUENCE FROM N.A.
RA MEDLINE=8606728; PubMed=2999715;
RA Ratner L., Starcich B., Josephs S.F., Hahn B.H., Reddy E.P., Arya S.K.,
RA Liyak K.J., Petteway S.R.Jr., Pearson M.L., Haseltine W.A., Arva S.K.,
RA Wong-staal F.;
RT "Polymorphism of the 3' open reading frame of the virus associated
RT with the acquired immune deficiency syndrome, human T-lymphotropic
RT virus type III.";
RL Nucleic Acids Res. 13:8219-8229(1985).
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; X03188; CAA26947.1; -.
DR HSSP; P03406; 1EFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23419 MW; 3B25EB332A479A46 CRC64;

Query Match 48.6%; Score 1096; DB 15; Length 206;
Best Local Similarity 96.6%; Pred. No. 1.2e-80;
Matches 199; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 110 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKHGAITSSNTAANNAACAWLEA 60

Qy 170 QEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLIHSQRQDILDWIYHTQGY 229
Db 61 QEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLIHSQRQDILDWIYHTQGY 120

Qy 230 FPDQNYTPGPGVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDPPEV 289
Db 121 FPDQNYTPGPGIRYPLTFGWRKLVPEPEKLEANKGENTSLHPVSLHGMDPPEV 180

Qy 290 LEWRDLSLAFHHVARELHPEYFKNC 315
Db 181 LEWRDLSLAFHHVARELHPEYFKNC 206

RESULT 11
Q78244 ID Q78244 PRELIMINARY; PRT; 206 AA.
AC Q78244;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Q.,
RA Verani P., Rossi G.B.;
RT "Sequence analysis of HIV-1 proviral DNA from a non producer
RT chronically infected HUT-78 cellular clone.";
RL J. Viral Diseases 1:40-55(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352106; PubMed=2765297;
RA Federico M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,
RA Macchi B., Mangiano N., Verani P., Rossi G.;
RT "Biological and molecular characterization of producer and non
RT producer clones from HUT-78 infected with a patient HIV isolate.";
RL AIDS Res. Hum. Retroviruses 5:385-396(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Titti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,

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RA Borsetti A., Saggio I., Verani P., Rossi G.;
RT "Variability of HIV-1 virus: characteristics of an infected but not
RT productive clone.";
RL Int. J. Immunopharmacol. 3:17-23(1990).
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; Z11530; CAA77629.1; -.
DR HSSP; P03406; 1EFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23398 MW; A31CC7244BBB2B43 CRC64;

Query Match 48.6%; Score 1096; DB 15; Length 206;
Best Local Similarity 96.6%; Pred. No. 1.2e-80;
Matches 199; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 110 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNADCAWLEA 60

Qy 170 QEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLIHSQRQDILDWIYHTQGY 229
Db 61 QEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLIHSQRQDILDWIYHTQGY 120

Qy 230 FPDQNYTPGPGVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDPPEV 289
Db 121 FPDQNYTPGPGIRYPLTFGWCYKLVPEPEKLEANKGENTSLHPVSLHGMDPPEV 180

Qy 290 LEWRDLSLAFHHVARELHPEYFKNC 315
Db 181 LEWRDLSLAFHHVARELHPEYFKNC 206

RESULT 12
Q9WLM7 ID Q9WLM7 PRELIMINARY; PRT; 206 AA.
AC Q9WLM7;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=18-SW;
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,
RA Johansson B., Vahne A., Sonnerborg A.;
RT "HIV-1 nef mutations and clinical long-term non progression: a
RT molecular epidemiology study.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF047084; AAD02458.1; -.
DR HSSP; P03406; 1EFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23512 MW; E09E3BEF828A83C0 CRC64;

Query Match 48.4%; Score 1092; DB 15; Length 206;
Best Local Similarity 95.6%; Pred. No. 2.6e-80;
Matches 197; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 110 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
Db 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNACAWLEA 60

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QY 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDLDWIYHTQY 229  
|||||  
DB 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDLDWIYHTQY 120  
|||||  
QY 230 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 289  
|||||  
DB 121 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
|||||  
QY 290 LEWRDLSRLAFHHVARELHPEYFKNC 315  
|||||  
DB 181 LEWRDLSRLAFHHVARELHPEYFKNC 206  
|||||  
RESULT 13  
Q74905 PRELIMINARY; PRT; 206 AA.  
ID Q74905;  
AC Q74905;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96400183; PubMed=8806559;  
RA Ratner L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,  
Hahn B., Powderly W., Arens M.;  
RT "Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects  
at different stages of disease."  
RL Virology 223:245-250(1996).  
CC -I- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL; U44443; AAB38195.1; -;  
DR HSP; Q70627; 2NEF.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
DR AIDS; GTP-binding; Myristate.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23617 MW; 5CAAB09C4730C38A CRC64;

Query Match 48.3%; Score 1090; DB 15; Length 206;  
Best Local Similarity 95.1%; Pred. No. 3.8e-80;  
Matches 196; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
QY 110 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNACAWLEA 169  
|||||  
DB 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNACAWLEA 60  
|||||  
QY 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDLDWIYHTQY 229  
|||||  
DB 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDLDWIYHTQY 120  
|||||  
QY 230 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 289  
|||||  
DB 121 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
|||||  
QY 290 LEWRDLSRLAFHHVARELHPEYFKNC 315  
|||||  
DB 181 LEWRDLSRLAFHHVARELHPEYFKNC 206  
|||||  
RESULT 14  
Q89561 PRELIMINARY; PRT; 206 AA.  
ID Q89561;  
AC Q89561;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.

OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Arens M.O., Ratner L., Joseph T., Bandres J.;  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
CC -I- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL; U44448; AAB38200.1; -;  
DR EMBL; U44447; AAB38199.1; -;  
DR HSP; Q70627; 2NEF.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
DR AIDS; GTP-binding; Myristate.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23629 MW; BF467FB1B7147CDE CRC64;

Query Match 48.2%; Score 1087; DB 15; Length 206;  
Best Local Similarity 94.7%; Pred. No. 6.6e-80;  
Matches 195; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
QY 110 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNACAWLEA 169  
|||||  
DB 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNACAWLEA 60  
|||||  
QY 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDLDWIYHTQY 229  
|||||  
DB 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDLDWIYHTQY 120  
|||||  
QY 230 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 289  
|||||  
DB 121 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
|||||  
QY 290 LEWRDLSRLAFHHVARELHPEYFKNC 315  
|||||  
DB 181 LEWRDLSRLAFHHVARELHPEYFKNC 206  
|||||

RESULT 15  
Q74913 PRELIMINARY; PRT; 206 AA.  
ID Q74913;  
AC Q74913;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96400183; PubMed=8806559;  
RA Ratner L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,  
Hahn B., Powderly W., Arens M.;  
RT "Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects  
at different stages of disease."  
RL Virology 223:245-250(1996).  
CC -I- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL; U44453; AAB38205.1; -;  
DR HSP; P03406; 1EFN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
DR AIDS; GTP-binding; Myristate.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23649 MW; E5B97FA0B70FC175 CRC64;

Query Match 48.1%; Score 1085; DB 15; Length 206;  
Best Local Similarity 95.6%; Pred. No. 9.6e-80;  
Matches 196; Conservative 5; Mismatches 4; Indels 0; Gaps 0;



QY 110 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 169  
DB 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
QY 170 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGLHSQRQDILDWIYHTQY 229  
DB 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGLHSQRQDILDWIYHTQY 120  
QY 230 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 289  
DB 121 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
QY 290 LEWREDSRLAFHHVARELHPEYFKN 314  
DB 181 LEWREDSRLAFHHVARELHPEYFKN 205  
RESULT 16  
Q74917 PRELIMINARY; PRT; 206 AA.  
ID Q74917;  
AC Q74917;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96400183; PubMed=8806559;  
RA Ratner L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,  
Hahn B., Powderly W., Arens M.;  
RT "Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects  
at different stages of disease."  
RL Virology 223:245-250(1996).  
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL; U44450; AAB38210.1; -;  
DR HSP; P03406; IEFN.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23562 MW; 478BBFA675CBC203 CRC64;

Query Match 47.9%; Score 1080; DB 15; Length 206;  
Best Local Similarity 94.7%; Pred. No. 2.4e-79;  
Matches 195; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 110 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 169  
DB 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
QY 170 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGLHSQRQDILDWIYHTQY 229  
DB 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGLHSQRQDILDWIYHTQY 120  
QY 230 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 289  
DB 121 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
QY 290 LEWREDSRLAFHHVARELHPEYFKN 315  
DB 181 LEWREDSRLAFHHVARELHPEYFKN 206  
RESULT 17  
Q74914 PRELIMINARY; PRT; 206 AA.  
ID Q74914;  
AC Q74914;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96400183; PubMed=8806559;  
RA Ratner L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,  
Hahn B., Powderly W., Arens M.;  
RT "Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects  
at different stages of disease."  
RL Virology 223:245-250(1996).  
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL; U44454; AAB38206.1; -;  
DR HSP; P03406; IEFN.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23615 MW; 08D97FA0B70FC17D CRC64;

Query Match 47.8%; Score 1079; DB 15; Length 206;  
Best Local Similarity 95.1%; Pred. No. 2.9e-79;  
Matches 195; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 110 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 169  
DB 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
QY 170 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGLHSQRQDILDWIYHTQY 229  
DB 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGLHSQRQDILDWIYHTQY 120  
QY 230 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 289  
DB 121 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
QY 290 LEWREDSRLAFHHVARELHPEYFKN 314  
DB 181 LEWREDSRLAFHHVARELHPEYFKN 205  
RESULT 18  
Q74915 PRELIMINARY; PRT; 206 AA.  
ID Q74915;  
AC Q74915;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96400183; PubMed=8806559;  
RA Ratner L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,  
Hahn B., Powderly W., Arens M.;  
RT "Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects  
at different stages of disease."  
RL Virology 223:245-250(1996).  
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL; U44455; AAB38207.1; -;  
DR HSP; P03406; IEFN.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.

SQ SEQUENCE 206 AA; 23648 MW; E5BD6FA0B70FC175 CRC64;

Query Match 47.8%; Score 1079; DB 15; Length 206;  
Best Local Similarity 95.6%; Pred. No. 2.9e-79;  
Matches 195; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 110 MGGKWSKSSVGVPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 169  
Db 1 MGGKWSKSSVGVPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
Qy 170 QEEVEGVFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDWIYHTQGY 229  
Db 61 QEEVEGVFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDWIYHTQGY 120  
Qy 230 FPDQNYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 289  
Db 121 FPDQNYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 180  
Qy 290 LEWRDLSRLAFHHVARELHPEYK 313  
Db 181 LEWRDLSRLAFHHVARELHPEYK 204

RESULT 19  
Q74909

ID Q74909 PRELIMINARY; PRT; 206 AA.  
AC Q74909;  
DT 01-NOV-1996 (TremBLrel. 01, Created)  
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.

OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=96400183; PubMed=8806559;  
RA Ratner L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,  
RA Hahn B., Powderly W., Arens M.;  
RT "Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects  
RT at different stages of disease."  
RL Virology 223:245-250(1996).  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

DR EMBL; U44449; AAB38201.1; -  
DR HSSP; Q70627; 2NEF.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS: GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23488 MW; F0596D6FAA81A05 CRC64;

Query Match 47.8%; Score 1077; DB 15; Length 206;  
Best Local Similarity 94.2%; Pred. No. 4.2e-79;  
Matches 194; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 110 MGGKWSKSSVGVPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 169  
Db 1 MGGKWSKSSVGVPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
Qy 170 QEEVEGVFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDWIYHTQGY 229  
Db 61 QEEVEGVFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDWIYHTQGY 120  
Qy 230 FPDQNYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 289  
Db 121 FPDQNYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 180  
Qy 290 LEWRDLSRLAFHHVARELHPEYK 315  
Db 181 LEWRDLSRLAFHHVARELHPEYK 206

RESULT 20  
Q9QPN3

ID Q9QPN3 PRELIMINARY; PRT; 202 AA.  
AC Q9QPN3;  
DT 01-MAY-2000 (TremBLrel. 13, Created)  
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN) (FRAGMENT).  
GN NEF.

OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=HIV-1LAI;  
RA Piedade J., Esteves A., Parreira R., Venenno T., Barros M.F.,  
RA Canas-Ferreira W.F.;  
RT "Cloning and expression of HIV-1 nef gene in the carrier-adjutant  
RT pVb3 expression system based on the major lipoprotein (Opr1) from the  
RT outer membrane of Pseudomonas aeruginosa."  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

DR EMBL; AF166101; AAD47831.1; -  
DR HSSP; P03406; 1EFN.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS: GTP-binding; Myristate.  
FT NON\_TER 202  
SQ SEQUENCE 202 AA; 23033 MW; CD61DFA6F386CC89 CRC64;

Query Match 47.7%; Score 1076; DB 15; Length 202;  
Best Local Similarity 97.5%; Pred. No. 5e-79;  
Matches 197; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 110 MGGKWSKSSVGVPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 169  
Db 1 MGGKWSKSSVGVPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
Qy 170 QEEVEGVFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDWIYHTQGY 229  
Db 61 QEEVEGVFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDWIYHTQGY 120  
Qy 230 FPDQNYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 289  
Db 121 FPDQNYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 180  
Qy 290 LEWRDLSRLAFHHVARELHPEY 311  
Db 181 LEWRDLSRLAFHHVARELHPEY 202

RESULT 21  
Q9Q596

ID Q9Q596 PRELIMINARY; PRT; 206 AA.  
AC Q9Q596;  
DT 01-MAY-2000 (TremBLrel. 13, Created)  
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.

OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Wang B., Saksena N.K.;  
RT "HIV-1 Strains from a cohort of American subjects reveal the presence  
RT of a V2 region extension unique to slow progressors and non-  
RT progressors."

```
RL AIDS 0:0-0(2000).
CC -I- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF203197; AAF25319.1; -.
DR HSSP; P03406; 1EFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23510 MW; 081DF3A12E5A7576 CRC64;

Query Match 47.5%; Score 1072; DB 15; Length 206;
Best Local Similarity 94.7%; Pred. No. 1.le-78;
Matches 195; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 110 MGGKWSKSSVGVVPTVPRMRRAEPAADGVGAASRDLEKKGAGTSSNTAATNAACAWLEA 169
Db 1 MGGKWSKRGIDGWPVAVRMRRAEPAADGVGAASRDLEKKGAGTSSNTAATNAACAWLEA 60

Qy 170 QEEEEVGFPVTPQVPLRPMYKAAVDLSHFLKKEGGLGSLHSQRQDILDLMWYHTQGY 229
Db 61 QEEEEVGFPVTPQVPLRPMYKAAVDLSHFLKKEGGLGSLHSQRQDILDLMWYHTQGY 120

Qy 230 FPDQNYTPGQVRYPLTFGMCKYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 289
Db 121 FPDQNYTPGQVRYPLTFGMCKYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180

Qy 290 LEWRFDLSRLAFHHVARELHPEYFKNC 315
Db 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206

RESULT 22
Q90595
ID Q90595 PRELIMINARY; PRT; 206 AA.
AC Q90595;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=8-IT;
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,
RA Johansson B., Vahlne A., Sonnerborg A.;
RT "HIV-1 nef mutations and clinical long-term non progression: a
RT molecular epidemiology study.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF011470; AAD01448.1; -.
DR HSSP; P03406; 1EFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 208 AA; 23681 MW; 1C891C3AD230C6A8 CRC64;

Query Match 47.5%; Score 1071; DB 15; Length 208;
Best Local Similarity 94.2%; Pred. No. 1.3e-78;
Matches 196; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 110 MGGKWSKSSVGVVPTVPRMRRAEPA--ADGVGAASRDLEKKGAGTSSNTAATNAACAWL 167
Db 1 MGGKWSKRSVIGWPVAVRMRRAEPAAXGAVSRDLEKKGAGTSSNTAATNAACAWL 60

Qy 168 EAQEEEEVGFPVTPQVPLRPMYKAAVDLSHFLKKEGGLGSLHSQRQDILDLMWYHTQ 227
Db 61 EAQEEEEVGFPVTPQVPLRPMYKAAVDLSHFLKKEGGLGSLHSQRQDILDLMWYHTQ 120

Qy 228 GYFPDQNYTPGQVRYPLTFGMCKYKLVPEPKVEEANKGENTSLHPVSLHGMDDPER 287
Db 121 GYFPDQNYTPGQVRYPLTFGMCKYKLVPEPKVEEANKGENTSLHPVSLHGMDDPER 180

Qy 288 EYLEWRFDLSRLAFHHVARELHPEYFKNC 315
Db 181 KYLEWRFDLSRLAFHHVARELHPEYFKNC 208

RESULT 24
Q9W7X3
ID Q9W7X3 PRELIMINARY; PRT; 206 AA.
AC Q9W7X3;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
```

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RL AIDS 0:0-0(2000).
CC -I- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF203197; AAF25319.1; -.
DR HSSP; P03406; 1EFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23510 MW; 081DF3A12E5A7576 CRC64;

Query Match 47.5%; Score 1072; DB 15; Length 206;
Best Local Similarity 94.7%; Pred. No. 1.le-78;
Matches 195; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 110 MGGKWSKSSVGVVPTVPRMRRAEPAADGVGAASRDLEKKGAGTSSNTAATNAACAWLEA 169
Db 1 MGGKWSKRGIDGWPVAVRMRRAEPAADGVGAASRDLEKKGAGTSSNTAATNAACAWLEA 60

Qy 170 QEEEEVGFPVTPQVPLRPMYKAAVDLSHFLKKEGGLGSLHSQRQDILDLMWYHTQGY 229
Db 61 QEEEEVGFPVTPQVPLRPMYKAAVDLSHFLKKEGGLGSLHSQRQDILDLMWYHTQGY 120

Qy 230 FPDQNYTPGQVRYPLTFGMCKYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 289
Db 121 FPDQNYTPGQVRYPLTFGMCKYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180

Qy 290 LEWRFDLSRLAFHHVARELHPEYFKNC 315
Db 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206

RESULT 22
Q90595
ID Q90595 PRELIMINARY; PRT; 206 AA.
AC Q90595;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC Wang B., Saksena N.K.;
RA "HIV-1 Strains from a cohort of American subjects reveal the presence
RT of a V2 region extension unique to slow progressors and non-
RT progressors";
RL AIDS 0:0-0(2000).
CC -I- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF203198; AAF25320.1; -.
DR HSSP; P03406; 1EFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23420 MW; A66FC8B78FFECFD2 CRC64;

Query Match 47.5%; Score 1072; DB 15; Length 206;
Best Local Similarity 93.7%; Pred. No. 1.le-78;
Matches 193; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 110 MGGKWSKSSVGVVPTVPRMRRAEPAADGVGAASRDLEKKGAGTSSNTAATNAACAWLEA 169
Db 1 MGGKWSKSGGWPVAVRMRRAEPAADGVGAASRDLEKKGAGTSSNTAATNAACAWLEA 60

Qy 170 QEEEEVGFPVTPQVPLRPMYKAAVDLSHFLKKEGGLGSLHSQRQDILDLMWYHTQGY 229
Db 61 QEEEEVGFPVTPQVPLRPMYKALDLSHFLKKEGGLGSLHSQRQDILDLMWYHTQGY 120
```

RP SEQUENCE FROM N.A.  
 RC STRAIN-PATIENT 27;  
 RA McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,  
 RA Pemberton L., Brew B.J.;  
 RT "Anomalies in Nef expression within the central nervous system of HIV-  
 RT 1 positive individuals/AIDS patients with or without AIDS dementia  
 RT complex";  
 RL J. Neurovirol. 4:0-0(1998).  
 CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 DR EMBL; AF064676; AAC18377.1;  
 DR HSSP; P03406; 1EFN.  
 DR InterPro; IPR001558; F-protein.  
 DR Pfam; PF00469; F-protein; 1.  
 KW AIDS; GTP-binding; Myristate.  
 SQ SEQUENCE 206 AA; 23499 MW; DEE21CAF05891D68 CRC64;

Query Match 47.4%; Score 1068; DB 15; Length 206;  
 Best Local Similarity 91.7%; Pred. No. 2.2e-78;  
 Matches 189; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

Qy 110 MGGKWSKSSVVGWPTVRMRRAEPAADGCGAASRDLEKKGAISSNTAATNAACAWLEA 169  
 Db 1 MGGKWSKSSVVGWPTVRMRRAEPAADGCGAASRDLEKKGAISSNTAATNAACAWLEA 60

Qy 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLHSORRODILDWIYHTQGY 229  
 Db 61 QKEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLHSORRODILDWIYHTQGY 120

Qy 230 FPDQNTYTPGVRYPPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 289  
 Db 121 FPDQNTYTPGVRYPPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180

Qy 290 LEWRFDLSRLAFHHARELHPEYKNC 315  
 Db 181 LEWRFDLSRLAFHHARELHPEYKDC 206

RESULT 25  
 ID Q900U1 PRELIMINARY; PRT; 206 AA.  
 AC Q900U1;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
 GN NEF.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RA McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,  
 RA Pemberton L., Brew B.J.;  
 RT "Anomalies in Nef expression within the central nervous system of HIV-  
 RT 1 positive individuals/AIDS patients with or without AIDS dementia  
 RT complex";  
 RL J. Neurovirol. 4:0-0(1998).  
 CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 DR EMBL; AF064676; AAC18376.1;  
 DR EMBL; AF064674; AAC18375.1;  
 DR HSSP; P03406; 1EFN.  
 DR InterPro; IPR001558; F-protein.  
 DR Pfam; PF00469; F-protein; 1.  
 KW AIDS; GTP-binding; Myristate.  
 SQ SEQUENCE 206 AA; 23514 MW; DC681CAF05891D68 CRC64;

Query Match 47.2%; Score 1064; DB 15; Length 206;  
 Best Local Similarity 91.7%; Pred. No. 4.7e-78;  
 Matches 189; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 110 MGGKWSKSSVVGWPTVRMRRAEPAADGCGAASRDLEKKGAISSNTAATNAACAWLEA 169  
 Db 1 MGGKWSKSSVVGWPTVRMRRAEPAADGCGAASRDLEKKGAISSNTAATNAACAWLEA 60

Qy 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLHSORRODILDWIYHTQGY 229  
 Db 61 QKEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLHSORRODILDWIYHTQGY 120

Qy 230 FPDQNTYTPGVRYPPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 289  
 Db 121 FPDQNTYTPGVRYPPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180

Qy 290 LEWRFDLSRLAFHHARELHPEYKNC 315  
 Db 181 LEWRFDLSRLAFHHARELHPEYKDC 206

Query Match 47.2%; Score 1065; DB 15; Length 206;  
 Best Local Similarity 93.2%; Pred. No. 3.9e-78;  
 Matches 192; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 110 MGGKWSKSSVVGWPTVRMRRAEPAADGCGAASRDLEKKGAISSNTAATNAACAWLEA 169  
 Db 1 MGGKWSKSSVVGWPTVRMRRAEPAADGCGAASRDLEKKGAISSNTAATNAACAWLEA 60

Qy 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLHSORRODILDWIYHTQGY 229  
 Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLHSORRODILDWIYHTQGY 120

Qy 230 FPDQNTYTPGVRYPPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 289  
 Db 121 FPDQNTYTPGVRYPPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180

Qy 290 LEWRFDLSRLAFHHARELHPEYKNC 315  
 Db 181 LEWRFDLSRLAFHHARELHPEYKDC 206

RESULT 26  
 ID Q9W7U0 PRELIMINARY; PRT; 206 AA.  
 AC Q9W7U0;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
 GN NEF.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RA McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,  
 RA Pemberton L., Brew B.J.;  
 RT "Anomalies in Nef expression within the central nervous system of HIV-  
 RT 1 positive individuals/AIDS patients with or without AIDS dementia  
 RT complex";  
 RL J. Neurovirol. 4:0-0(1998).  
 CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 DR EMBL; AF064675; AAC18376.1;  
 DR EMBL; AF064674; AAC18375.1;  
 DR HSSP; P03406; 1EFN.  
 DR InterPro; IPR001558; F-protein.  
 DR Pfam; PF00469; F-protein; 1.  
 KW AIDS; GTP-binding; Myristate.  
 SQ SEQUENCE 206 AA; 23514 MW; DC681CAF05891D68 CRC64;

Query Match 47.2%; Score 1064; DB 15; Length 206;  
 Best Local Similarity 91.7%; Pred. No. 4.7e-78;  
 Matches 189; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 110 MGGKWSKSSVVGWPTVRMRRAEPAADGCGAASRDLEKKGAISSNTAATNAACAWLEA 169  
 Db 1 MGGKWSKSSVVGWPTVRMRRAEPAADGCGAASRDLEKKGAISSNTAATNAACAWLEA 60

Qy 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLHSORRODILDWIYHTQGY 229  
 Db 61 QKEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLHSORRODILDWIYHTQGY 120

Qy 230 FPDQNTYTPGVRYPPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 289  
 Db 121 FPDQNTYTPGVRYPPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180

Qy 290 LEWRFDLSRLAFHHARELHPEYKNC 315  
 Db 181 LEWRFDLSRLAFHHARELHPEYKDC 206

RESULT 27  
 Q93010

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ID O93010 PRELIMINARY; PRT: 206 AA.
AC O93010;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PATIENT 9;
RX MEDLINE=98097260; PubMed=9436760;
RA Kang M.R., Cho Y.K., Chun J., Kim Y.B., Lee I., Lee H.J., Kim S.H.,
RA Kim Y.K., Yoon K., Yang J.M., Kim J.M., Shin Y.O., Kang C., Lee J.S.,
RA Choi K.W., Kim D.G., Fitch W.M., Kim S.;
RT "Phylogenetic analysis of the nef gene reveals a distinctive
RT monophyletic clade in Korean HIV-1 cases."
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 17:58-68(1998).
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF063922; AAC17893.1; -.
DR HSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; GTP-binding; Myristate.
KW SEQUENCE 206 AA; 23348 MW; 4D5AEDF55FAE93E3 CRC64;
SQ
```

Query Match 47.1%; Score 1062; DB 15; Length 206;  
Best Local Similarity 94.6%; Pred. No. 6.8e-78;  
Matches 194; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

```
QY 110 MGGKSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169
DB 1 MGGKSKSSVIGWPAVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60
QY 170 QEEVEGFPVTPQVLRPMPTTKAAYDLSHFLKEKGLGSLIHSQRQDILDWIYHTQY 229
DB 61 QEEVEGFPVTPQVLRPMPTTKAAYDLSHFLKEKGLGSLIHSQRQDILDWIYHTQY 120
QY 230 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 289
DB 121 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 180
QY 290 LEWRDLSRLAFHHVARELHPEYKNC 314
DB 181 LEWRDLSRLAFHHVARELHPEYKNC 205
QY 290 LEWRDLSRLAFHHVARELHPEYKNC 314
DB 181 LEWRDLSRLAFHHVARELHPEYKNC 205
```

RESULT 28

Query Match 47.1%; Score 1062; DB 15; Length 206;  
Best Local Similarity 94.6%; Pred. No. 6.8e-78;  
Matches 194; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

```
QY 110 MGGKSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169
DB 1 MGGKSKSSVIGWPAVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60
QY 170 QEEVEGFPVTPQVLRPMPTTKAAYDLSHFLKEKGLGSLIHSQRQDILDWIYHTQY 229
DB 61 QEEVEGFPVTPQVLRPMPTTKAAYDLSHFLKEKGLGSLIHSQRQDILDWIYHTQY 120
QY 230 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 289
DB 121 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 180
QY 290 LEWRDLSRLAFHHVARELHPEYKNC 314
DB 181 LEWRDLSRLAFHHVARELHPEYKNC 205
QY 290 LEWRDLSRLAFHHVARELHPEYKNC 314
DB 181 LEWRDLSRLAFHHVARELHPEYKNC 205
```

RESULT 28

Query Match 47.1%; Score 1062; DB 15; Length 206;  
Best Local Similarity 94.6%; Pred. No. 6.8e-78;  
Matches 194; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

```
QY 110 MGGKSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169
DB 1 MGGKSKSSVIGWPAVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60
QY 170 QEEVEGFPVTPQVLRPMPTTKAAYDLSHFLKEKGLGSLIHSQRQDILDWIYHTQY 229
DB 61 QEEVEGFPVTPQVLRPMPTTKAAYDLSHFLKEKGLGSLIHSQRQDILDWIYHTQY 120
QY 230 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 289
DB 121 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 180
QY 290 LEWRDLSRLAFHHVARELHPEYKNC 314
DB 181 LEWRDLSRLAFHHVARELHPEYKNC 205
QY 290 LEWRDLSRLAFHHVARELHPEYKNC 314
DB 181 LEWRDLSRLAFHHVARELHPEYKNC 205
```

```
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF064673; AAC18374.1; -.
DR HSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; GTP-binding; Myristate.
KW SEQUENCE 206 AA; 23472 MW; 2255A447ECE85456 CRC64;
SQ
```

Query Match 47.1%; Score 1061; DB 15; Length 206;  
Best Local Similarity 91.7%; Pred. No. 8.2e-78;  
Matches 189; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

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QY 110 MGGKSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169
DB 1 MGGKSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60
QY 170 QEEVEGFPVTPQVLRPMPTTKAAYDLSHFLKEKGLGSLIHSQRQDILDWIYHTQY 229
DB 61 QEEVEGFPVTPQVLRPMPTTKAAYDLSHFLKEKGLGSLIHSQRQDILDWIYHTQY 120
QY 230 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 289
DB 121 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 180
QY 290 LEWRDLSRLAFHHVARELHPEYKNC 315
DB 181 LEWRDLSRLAFHHVARELHPEYKNC 206
```

RESULT 29

Query Match 47.0%; Score 1060; DB 15; Length 206;  
Best Local Similarity 92.7%; Pred. No. 9.9e-78;  
Matches 191; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

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QY 110 MGGKSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169
DB 1 MGGKSKSGVGWPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTPTNNADCAWLEA 60
QY 170 QEEVEGFPVTPQVLRPMPTTKAAYDLSHFLKEKGLGSLIHSQRQDILDWIYHTQY 229
DB 61 QEEVEGFPVTPQVLRPMPTTKAAYDLSHFLKEKGLGSLIHSQRQDILDWIYHTQY 120
QY 230 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 289
DB 121 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 180
QY 290 LEWRDLSRLAFHHVARELHPEYKNC 315
DB 181 LEWRDLSRLAFHHVARELHPEYKNC 206
```

RESULT 29

Query Match 47.0%; Score 1060; DB 15; Length 206;  
Best Local Similarity 92.7%; Pred. No. 9.9e-78;  
Matches 191; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

```
QY 110 MGGKSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169
DB 1 MGGKSKSGVGWPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTPTNNADCAWLEA 60
QY 170 QEEVEGFPVTPQVLRPMPTTKAAYDLSHFLKEKGLGSLIHSQRQDILDWIYHTQY 229
DB 61 QEEVEGFPVTPQVLRPMPTTKAAYDLSHFLKEKGLGSLIHSQRQDILDWIYHTQY 120
QY 230 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 289
DB 121 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 180
QY 290 LEWRDLSRLAFHHVARELHPEYKNC 315
DB 181 LEWRDLSRLAFHHVARELHPEYKNC 206
```

RESULT 29

Query Match 47.0%; Score 1060; DB 15; Length 206;  
Best Local Similarity 92.7%; Pred. No. 9.9e-78;  
Matches 191; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

```
QY 110 MGGKSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 169
DB 1 MGGKSKSGVGWPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTPTNNADCAWLEA 60
QY 170 QEEVEGFPVTPQVLRPMPTTKAAYDLSHFLKEKGLGSLIHSQRQDILDWIYHTQY 229
DB 61 QEEVEGFPVTPQVLRPMPTTKAAYDLSHFLKEKGLGSLIHSQRQDILDWIYHTQY 120
QY 230 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 289
DB 121 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 180
QY 290 LEWRDLSRLAFHHVARELHPEYKNC 315
DB 181 LEWRDLSRLAFHHVARELHPEYKNC 206
```

Db 121 FPDQNTYTPGIRYPLTFGWCYKLVPEQEKVKKANEKGNKNTSLHHPMSLHGMDDDPEREV 180  
Qy 290 LEWRFDSRLAFHHVARELHPEYFKNC 315  
Db 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

## RESULT 30

Q9W7X2  
ID Q9W7X2 PRELIMINARY; PRT; 206 AA.  
AC Q9W7X2;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN-PATIENT 27;  
RA McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,  
Pemberton L., Brew B.J.;  
RT "Anomalies in Nef expression within the central nervous system of HIV-  
1 positive individuals/AIDS patients with or without AIDS dementia  
complex".  
RL J. Neurovirol. 4:0-0(1998).  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL; AF064677; AAC18378.1; -;  
DR HSSP; P03406; 1EFN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate;  
SQ SEQUENCE 206 AA; 23442 MW; DC6A96AF05891D6B CRC64;

Query Match 46.9%; Score 1057; DB 15; Length 206;  
Best Local Similarity 91.3%; Pred. No. 1.7e-77;  
Matches 188; Conservative 13; Mismatches 5; Indels 0; Gaps 0;  
Qy 110 MGGKWSKSSVVGWPTVRRMRRAEPADGVGAASRDLEKKGAITSSNTAATNAACAWLEA 169  
Db 1 MGGKWSKSSVVGWPTVRRMRRAEPADGVGAASRDLEKKGAITSSNTAATNAACAWLEA 60  
Qy 170 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKXGGLGGLHSORRQDILDWIYHTQY 229  
Db 61 QKEEVGFPVTPQVPLRPMTYKAAVDLSHFLKXGGLGGLHSORRQDILDWIYHTQY 120  
Qy 230 FPDQNTYTPGIRYPLTFGWCYKLVPEQEKVKKANEKGNKNTSLHHPMSLHGMDDDPEREV 289  
Db 121 FPDQNTYTPGIRYPLTFGWCYKLVPEQEKVKKANEKGNKNTSLHHPMSLHGMDDDPEREV 180  
Qy 290 LEWRFDSRLAFHHVARELHPEYFKNC 315  
Db 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

Search completed: August 26, 2002, 08:14:56  
Job time: 384 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2002, 08:12:27 ; Search time 99.16 Seconds  
(without alignments)  
462.621 Million cell updates/sec

Title: US-09-509-239-21

Perfect score: 2264

Sequence: 1 MDPSSSHSNMANTQMSDKI.....QSRGDPGPKETSGHHHHH 413

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802:\*\*

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- 2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*
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- 4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.\*
- 6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.\*
- 7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.\*
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- 9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.\*
- 10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.\*
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- 19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2264	100.0	413	20 AAY02355	A representative L
2	2264	100.0	413	22 AAG63237	Amino acid sequenc
3	2246	99.2	411	22 AAG63235	Amino acid sequenc
4	2233	98.6	411	20 AAY02353	A representative L
5	1715.5	75.8	326	20 AAY02354	A representative L
6	1715.5	75.8	326	22 AAG63236	Amino acid sequenc
7	1697.5	75.0	324	20 AAY02352	A representative L
8	1697.5	75.0	324	22 AAG63234	Amino acid sequenc
9	1688	74.6	302	20 AAY02351	A representative H
10	1688	74.6	302	22 AAG63233	Amino acid sequenc
11	1675	74.0	302	20 AAY02357	A representative H

12	1675	74.0	302	22	AAG63239	Amino acid sequenc
13	1139.5	50.3	215	20	AAY02349	A representative H
14	1139.5	50.3	215	22	AAG63231	Amino acid sequenc
15	1120	49.5	206	14	AAY50795	Human NEF protein/
16	1116	49.3	206	14	AAR38893	Nef protein of HIV
17	1115	49.2	206	21	AAB10054	HIV-1 nef protein.
18	1114	49.2	206	20	AAR69326	HIV-1 nef protein
19	1111	49.1	206	7	AAP61515	Sequence of E' pro
20	1107	48.9	216	7	AAP60423	Sequence of LAV v1
21	1092	48.2	206	20	AAM90479	HTLV-III E' protei
22	1011	44.7	216	22	AAE04960	HIV-1 jrf1 Nef pro
23	997	44.0	210	19	AAW53113	Protein 6 containe
24	997	44.0	210	21	AAW77299	HIV-1 (ATCC CRL 85
25	996	44.0	217	22	AAE04962	HIV-1 jrf1 Nef (G2
26	983	43.4	210	12	AAE12262	HIV-1 strain OYI o
27	978	43.2	237	22	AAE04961	Human tPA leader p
28	968	42.8	237	22	AAE04963	Human tPA leader p
29	952	42.0	206	21	AAE04963	HIV-1 non-subtype
30	948.5	41.9	3025	22	AAE04963	HIV-1 subtype C.pr
31	934	41.3	206	21	AAE04963	HIV-1 non-subtype
32	927.5	41.0	206	9	AAP81859	Sequence encoded b
33	910.5	40.2	207	21	AAE04963	HIV-1 non-subtype
34	903.5	39.9	207	11	AAR08407	Sequence deduced f
35	901.5	39.8	207	21	AAE04963	HIV-1 non-subtype
36	901.5	39.8	208	21	AAE04963	HIV-1 non-subtype
37	895.5	39.6	219	21	AAE04963	HIV-1 non-subtype
38	893.5	39.5	217	21	AAE04963	HIV-1 non-subtype
39	885.5	39.1	207	21	AAE04963	HIV-1 non-subtype
40	878.5	38.8	207	21	AAE04963	HIV-1 non-subtype
41	867	38.3	206	21	AAE04963	HIV-1 non-subtype
42	860	38.0	206	21	AAE04963	HIV-1 non-subtype
43	834.5	36.9	209	19	AAW72998	HIV isolate LAV.MA
44	831.5	36.7	209	9	AAP81866	Sequence encoded b
45	796	35.2	212	19	AAW68481	HIV-1 strain YBF30

#### ALIGNMENTS

RESULT 1

AAV02355

ID AAY02355 standard; Protein; 413 AA.

XX AC AAY02355;

XX DT 09-JUL-1999 (first entry)

XX DE A representative Lipod-Tat fusion protein.

XX KW HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;

XX KW vaccine; HIV infection; protein D.

XX OS Synthetic.

XX OS Human immunodeficiency virus type 1.

XX PN WO9916884-AL.

XX PD 08-APR-1999.

XX PF 17-SEP-1998; 98WO-EP06040.

XX PR 26-SEP-1997; 97GB-0020585.

XX PR (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Bruck C, Godart SAG, Marchand M;

XX XX WPI; 1999-302282/25.

XX DR N-PSDB; AAX35691.

XX XX HIV Tat or Nef protein linked to a fusion partner

XX PS Disclosure; Fig 2; 66pp; English.

```

XX CC The present sequence represents a fusion protein comprising Lipod-HIV-1
CC Tat. The protein is exemplified the fusion proteins of
CC the invention. The specification also describes fusion proteins
CC comprising HIV-1 Nef protein. The fusion protein can be used in a
CC vaccine to prevent HIV infection.
XX CC
XX SQ Sequence 413 AA;

Query Match 100.0%; Score 2264; DB 20; Length 413;
Best Local Similarity 100.0%; Pred. No. 3.1e-205;
Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPSSHSNMANTQMSDKIIIAHRGASGYLPETHLESKALAFQAQADYLFQDLAMTKDG 60
Db 1 mdpsshsnmantqmsdkiiiahrgasgyipehtleskalafqaqadyleqdlamtkdg 60
Qy 61 RLVTVDHFLDGLTDVAKKFPHRHDKGRYYVIDFTLKEIQSLEMTENFETMGKWSKSS 120
Db 61 rlvtvdhflgldtdvakkfphrhrkdgryyvidftlkeiqslemtentfmgkwsks 120
Qy 121 VVGWPTVRMRRAEPADGVAASRDLEKHAITSSNTAATNAACAWLEAQEEVEVGFP 180
Db 121 vvgwptvrmerraepaadgvaasrdlekhaitsntaatnaacawleaqeevevgfp 180
Qy 181 VTPQVPLRPMTYKAAVDLSHFLKEKGLGLIHSORRODILDLWIYHTQGYPDMQNTYP 240
Db 181 vtpqvplrpmtykaavdlsfhflkekglglihsorrodildlwiyhtqgyfpmqnytp 240
Qy 241 GPGVRYPLTTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPEREVLWRFDSRL 300
Db 241 gpgvrypltfwgcyklvpdpdkveeankgentsllhpsvslhgmddperevlewrfdsr 300
Qy 301 AFHHVARELHPEYFNKCTSEPVDPRLPEWPKHGPSQPKTACTNCYCKKCCFHCQVCFTKA 360
Db 301 afhhvarelhpeyfnkctsevpdprlepwbkpgsqpktactncycckkccfchqvcfika 360
Qy 361 LGISYGRKKRRQRPRPGSQTHQVSLSKQPTSQSRGDPGTGPKETSGHHHHH 413
Db 361 lgisygrkrrqrprpgsqthqvskskqtsqrgdgtgpketsgghhhhh 413

RESULT 2
AAG63237 standard; Protein: 413 AA.
XX AC
XX DT 01-OCT-2001 (first entry)
XX DT
DE Amino acid sequence of a His tagged ProTD-Nef-Tat fusion protein.
XX KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.
XX OS Synthetic.
XX OS Human immunodeficiency virus.
XX FH Key Location/Qualifiers
XX FT Peptide 1..111
XX FT /note= "ProTD fusion partner"
XX PN WO200154719-A2.
XX PD 02-AUG-2001.
XX PF
XX PF 29-JAN-2001; 2001WO-EP00944.
XX PR 31-JAN-2000; 2000GB-0002200.
XX PR 14-APR-2000; 2000GB-0009336.
XX PR 06-JUN-2000; 2000GB-0013806.
XX PR 28-JUN-2000; 2000WO-EP05998.
XX OS

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```

PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX Voss G;
PI WPI: 2001-476172/51.
DR N-PSDB; AAH42881.
XX PT
XX PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef
XX linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120
XX protein or polynucleotide for the manufacture of a vaccine -
XX Disclosure: Fig 1; 90pp; English.
XX CC
XX CC The present sequence represents a His-tagged ProTD-Nef-Tat fusion
XX protein. The protein is expressed in Escherichia coli, and is used to
XX produce the vaccine of the invention. The specification describes
XX the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the
XX manufacture of a vaccine. The vaccine is used for the prophylactic or
XX therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act
XX in synergy with gp120 in the treatment and prevention of HIV. The
XX vaccine reduces the HIV viral load in HIV infected humans and results
XX in a maintenance of CD4+ levels over those levels found in the absence
XX of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.
XX SQ Sequence 413 AA;

Query Match 100.0%; Score 2264; DB 22; Length 413;
Best Local Similarity 100.0%; Pred. No. 3.1e-205;
Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPSSHSNMANTQMSDKIIIAHRGASGYLPETHLESKALAFQAQADYLFQDLAMTKDG 60
Db 1 mdpsshsnmantqmsdkiiiahrgasgyipehtleskalafqaqadyleqdlamtkdg 60
Qy 61 RLVTVDHFLDGLTDVAKKFPHRHDKGRYYVIDFTLKEIQSLEMTENFETMGKWSKSS 120
Db 61 rlvtvdhflgldtdvakkfphrhrkdgryyvidftlkeiqslemtentfmgkwsks 120
Qy 121 VVGWPTVRMRRAEPADGVAASRDLEKHAITSSNTAATNAACAWLEAQEEVEVGFP 180
Db 121 vvgwptvrmerraepaadgvaasrdlekhaitsntaatnaacawleaqeevevgfp 180
Qy 181 VTPQVPLRPMTYKAAVDLSHFLKEKGLGLIHSORRODILDLWIYHTQGYPDMQNTYP 240
Db 181 vtpqvplrpmtykaavdlsfhflkekglglihsorrodildlwiyhtqgyfpmqnytp 240
Qy 241 GPGVRYPLTTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPEREVLWRFDSRL 300
Db 241 gpgvrypltfwgcyklvpdpdkveeankgentsllhpsvslhgmddperevlewrfdsr 300
Qy 301 AFHHVARELHPEYFNKCTSEPVDPRLPEWPKHGPSQPKTACTNCYCKKCCFHCQVCFTKA 360
Db 301 afhhvarelhpeyfnkctsevpdprlepwbkpgsqpktactncycckkccfchqvcfika 360
Qy 361 LGISYGRKKRRQRPRPGSQTHQVSLSKQPTSQSRGDPGTGPKETSGHHHHH 413
Db 361 lgisygrkrrqrprpgsqthqvskskqtsqrgdgtgpketsgghhhhh 413

RESULT 3
AAG63235 standard; Protein: 411 AA.
XX AC
XX AC AAG63235;
XX DT 01-OCT-2001 (first entry)
XX DT
DE Amino acid sequence of a His tagged LipD-Nef-Tat linked protein.
XX KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.
XX OS Synthetic.

```



OS Human immunodeficiency virus.

PH Key Location/Qualifiers  
FT Peptide 1..109  
TT /note= "ProtD fusion partner"

PN WO200154719-A2.

XX PD 02-AUG-2001.

XX PF 29-JAN-2001; 2001WO-EP00944.

XX PR 31-JAN-2000; 2000GB-0002200.

XX PR 14-APR-2000; 2000GB-0009336.

XX PR 06-JUN-2000; 2000GB-0013806.

XX PR 28-JUN-2000; 2000WO-EP05998.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Voss G;

XX WPI; 2001-476172/51.

XX DR N-PSDB; AAH42879.

XX New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef

XX PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120

XX PT protein or polynucleotide for the manufacture of a vaccine -

XX PS Disclosure: Fig 1; 90pp; English.

XX The present sequence represents a His-tagged Nef-Tat linked protein of  
CC HIV, with a lipidation signal sequence (lipod) which is removed after  
CC processing and a ProtD fusion partner. The protein is expressed in  
CC Escherichia coli, and is used to produce the vaccine of the invention.  
CC The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat;  
CC and HIV gp120 in the manufacture of a vaccine. The vaccine is used for  
CC the prophylactic or therapeutic immunization of humans against HIV.  
CC Tat, Nef or Nef-Tat act in synergy with gp120 in the treatment and  
CC prevention of HIV. The vaccine reduces the HIV viral load in HIV  
CC infected humans and results in a maintenance of CD4+ levels over those  
CC levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat  
CC and HIV gp120.

XX Sequence 411 AA;

Query Match 99.2%; Score 2246; DB 22; Length 411;  
Best Local Similarity 100.0%; Pred. No. 1.5e-203;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SHSSNMANTQMSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEODLAWTKDGRV 63

DB 2 shssnmantqmsdkiiiahrgasgylpehtleskalfaqadyleqdlamtkdgriv 61

QY 64 VIHDFDLGLTQVAKKFPHRHRKDGRIYVIDFTLKEIQSLEMTENFETMGKWSKSSVVG 123

DB 62 vlnhdflgltqvakkfphrhrkdgryyvidftlkeiqslemtentfmgkwsksvvg 121

QY 124 WPTVRMRRAEPAADGVGAASRDLEKHAITSNTAATNAACAWLEAQEEVEEVPVTP 183

DB 122 wptvrermraepaadvgaasrdlekhgaitssntaataacawleaqeeveevfpvtp 181

QY 184 QVPLRPMTYKAADVLSHFLEKGGLEGLTHSRRQDILDILWIYHTGYPFQWNYTPPGG 243

DB 182 qvplrpmtykaadvlsfhflekkggleglthsgrrqldilwihtgyfpdwgnytpgpg 241

QY 244 VRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREVLWFDSRLAFH 303

DB 242 vrypltfgcylvppepkveankgentsllhpsvslhgmddperewlwfdsrlafh 301

QY 304 HVARELHPYFKNCTSEPDPRLEPKHPGSPKTACTNCYCKKCCFHCQVCFITKALGI 363

DB 302 hvarelhpeyfnctsepdprlepkhpgspktaactncycckccfchcqvcfitalgi 361

QY 364 SYGRKKRRQRRRPOGSOHQVLSKQPTSQSRGDPGTGPKETSGHHHHH 413  
DB 362 sygrkkrrqrrppqsgqthqvsksqptsqsgdptgpketsghhhhh 411

#### RESULT 4

AAV02353

ID AAY02353 standard; Protein; 411 AA.

XX AC AAY02353;

XX DT 09-JUL-1999 (first entry)

XX DE A representative Lipod-Tat-His fusion protein.

XX KW HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
XX KW vaccine; HIV infection; protein D.

XX OS Synthetic.

OS Human immunodeficiency virus type 1.

XX PN WO9916884-A1.

XX PD 08-APR-1999.

XX PF 17-SEP-1998; 98WO-EP06040.

XX PR 26-SEP-1997; 97GB-0020585.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Bruck C, Godart SAG, Marchand M;

XX DR WPI; 1999-302282/25.

XX N-PSDB; AAX35689.

XX HIV Tat or Nef protein linked to a fusion partner

XX Disclosure: Fig 2; 66pp; English.

XX The present sequence represents a fusion protein comprising Lipod-Hiv-1  
CC Tat-His. The protein is exemplified the fusion proteins of  
CC the invention. The specification also describes fusion proteins  
CC comprising HIV-1 Nef protein. The fusion protein can be used in a  
CC vaccine to prevent HIV infection.

XX Sequence 411 AA;

Query Match 98.6%; Score 2233; DB 20; Length 411;  
Best Local Similarity 99.8%; Pred. No. 2.6e-202;  
Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 SHSSNMANTQMSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEODLAWTKDGRV 63

DB 2 shssnmantqmsdkiiiahrgasgylpehtleskalfaqadyleqdlamtkdgriv 61

QY 64 VIHDFDLGLTQVAKKFPHRHRKDGRIYVIDFTLKEIQSLEMTENFETMGKWSKSSVVG 123

DB 62 vlnhdflgltqvakkfphrhrkdgryyvidftlkeiqslemtentfmgkwsksvvg 121

QY 124 WPTVRMRRAEPAADGVGAASRDLEKHAITSNTAATNAACAWLEAQEEVEEVPVTP 183

DB 122 wptvrermraepaadvgaasrdlekhgaitssntaataacawleaqeeveevfpvtp 181

QY 184 QVPLRPMTYKAADVLSHFLEKGGLEGLTHSRRQDILDILWIYHTGYPFQWNYTPPGG 243

DB 182 qvplrpmtykaadvlsfhflekkggleglthsgrrqldilwihtgyfpdwgnytpgpg 241

QY 244 VRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREVLWFDSRLAFH 303

DB 242 vrypltfgcylvppepkveankgentsllhpsvslhgmddperewlwfdsrlafh 301

QY 304 HVARLHPEYFKNCTSEPVDRLEPDKVVEANKGENTSLHLPVSLHGMDDPEREVLHFRDRL 363  
Db 302 hvarelhpeyfkntsepvdrlepkvpepdkveeankgentsllhpsalhgmdpervlewrfdsl 361  
QY 364 SYGRKKRRORRRPQGSQTHOVSLSKQPTQSOSGDPTGPKETSGHHHHH 413  
Db 362 sygrkrrrrrrppqgqthgvsksqptsgsrqgdpckpsetsghnnhhh 411

RESULT 5  
AAY02354  
ID AAY02354 standard; Protein: 326 AA.  
XX AC AAY02354;  
XX DT 09-JUL-1999 (first entry)  
XX DE A representative Lipod-Nef fusion protein.  
XX KW HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
XX KW vaccine; HIV infection; protein D.  
XX OS Synthetic.  
XX OS Human immunodeficiency virus type 1.  
XX PN WO9916884-A1.  
XX PD 08-APR-1999.  
XX PF 17-SEP-1998; 98WO-EP06040.  
XX PR 26-SEP-1997; 97GB-0020585.  
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX PI Bruck C, Godart SAG, Marchand M;  
XX WPI; 1999-302282/25.  
DR N-PSDB; AAX35690.  
XX HIV Tat or Nef protein linked to a fusion partner  
XX PS Disclosure; Fig 2; 56pp; English.  
XX The present sequence represents a fusion protein comprising Lipod-HIV-1  
CC Nef. The protein is exemplified by the fusion proteins of  
CC the invention. The specification also describes fusion proteins  
CC comprising HIV-1 Tat protein. The fusion protein can be used in a  
CC vaccine to prevent HIV infection.  
XX SQ Sequence 326 AA;

Query Match 75.8%; Score 1715.5; DB 20; Length 326;  
Best Local Similarity 78.9%; Pred. No. 1.5e-153;  
Matches 326; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 MDPSSSHSNMANTQMSKIIIAHARGAGYLPEHTLESKALAFQAQADYLEODLAMTKDG 60  
Db 1 mdpsshsnmanmqmskiiiahrgagylpehtleskalahafaqadyleodlamtkdg 60  
QY 61 RLUVTHDFLDGLTOVAKKFPHRHRKDRYVIDFTLKEIQSLEMTENFETMGKWSKSS 120  
Db 61 rlviwhdfldgltdvakkfphrhrkdrgyvidftlkeiqslemtenfetmgkwsks 120  
QY 121 VVGWPTVREMRRAEPAADGVCAASRDLEKHGCAITSSNTAATNAACALEAQEEVEVGFP 180  
Db 121 vvgwptvremrraeapaadgvcaasrdlekhhgcaitssntaataacaleaqeevevgfp 180  
QY 181 VTPQVPLRPMTYKAAVDLSHFLKKEGLELIHSORRODILDIWIYHTQGYPPDQWNTYP 240  
Db 181 vtpqvplrpmtykaavdlsfhflkkggleglihsqrrqdildwiyhtqgyfpdqwnytp 240

QY 241 GPGVRYPLTFTGWCYKLYVPEPDKVVEANKGENTSLHLPVSLHGMDDPEREVLHFRDRL 300  
Db 241 gpgvryplftfgwcyklyvpepdkveeankgentsllhpsalhgmdpervlewrfdsl 300  
QY 301 AFHHVARELHPEYFKNCTSEPVDRLEPDKVVEANKGENTSLHLPVSLHGMDDPEREVLHFRDRL 360  
Db 301 afhhvarelhpeyfknc-----tsghnnhhh 317  
QY 361 LGISYGRKKRRRRPQGSQTHOVSLSKQPTQSOSGDPTGPKETSGHHHHH 413  
Db 318 -----tsghnnhhh 326

RESULT 6  
AAG63236  
ID AAG63236 standard; Protein: 326 AA.  
XX AC AAG63236;  
XX DT 01-OCT-2001 (first entry)  
XX DE Amino acid sequence of a His tagged ProtD-Nef fusion protein.  
XX KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.  
XX OS Synthetic.  
XX OS Human immunodeficiency virus.  
XX FH Key Location/Qualifiers  
XX FT Peptide 1..111 /note= "ProtD fusion partner"  
XX PN WO200154719-A2.  
XX PD 02-AUG-2001.  
XX PF 29-JAN-2001; 2001WO-EP00944.  
XX PR 31-JAN-2000; 2000GB-0002200.  
XX PR 14-APR-2000; 2000GB-0009336.  
XX PR 06-JUN-2000; 2000GB-0013806.  
XX PR 28-JUN-2000; 2000WO-EP05998.  
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX Voss G;  
XX WPI; 2001-476172/51.  
DR N-PSDB; AAH42880.  
XX New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
XX linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
XX protein or polynucleotide for the manufacture of a vaccine -  
XX Disclosure; Fig 1; 90pp; English.  
XX The present sequence represents a His-tagged ProtD-Nef fusion protein.  
XX The protein is expressed in Escherichia coli, and is used to  
XX produce the vaccine of the invention. The specification describes  
XX the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the  
XX manufacture of a vaccine. The vaccine is used for the prophylactic or  
XX therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
XX in synergy with gp120 in the treatment and prevention of HIV. The  
XX vaccine reduces the HIV viral load in HIV infected humans and results  
XX in a maintenance of CD4+ levels over those levels found in the absence  
XX of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.  
XX SQ Sequence 326 AA;

Query Match 75.8%; Score 1715.5; DB 22; Length 326;  
Best Local Similarity 78.9%; Pred. No. 1.5e-153;

Matches 326; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 MDPSSSHSNWANTQMSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEQDLAMTKDG 60  
 |||||  
 Db 1 mdpssshsnmantqmsdkiiiahrgasgylpehtleskalafagadyleqdlamtkdg 60  
 |||||

QY 61 RLVVTHDFLDGLTDVAKKFPFHRHRKDGYYVIDFTLKEIQSLEMTENFETMGKWSKSS 120  
 |||||  
 Db 61 rlvvthdflldgltdvakkfphrhrkdgryyvidftlkeiqslemtentfmggkwsks 120  
 |||||

QY 121 VVGWPTVRMRRAEPAADGVGAASRDLEKKGAIITSSNTAATNAACAWLEAQEEVEEVGFP 180  
 |||||  
 Db 121 vvgwptvrmerraepaadvgaasrdlekgaiitssntaatnaacawleaqeeveevgfp 180  
 |||||

QY 181 VTPQVPLRPMTYKAADVLSHFLKEKGGLEGGLIHSORRQDILDLIWIYHTQGYFPDQNYTP 240  
 |||||  
 Db 181 vtpqvplrpmtykaadvlsfhflkekgglegglihsqrrqdildliwyhtqgyfpdgnytp 240  
 |||||

QY 241 GPGVRYPTFTGVCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREVLEWRDSDL 300  
 |||||  
 Db 241 gpgvryptftgvcylvppepkveeankgentsllhpsvlhgmddperevlewrfdsl 300  
 |||||

QY 301 AFHHVARELHPEYFKNCTSEPVDPRLPEPMKHPGSPQKTACTNCKKCCFHCQVCFTKA 360  
 |||||  
 Db 301 afhhvarelhpeyfknc-----tsghhhhh 317

QY 361 LGISYGRKKRRRRPPQGSQTHQVSLSKQPTSQSRGDPGPKETSGHHHHH 413  
 |||||  
 Db 318 -----tsghhhhh 326

RESULT 7  
 AAY02352  
 ID AAY02352 standard; Protein; 324 AA.  
 AC AAY02352;  
 XX  
 DT 09-JUL-1999 (first entry)  
 XX  
 DE A representative LipD-Nef-His fusion protein.  
 XX  
 KW HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
 XX vaccine; HIV infection; protein D.  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO9916884-A1.  
 XX  
 PD 08-APR-1999.  
 XX  
 PF 17-SEP-1998; 98WO-EP06040.  
 XX  
 PR 26-SEP-1997; 97GB-0020585.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA  
 PI Bruck C, Godart SAG, Marchand M;  
 XX  
 DR WPI; 1999-302282/25.  
 XX  
 DR N-PSDB; AAX35688.  
 XX  
 PT HIV Tat or Nef protein linked to a fusion partner  
 XX  
 PS Disclosure; Fig 2; 66pp; English.  
 XX  
 CC The present sequence represents a fusion protein comprising LipD-HIV-1  
 CC Nef-His. The protein is exemplified the fusion proteins of  
 CC the invention. The specification also describes fusion proteins  
 CC comprising HIV-1 Tat protein. The fusion protein can be used in a  
 CC vaccine to prevent HIV infection.  
 XX  
 SQ Sequence 324 AA;

Query Match 75.0%; Score 1697.5; DB 20; Length 324;  
 Best Local Similarity 78.8%; Pred. No. 7.5e-152;  
 Matches 323; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 4 SSSSNWANTQMSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEQDLAMTKDGLRV 63  
 |||||  
 Db 2 ssssnmantqmsdkiiiahrgasgylpehtleskalafagadyleqdlamtkdgrlv 61  
 |||||

QY 64 VTHDHFLDGLTDVAKKFPFHRHRKDGYYVIDFTLKEIQSLEMTENFETMGKWSKSSVVG 123  
 |||||  
 Db 62 vihdhflldgltdvakkfphrhrkdgryyvidftlkeiqslemtentfmggkwsksvvg 121  
 |||||

QY 124 WPTVRMRRAEPAADGVGAASRDLEKKGAIITSSNTAATNAACAWLEAQEEVEEVGFPVTP 183  
 |||||  
 Db 122 wptvrmerraepaadvgaasrdlekgaiitssntaatnaacawleaqeeveevgfpvtp 181  
 |||||

QY 184 QVPLRPMTYKAADVLSHFLKEKGGLEGGLIHSORRQDILDLIWIYHTQGYFPDQNYTPGPG 243  
 |||||  
 Db 182 qvplrpmtykaadvlsfhflkekgglegglihsqrrqdildliwyhtqgyfpdgnytpgpg 241  
 |||||

QY 244 VRYPTFTGVCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREVLEWRDSDLAFH 303  
 |||||  
 Db 242 vryptftgvcylvppepkveeankgentsllhpsvlhgmddperevlewrfdslafh 301  
 |||||

QY 304 HVARELHPEYFKNCTSEPVDPRLPEPMKHPGSPQKTACTNCKKCCFHCQVCFTKALGI 363  
 |||||  
 Db 302 hvarelhpeyfknc-----tsghhhhh 315

QY 364 SYGRKKRRRRPPQGSQTHQVSLSKQPTSQSRGDPGPKETSGHHHHH 413  
 |||||  
 Db 316 -----tsghhhhh 324

RESULT 8  
 AAG63234  
 ID AAG63234 standard; Protein; 324 AA.  
 XX  
 AC AAG63234;  
 XX  
 DT 01-OCT-2001 (first entry)  
 XX  
 DE Amino acid sequence of a His tagged LipD-Nef of HIV.  
 XX  
 KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..109  
 FT /note= "protD fusion partner"  
 XX  
 PN WO200154719-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 29-JAN-2001; 2001WO-EP00944.  
 XX  
 PR 31-JAN-2000; 2000GB-0002200.  
 PR 14-APR-2000; 2000GB-0009336.  
 PR 06-JUN-2000; 2000GB-0013806.  
 PR 28-JUN-2000; 2000WO-EP05998.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA  
 PI Voss G;  
 XX  
 DR WPI; 2001-476172/51.  
 DR N-PSDB; AAX42878.  
 XX  
 PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef

PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
 XX protein or polynucleotide for the manufacture of a vaccine  
 PS Disclosure; Fig 1; 90pp; English.

XX The present sequence represents a His-tagged Nef protein of HIV, with  
 CC a lipidation signal sequence (lipod) which is removed after processing.  
 CC The protein is expressed in Escherichia coli, and is used to  
 CC produce the vaccine of the invention. The specification describes  
 CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the  
 CC manufacture of a vaccine. The vaccine is used for the prophylactic or  
 CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
 CC in synergy with gp120 in the treatment and prevention of HIV. The  
 CC vaccine reduces the HIV viral load in HIV infected humans and results  
 CC in a maintenance of CD4+ levels over those levels found in the absence  
 CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.

XX Sequence 324 AA;

Query Match 75.0%; Score 1697.5; DB 22; Length 324;  
 Best Local Similarity 78.8%; Pred. No. 7.5e-152;  
 Matches 323; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 4 SSSSSNANTOMKSDKIIIAHRAAGSYLPHTLESKALAFQAQADYLEQDLAMTKDGRLV 63  
 DB 2 SSSSSNANTOMKSDKIIIAHRAAGSYLPHTLESKALAFQAQADYLEQDLAMTKDGRLV 61  
 QY 64 VIHDFLDGLTDVAKKPHRHRDGRYYVDFTLKEIQSLEMTENFTMGKWSKSSVVG 123  
 DB 62 VIHDFLDGLTDVAKKPHRHRDGRYYVDFTLKEIQSLEMTENFTMGKWSKSSVVG 121  
 QY 124 WPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEAEQEEVGFVTP 183  
 DB 122 WPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEAEQEEVGFVTP 181  
 QY 184 QVLRPMTYKAAVDLSHFLKEKGLGLIHSQRRQDILDLYHTQGYFPDQWNTPGPG 243  
 DB 182 QVLRPMTYKAAVDLSHFLKEKGLGLIHSQRRQDILDLYHTQGYFPDQWNTPGPG 241  
 QY 244 VRYPLTGWCKYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPEREVLWRDLSLAFH 303  
 DB 242 VRYPLTGWCKYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPEREVLWRDLSLAFH 301  
 QY 304 HVARELHPEYFKNCTSEPVDRPLEPWPKHGSGQPKTACTNCYCKKCCFHCQVCFITKALGI 363  
 DB 302 HVARELHPEYFKNCTSEPVDRPLEPWPKHGSGQPKTACTNCYCKKCCFHCQVCFITKALGI 315  
 QY 364 SYGRKKRRRRRPPQGSQTHQVSLSKQPTSGSRGDPGPKETSGHHHHH 413  
 DB 316 SYGRKKRRRRRPPQGSQTHQVSLSKQPTSGSRGDPGPKETSGHHHHH 324

RESULT 9

AY02351  
 ID AAY02351 standard; Protein; 302 AA.

XX AC AAY02351;

XX DT 09-JUL-1999 (first entry)

XX DE A representative HIV-1 Nef-Tat-His protein.

XX HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
 KW vaccine; HIV infection; protein D.

XX OS Synthetic.  
 OS Human immunodeficiency virus type 1.

XX PN WO9916884-A1.

XX PD 08-APR-1999.

XX

PF 17-SEP-1998; 98WO-EP06040.  
 XX  
 PR 26-SEP-1997; 97GB-0020585.  
 XX  
 XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX Bruck C, Godart SAG, Marchand M;

XX WPI; 1999-302282/25.

DR N-PSDB; AAX35687.

XX HIV Tat or Nef protein linked to a fusion partner

XX Disclosure; Fig 2; 66pp; English.

CC The present sequence represents a representative HIV-1 Nef-Tat-His  
 CC protein. The protein is used in the creation of the fusion proteins of  
 CC the invention, in conjunction with a fusion partner (e.g. protein D).  
 CC The fusion protein can be used in a vaccine to prevent HIV infection.

XX Sequence 302 AA;

Query Match 74.6%; Score 1688; DB 20; Length 302;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-151;  
 Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 MGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 171  
 DB 1 MGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 QY 172 QEEEEYGFVTPQVLRPMTYKAAVDLSHFLKEKGLGLIHSQRRQDILDLYHTQGY 231  
 DB 61 QEEEEYGFVTPQVLRPMTYKAAVDLSHFLKEKGLGLIHSQRRQDILDLYHTQGY 120  
 QY 232 FPDQWNTPGGYRPLTGWCKYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPEREV 291  
 DB 121 FPDQWNTPGGYRPLTGWCKYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPEREV 180  
 QY 292 LEWRFSRLAFHVAELHPEYFKNCTSEPVDRPLEPWPKHGSGQPKTACTNCYCKKCCFH 351  
 DB 181 LEWRFSRLAFHVAELHPEYFKNCTSEPVDRPLEPWPKHGSGQPKTACTNCYCKKCCFH 240  
 QY 352 CQVCFITKALGISYGRKKRRRRRPPQGSQTHQVSLSKQPTSGSRGDPGPKETSGHHHH 411  
 DB 241 CQVCFITKALGISYGRKKRRRRRPPQGSQTHQVSLSKQPTSGSRGDPGPKETSGHHHH 300  
 QY 412 HH 413  
 DB 301 hh 302

RESULT 10

AG63233  
 ID AAG63233 standard; Protein; 302 AA.

XX AC AAG63233;

XX DT 01-OCT-2001 (first entry)

XX DE Amino acid sequence of a His-tagged Nef-Tat linked protein of HIV.

XX HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.

XX OS Synthetic.  
 OS Human immunodeficiency virus.

XX PN WO200154719-A2.

XX PD 02-AUG-2001.

XX 29-JAN-2001; 2001WO-EP00944.

XX

PR 31-JAN-2000; 2000GB-0002200.  
PR 14-APR-2000; 2000GB-0009336.  
PR 06-JUN-2000; 2000GB-0013806.  
PR 28-JUN-2000; 2000WO-EP05998.  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX PA  
XX PI Voss G;  
XX XX  
XX WPI; 2001-476172/51.  
DR N-PSDB; AAH42877.  
XX  
XX New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
PT protein or Polynucleotide for the manufacture of a vaccine -  
XX  
XX Disclosure; Fig 1; 90pp; English.  
XX  
XX The present sequence represents a His-tagged Nef-Tat linked protein of  
CC HIV. The protein is expressed in the yeast Pichia pastoris, and is used  
CC to produce the vaccine of the invention. The specification describes  
CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the  
CC manufacture of a vaccine. The vaccine is used for the prophylactic or  
CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
CC in synergy with gp120 in the treatment and prevention of HIV. The  
CC vaccine reduces the HIV viral load in HIV infected humans and results  
CC in a maintenance of CD4+ levels over those levels found in the absence  
CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.  
XX  
XX Sequence 302 AA;  
SQ

Query Match 74.6%; Score 1688; DB 22; Length 302;  
Best Local Similarity 100.0%; Pred. No. 5.4e-151;  
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 112 MGGKWSKSVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 171  
Db 1 mggkwsksvsgvptvrermraraepaadvgaasrdlekhgaitssntaatnaacawlea 50  
QY 172 QEEEEVGFPVTPQVPLRPMYTYKAAVDLSHFLKEKGLGLIHSQRRQDILDWYHTQGY 231  
Db 61 qeeeevgfptvpqplrpmttykaavdlshflkekggleglihsqrqrdildwiyhtqgy 120  
QY 232 FPDWNYTPGPGVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 291  
Db 121 fpdwnytpgpgvryplttfgwcyklvppepkveeankgentsllhpsvlhgmddperev 180  
QY 292 LEWRDLSRLAFHHVARELHPEYFKNCTSEPDPRLEPKHGPSQPKTACTNCKKCCFH 351  
Db 181 lewrdsrlafhhvarelhpeyfkntsepdprlep\*khpsqpkactactnckkccfh 240  
QY 352 CQVCFTIKALGISYGRKKRRRRPPQGSQTHQVSLSKOPTSQSRGDPGPKETSGHHHH 411  
Db 241 cqvcftikalgisyrkrrrrppqgsqthqvslskptsqsgsdgdpkpketsgghhhh 300  
QY 412 HH 413  
Db 301 hh 302

RESULT 11  
AAV02357  
ID AAV02357 standard; Protein; 302 AA.  
XX AC AAV02357;  
XX XX  
XX 09-JUL-1999 (first entry)  
XX DT  
XX A representative HIV-1 mutant Tat-His protein.  
XX DE  
XX HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
KW vaccine; HIV infection; protein D.

XX Synthetic.  
OS Human immunodeficiency virus type 1.  
XX  
XX WO9916884-A1.  
XX  
XX 08-APR-1999.  
XX  
XX PF 17-SEP-1998; 98WO-EP06040.  
XX  
XX PR 26-SEP-1997; 97GB-0020585.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
XX Bruck C, Godart SAG, Marchand M;  
XX  
XX WPI; 1999-302282/25.  
DR N-PSDB; AAX35693.  
XX  
XX HIV Tat or Nef protein linked to a fusion partner  
PT  
XX Disclosure; Fig 2; 66pp; English.  
XX  
XX The present sequence represents a representative HIV-1 mutant Tat-His  
CC protein. The protein is used in the creation of the fusion proteins of  
CC the invention, in conjunction with a fusion partner (e.g. protein D).  
CC The specification also describes fusion proteins comprising HIV-1 Nef  
CC protein. The fusion protein can be used in a vaccine to prevent HIV  
CC infection.  
XX  
XX Sequence 302 AA;  
SQ

Query Match 74.0%; Score 1675; DB 20; Length 302;  
Best Local Similarity 99.0%; Pred. No. 9.1e-150;  
Matches 299; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 112 MGGKWSKSVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 171  
Db 1 mggkwsksvsgvptvrermraraepaadvgaasrdlekhgaitssntaatnaacawlea 60  
QY 172 QEEEEVGFPVTPQVPLRPMYTYKAAVDLSHFLKEKGLGLIHSQRRQDILDWYHTQGY 231  
Db 61 qeeeevgfptvpqplrpmttykaavdlshflkekggleglihsqrqrdildwiyhtqgy 120  
QY 232 FPDWNYTPGPGVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 291  
Db 121 fpdwnytpgpgvryplttfgwcyklvppepkveeankgentsllhpsvlhgmddperev 180  
QY 292 LEWRDLSRLAFHHVARELHPEYFKNCTSEPDPRLEPKHGPSQPKTACTNCKKCCFH 351  
Db 181 lewrdsrlafhhvarelhpeyfkntsepdprlep\*khpsqpkactactnckkccfh 240  
QY 352 CQVCFTIKALGISYGRKKRRRRPPQGSQTHQVSLSKOPTSQSRGDPGPKETSGHHHH 411  
Db 241 cqvcftikalgisyrkrrrrppqgsqthqvslskptsqsgsdgdpkpketsgghhhh 300  
QY 412 HH 413  
Db 301 hh 302

RESULT 12  
AAG63239  
ID AAG63239 standard; Protein; 302 AA.  
XX AC AAG63239;  
XX XX  
XX 01-OCT-2001 (first entry)  
XX DT  
XX Amino acid sequence of a His-tagged mutant His protein of HIV.  
XX DE  
XX HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.  
KW

XX Synthetic.  
OS Human immunodeficiency virus.  
XX WO200154719-A2.  
XX 02-AUG-2001.  
XX 29-JAN-2001; 2001WO-EP00944.  
XX 31-JAN-2000; 2000GB-0002200.  
XX 14-APR-2000; 2000GB-0009336.  
XX 06-JUN-2000; 2000GB-0013806.  
XX 28-JUN-2000; 2000WO-EP05998.  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX Voss G;  
XX WPI; 2001-476172/51.  
XX N-PSDB; AAH42883.  
XX New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
XX linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
XX protein or polynucleotide for the manufacture of a vaccine .  
XX Disclosure; Fig 1; 90pp; English.  
XX The present sequence represents a His-tagged mutant His protein of HIV.  
XX The protein is expressed in the yeast Pichia pastoris, and is used to  
XX produce the vaccine of the invention. The specification describes  
XX the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the  
XX manufacture of a vaccine. The vaccine is used for the prophylactic or  
XX therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
XX in synergy with gp120 in the treatment and prevention of HIV. The  
XX vaccine reduces the HIV viral load in HIV infected humans and results  
XX in a maintenance of CD4+ levels over those levels found in the absence  
XX of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.  
XX Sequence 302 AA;

Query Match 74.0%; Score 1675; DB 22; Length 302;  
Best Local Similarity 99.0%; Pred. No. 9.1e-150;  
Matches 299; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 112 MGGKWSKSVVGVPTVRRMRRAEPAADGGAASRDLEKHGAITSNTAATNAACAWLEA 171  
DB 1 mggkwsksvvgvptvrrmraraepaadvgaasrdlekhgaitsntaataacawlea 60  
QY 172 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLIHSQRQDILDWYHTQGY 231  
DB 61 qeeevgfpvtpqvlrpmtykaavdlshflkekggleghlsqrqrldldwlyhtggy 120  
QY 232 FPDWQNYTPGCVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 291  
DB 121 fpdwnytpgpgvrypltfgcylkvppepkveeankgentsllhpvsilhgmddperev 180  
QY 292 LEWRDLSRLAFHHVARELHPEYFKNCTSEPDVPRLEPKHGPSQPKTACTNCYCKKCCFH 351  
DB 181 lewrfdslafhhvarelhpeyfkntsepdvprlepkhpgsqpkactnctcyckkccfh 240  
QY 352 CQVCFITKALGISYGRKKRRRRPPQGSQTHVSLSKOPTSOSRGDPTGPKETSGHHHH 411  
DB 241 cqvcfitaalgisygrkrrrrppqgsqthvslskoptsqskgeptgktsghhhh 300  
QY 412 HH 413  
DB 301 hh 302  
RESULT 13  
AAY02349

ID AAY02349 standard; Protein; 215 AA.  
XX AAY02349;  
XX 09-JUL-1999 (first entry)  
XX A representative HIV-1 Nef-His protein.  
XX HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
XX vaccine; HIV infection; protein D.  
XX Synthetic.  
XX Human immunodeficiency virus type 1.  
XX WO9916884-A1.  
XX 08-APR-1999.  
XX 17-SEP-1998; 98WO-EP06040.  
XX 26-SEP-1997; 97GB-0020585.  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX Bruck C, Godart SAG, Marchand M;  
XX WPI; 1999-302282/25.  
XX N-PSDB; AAX35685.  
XX HIV Tat or Nef protein linked to a fusion partner  
XX Disclosure; Fig 2; 66pp; English.  
XX The present sequence represents a representative HIV-1 Nef-His protein.  
XX The protein is used in the creation of the fusion proteins of  
XX the invention, in conjunction with a fusion partner (e.g. protein D).  
XX The specification also describes fusion proteins comprising HIV-1 Tat  
XX protein. The fusion protein can be used in a vaccine to prevent HIV  
XX infection.  
XX Sequence 215 AA;  
Query Match 50.3%; Score 1139.5; DB 20; Length 215;  
Best Local Similarity 71.2%; Pred. No. 2.3e-99;  
Matches 215; Conservative 0; Mismatches 0; Indels 87; Gaps 1;  
QY 112 MGGKWSKSVVGVPTVRRMRRAEPAADGGAASRDLEKHGAITSNTAATNAACAWLEA 171  
DB 1 mggkwsksvvgvptvrrmraraepaadvgaasrdlekhgaitsntaataacawlea 60  
QY 172 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLIHSQRQDILDWYHTQGY 231  
DB 61 qeeevgfpvtpqvlrpmtykaavdlshflkekggleghlsqrqrldldwlyhtggy 120  
QY 232 FPDWQNYTPGCVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 291  
DB 121 fpdwnytpgpgvrypltfgcylkvppepkveeankgentsllhpvsilhgmddperev 180  
QY 292 LEWRDLSRLAFHHVARELHPEYFKNCTSEPDVPRLEPKHGPSQPKTACTNCYCKKCCFH 351  
DB 181 lewrfdslafhhvarelhpeyfkntsepdvprlepkhpgsqpkactnctcyckkccfh 206  
QY 352 CQVCFITKALGISYGRKKRRRRPPQGSQTHVSLSKOPTSOSRGDPTGPKETSGHHHH 411  
DB 207 -----tsghhhh 213  
QY 412 HH 413  
DB 214 hh 215  
RESULT 14

AAG63231  
ID AAG63231 standard; Protein; 215 AA.

XX AC AAG63231;

XX DT 01-OCT-2001 (first entry)

XX DE Amino acid sequence of a His-tagged Nef protein of HIV.

XX KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.

XX OS Synthetic.

XX OS Human immunodeficiency virus.

XX PN WO200154719-A2.

XX PD 02-AUG-2001.

XX PF 29-JAN-2001; 2001WO-EP00944.

XX PR 31-JAN-2000; 2000GB-0002200.

XX PR 14-APR-2000; 2000GB-0009336.

XX PR 06-JUN-2000; 2000GB-0013806.

XX PR 28-JUN-2000; 2000WO-EP05998.

XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Voss G;

XX DR WPI; 2001-476172/51.

XX DR N-PSDB; AAH42875.

XX PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120 protein or polynucleotide for the manufacture of a vaccine -

XX PS Disclosure; Fig 1; 90pp; English.

XX CC The present sequence represents a His-tagged Nef protein of HIV. The protein is expressed in the yeast *Pichia pastoris*, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gp120 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.

XX SQ Sequence 215 AA;

Query Match 50.3%; Score 1139.5; DB 22; Length 215;  
Best Local Similarity 71.2%; Pred. No. 2.3e-99;  
Matches 215; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 112 MGGKWSKSVVGPVTRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 171

Db 1 mggkwsksvvgpvrermraepaadvgaasrdlekhgaitsntaataacawlea 60

QY 172 QEEVEVGFPTVPQVPLRPMTYKAAVDLSHFLKEKGLGELIHSQRQDILDWYHTOGY 231

Db 61 qeevevgfptvpqvlrpmtykaavdlshflkekggleglhsqrqrdildwlyhtggy 120

QY 232 FPDWQNYTPGQVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 291

Db 121 fpdwnytpgpgvrypltfgcylkvppepkveeankgentsllhpsvslhgmddperev 180

QY 292 LEWRDLSRLAFHHVARELHPEYFKNC 351

Db 181 lewrdsrlafhhvarelhpeyfknc----- 206

QY 352 QVCFITRALGISYGRKKRRRRRPPQSGQTHQVSLSKQPTSQSRGDPGPKETSGHHHH 411

Db 207 -----|||||  
QY 412 RH 413  
||  
Db 214 hh 215 -----tsghhhh 213

RESULT 15

AAAY50795

ID AAAY50795 standard; protein; 206 AA.

XX AC AAAY50795;

XX DT 17-FEB-2000 (first entry)

XX DE Human NEF protein/calmodulin binding inhibitor.

XX KW NEF protein; calmodulin; negative factor protein; binding inhibitor; diagnosis; detection; infection; treatment; HIV.

XX OS Homo sapiens.

XX PN WO9957136-A2.

XX PD 11-NOV-1999.

XX PF 06-MAY-1999; 99WO-EP03105.

XX PR 06-MAY-1998; 98DE-1020224.

XX PA (SCHO/) SCHOTT M.

XX PA (SCHO/) SCHORR J.

XX PA (ANTZ/) ANTZ C.

XX PI Schott M, Schorr J, Antz C;

XX DR WPI; 2000-038789/03.

XX CC Binding agents used for treatment, prevention and diagnosis of human immune deficiency virus infection -

XX PS Claim 3; Fig 1; 29pp; German.

XX CC This invention describes novel binding partners (A) (i) for negative factor protein (Nef) that competitively inhibit binding of calmodulin (I) to Nef, or (ii) for (I) that competitively inhibit binding of Nef to (I). (A) are used for prevention, diagnosis (by specific detection of intra- and/or extra-cellular Nef, including staging of infection), and/or treatment of infections with human immune deficiency virus (HIV).

XX SQ Sequence 206 AA;

Query Match 49.5%; Score 1120; DB 21; Length 206;  
Best Local Similarity 99.0%; Pred. No. 1.5e-97;  
Matches 204; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 112 MGGKWSKSVVGPVTRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 171

Db 1 mggkwsksvvgpvrermraepaadvgaasrdlekhgaitsntaanaacawlea 60

QY 172 QEEVEVGFPTVPQVPLRPMTYKAAVDLSHFLKEKGLGELIHSQRQDILDWYHTOGY 231

Db 61 qeevevgfptvpqvlrpmtykaavdlshflkekggleglhsqrqrdildwlyhtggy 120

QY 232 FPDWQNYTPGQVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 291

Db 121 fpdwnytpgpgvrypltfgcylkvppepkveeankgentsllhpsvslhgmddperev 180

QY 292 LEWRDLSRLAFHHVARELHPEYFKNC 317

Db 181 lewrdsrlafhhvarelhpeyfknc 206

## RESULT 16

AAR38893  
ID AAR38893 standard; Protein; 206 AA.XX AC AAR38893;  
XX DT 10-NOV-1993 (first entry)  
XX DE Nef protein of HIV-1.  
XX KW AIDS; antibody; p25; gp110; gp41; assay; detection;  
XX OS Immunity; vaccine.  
XX Human immunodeficiency virus-1.

XX OS US5221610-A.

XX PN 22-JUN-1993.

XX PD 26-MAY-1988; 88US-0199143.

XX PF 26-MAY-1988; 88US-0199143.

XX PR 04-SEP-1991; 91US-0754300.

XX PA (INRM ) INST NAT SANTE &amp; RECH MEDICALE.

XX PI (INSP ) INST PASTEUR.

XX PI Bahraoui EM, Chamaret S, Ferris S, Granier C, Montagnier L;

XX PI Rietschoten JV, Rochat H, Sabatier JM;

XX DR WPI; 1993-213434/26.

XX PT Diagnosis of HIV infection - by detecting HIV antibodies using

XX PT antigenic polypeptide derived from nef protein of HIV-1

XX PS Disclosure; Fig 2; 15pp; English.

XX CC The nef protein comprises peptides which are expressed in vivo in HIV

XX CC infected patients before detectable ams. of p25, gp110 and gp41 are

XX CC expressed. Thus, they can be used in assays for early detection of HIV.

XX CC They can also be used to raise antibodies for use in detection.

XX CC to induce cellular immunity or to raise neutralising antibodies

XX CC that either inactivate the AIDS virus or reduce the viability of

XX CC the virus in vivo or destroy infected cells.

XX CC The peptides may be used in viral vaccines.

XX SQ Sequence 206 AA;

## Query Match

Best Local Similarity 49.3%; Score 1116; DB 14; Length 206;

Matches 204; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 171

DB 1 mggkwsksvvgwptvrermraepaadvgaasrdlekhgaitsntaataacawlea 60

QY 172 QEEVEVGFPTVPOVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDILDLYHTOGY 231

DB 61 qeevevgfptvpqplrpmtykaavdlshflkekgleglshqrqdlldlyhtggy 120

QY 232 FPDWQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHHPVSLHGMDDPEREV 291

DB 121 fpdwnytpgcvrypltfwgcyklvppepkveeankgentsllhpsvslhgmddperev 180

QY 292 LEWRDSDSLAFHHVARELHPEYFKNC 317

DB 181 lewrdsrlafhhvarelhpeyfknc 206

## RESULT 17

## AAB10054

ID AAB10054 standard; Protein; 206 AA.

XX AC AAB10054;

XX DT 02-NOV-2000 (first entry)

XX DE HIV-1 nef protein.

XX KW Glycoprotein; gag; pol; GP-1; GP-2; anti-HIV; cytostatic;

XX KW gene therapy; treatment; infectious disease; HIV; AIDS; neoplasm;

XX KW Carcinoma; melanoma; nef protein.

XX OS Human immunodeficiency virus type 1.

XX PN EP1006196-A2.

XX PD 07-JUN-2000.

XX PF 25-NOV-1999; 99EP-0250415.

XX PR 26-NOV-1998; 98DE-1056463.

XX PA (PETT-) PETTE INST HEINRICH.

XX PI Von Laer MD;

XX WPI; 2000-378268/33.

XX N-PSDB; AAA40298, AAB10053, AAB10054.

XX New retroviral packing cell useful as pharmaceutical carrier in gene

XX therapy for treatment of HIV and neoplasms, comprises retroviral genes

XX PT and glycoproteins -

XX PS Disclosure; Page 48; 69pp; German.

XX CC This invention describes a novel retroviral packing cell (I), comprising

XX CC the retroviral genes gag, pol and glycoproteins GP-1 and GP-2 of the LCMV

XX CC coding gene gp, or a part of these. The products of the invention have

XX CC anti-HIV and cytostatic activity and can be used for gene therapy. (I) is

XX CC useful for in vitro infection of cells, especially hematopoietic stem

XX CC cells, for expression of transgenes in cells and as a pharmaceutical

XX CC carrier for gene therapy. (I) is therefore useful in the treatment of

XX CC infectious diseases (HIV or AIDS), neoplasms (carcinomas), melanomas and

XX CC other diseases. This sequence represents the Human immunodeficiency virus

XX CC (HIV-1) nef protein described in the method of the invention.

XX SQ Sequence 206 AA;

## Query Match

Best Local Similarity 49.2%; Score 1115; DB 21; Length 206;

Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 171

DB 1 mggkwsksvvgwptvrermraepaadvgaasrdlekhgaitsntaanaacawlea 60

QY 172 QEEVEVGFPTVPOVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDILDLYHTOGY 231

DB 61 qeevevgfptvpqplrpmtykaavdlshflkekgleglshqrqdlldlyhtggy 120

QY 232 FPDWQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHHPVSLHGMDDPEREV 291

DB 121 fpdwnytpgcvrypltfwgcyklvppepkveeankgentsllhpsvslhgmddperev 180

QY 292 LEWRDSDSLAFHHVARELHPEYFKNC 317

DB 181 lewrdsrlafhhvarelhpeyfknc 206

## \*RESULT 18

AAW89326



```

ID AAM89326 standard; Protein; 206 AA.
XX
AC AAM89326;
XX
DT 01-JUN-1999 (first entry)
XX
DE HIV-1 nef protein sequence.
XX
KW Antigenic composition; primate; lentivirus; nef gene; vaccine;
infection; AIDS; HIV-1; nef protein.
XX
OS Human immunodeficiency virus type 1.
XX
PN US851813-A.
XX
PD 22-DEC-1998.
XX
PF 27-JAN-1994; 94US-0188583.
XX
PR 27-JAN-1994; 94US-0188583.
PR 12-JUL-1990; 90US-0551945.
PR 09-JUL-1991; 91US-0727494.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Destosiers RC;
XX
WPI; 1999-080408/07.
DR N-PSDB; AAV81866.
XX
PT Lentivirus antigenic compositions - containing lentivirus with nef
gene deletion
XX
PS Disclosure; Fig 2A-R; 93pp; English.
XX
CC The invention relates to an antigenic composition comprising an isolated
primate lentivirus whose genome contains an engineered non-reversible
null mutation in the nef gene, or an infectious DNA clone in a carrier.
CC The antigenic composition is used in vaccines against infection by the
lentivirus, e.g. AIDS.
XX
SQ Sequence 206 AA;

Query Match 49.2%; Score 1114; DB 20; Length 206;
Best Local Similarity 97.6%; Pred. No. 5.4e-97;
Matches 201; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 112 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGALTSSNTAATNAACAWLEA 171
Db 1 mggkwsksvvgwptvrrmrreapadvggaasrdlekhgaltssntaannaacawlea 60

QY 172 QEEEEYGFVPTQVPLRPMTYKAAVDLSHFLKEKGLEGILHSQRRQDILDLYIHTQGY 231
Db 61 qeeekvgfvtqvpvlrmpmtykaavdlsflkkglegilhsqrrqdlldlyihtqgy 120

QY 232 FPDQNYTFCGPGVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPEREV 291
Db 121 fpdqnytpgpggirypltfgwcyklypvepdkveeankgentsllhpvslhgmdperv 180

QY 292 LEWRFDRLAFHHVARELHPEYFKNC 317
Db 181 lewrfdslafhhvarelhpeyfknc 206

RESULT 19
AAP61515
ID AAP61515 standard; Protein; 206 AA.
XX
AC AAP61515;
XX
DT 08-JUN-1991 (first entry)
XX

DE Sequence of E' protein.
XX
HIV; LAV; AIDS; diagnosis; vaccine.
XX
HTLV-IIIb/H9 cells (ATCC CRL 8543).
XX
EPI87041-A.
XX
09-JUL-1986.
XX
23-DEC-1985; 85EP-0309454.
XX
24-DEC-1984; 84US-0685272.
XX
04-DEC-1985; 85US-0805069.
XX
( GETH ) GENENTECH INC.
XX
Capon DJ, Lasky LA;
XX
WPI; 1986-177602/28.
XX
N-PSDB; AAN60288.
XX
Acquired immune deficiency syndrome polypeptide(s) ; obt'd. by
molecular cloning etc. and used for diagnosis and in vaccines
against virus disease
XX
Example; fig 2; 125pp; English.
XX
A comparison of AAN60287 with the cDNA of the HTLV-III genome
revealed one particular clone, designated p7.11 which contained a
DNA sequence encoding this peptide (AAP60308) sequence. This approx.
2.2 kilobase covers the precursor gag region and encodes, 5' to 3',
p-12, p-15, p-24 a second p-15 protein, and approx. 300 extra base
pairs 3' to the gag region (see AAN60288).
XX
SQ Sequence 206 AA;

Query Match 49.1%; Score 1111; DB 7; Length 206;
Best Local Similarity 97.1%; Pred. No. 1e-96;
Matches 200; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 112 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGALTSSNTAATNAACAWLEA 171
Db 1 mggkwsksvvgwptvrrmrreapadvggaasrdlekhgaltssntaannaacawlea 60

QY 172 QEEEEYGFVPTQVPLRPMTYKAAVDLSHFLKEKGLEGILHSQRRQDILDLYIHTQGY 231
Db 61 qeeekvgfvtqvpvlrmpmtykaavdlsflkkglegilhsqrrqdlldlyihtqgy 120

QY 232 FPDQNYTFCGPGVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDPEREV 291
Db 121 fpdqnytpgpggirypltfgwcyklypvepdkveeankgentsllhpvslhgmdperv 180

QY 292 LEWRFDRLAFHHVARELHPEYFKNC 317
Db 181 lewrfdslafhhvarelhpeyfknc 206

RESULT 20
AAP60423
ID AAP60423 standard; Protein; 216 AA.
XX
AC AAP60423;
XX
DT 20-AUG-1991 (first entry)
XX
DE Sequence of LAV virus ORF F protein.
XX
AIDS vaccine; diagnosis; immunoassay; HIV; HTLV-III.
XX
Lymphadenopathy virus.
XX

```

PN W08602383-A.  
XX  
PD 24-APR-1986.  
XX  
XX 18-OCT-1985; 85WO-EP00548.  
XX  
XX 21-JAN-1985; 85GB-0001473.  
PR  
PR 18-OCT-1984; 84FR-0016013.  
PR  
PR 16-NOV-1984; 84GB-0029099.  
XX  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
PA (INSP ) INST PASTEUR.  
XX  
XX Montagnier L, Krust B, Charnaret S, Clavel F, Chermann J-C;  
PI Barre-Sinoussi F, Allizon M, Sonigo P, Stewart C, Danos O;  
PI Wain-Hobson S;  
XX  
XX WPI: 1986-119166/18.  
DR N-PSDB; AAN60365.  
XX  
XX Purified glyco:protein and peptide(s) - are recognised by sera contg.  
FT antibodies against lymphadenopathy virus and useful in detecting  
PT AIDS antibodies or in vaccines  
XX  
XX Disclosure; Fig 4; 75pp; English.  
XX  
XX The inventors claim a polypeptide which is recognised by sera of  
CC human origin contg. antibodies against the virus of  
CC lymphadenopathies (LAV) or acquired immune deficiency syndrome  
CC (AIDS). Also claimed are various peptides corresp. to the AA  
CC sequences deducible from proteins encoded by LAV DNA, defined by  
CC specific residues (e.g. 12-32, 37-46, 49-79, 88-153) in accordance  
CC with a formula given in the specification.  
XX  
SQ Sequence 216 AA;  
  
Query Match 48.9%; Score 1107; DB 7; Length 216;  
Best Local Similarity 98.1%; Pred. No. 2.7e-96;  
Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
QY 112 MGGKWSKSVVGVWPTVRERMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 171  
Db 11 mggkwsksvvgwptvrermtraepaahgvgaaaspdlkghaigtsntaatnaacawlea 70  
  
QY 172 QEEEVGFPTVPQVPLRPMYKAAVDLSHFLKEKGLGGLIHSQRQDILDWIYHTOGY 231  
Db 71 qeeevgfptvpqplrpmtykaavdlshflkekggleglihsqrqrqldilwihtggy 130  
  
QY 232 RPDQNYTPGVRVPLTFGCYKLVPEPKVVEANKGENTSLHPSVSLHGMDDPEREV 291  
Db 131 fpdwnytpgpvrpvltfgcylvpepkvveankgentsllhpsvslhgmdpper 190  
  
QY 292 LEWRFDLSRLAFHHVARELHPYFKNC 317  
Db 191 lewrfdlsrlafhhvarelhpyfknc 216.  
  
RESULT 21  
AAW90179  
ID AAW90179 standard; Protein; 206 AA.  
XX  
AC AAW90179;  
XX  
DT 14-JUN-1999 (first entry)  
XX  
DE HTLV-III E' protein.  
XX  
KW AIDS; acquired immunodeficiency syndrome; viral infection; env protein;  
KW fusion polypeptide; E' protein; gag protein; pol protein; p' protein;  
KW gD signal peptide; detection; vaccination; etiological agent;  
KW infection inhibitor; AIDS associated retrovirus; p24; gp41.  
XX

OS Human lymphotropic virus type III.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 11 /label= Val, Ile  
FT Misc-difference 51 /label= Thr, Asn  
FT Misc-difference 54 /label= Asp, Ala  
FT Misc-difference 65 /label= Glu, Lys  
FT Misc-difference 151 /label= Glu, Asp  
FT Misc-difference 153 /label= Leu, Val  
XX  
XX US5853978-A.  
XX  
XX 29-DEC-1998.  
PD  
XX 29-JUL-1994; 94US-0282857.  
PF  
XX 08-MAY-1986; 86US-0861016.  
PR 24-DEC-1984; 84US-0685272.  
PR 04-DEC-1985; 85US-0805069.  
PR 02-AUG-1988; 88US-0227568.  
PR 19-NOV-1992; 92US-0979391.  
PR 29-SEP-1993; 93US-0129009.  
PR 29-JUL-1994; 94US-0282857.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Berman PW, Capon DJ, Lasky LA;  
PI  
XX WPI: 1999-094894/08.  
DR N-PSDB; AAV74271.  
XX  
XX New AIDS-associated fusion polypeptide(s) - used for the detection  
PT of AIDS or to inhibit infection by AIDS associated retrovirus or  
PT dissemination of such retrovirus in infected individuals  
XX  
XX Example 1; Fig 2A-J; 47pp; English.  
PS  
XX This invention describes a novel fusion polypeptide which comprises  
CC (a) a first polypeptide sequence of an AIDS associated E', env, or gag  
CC polypeptide, that specifically binds complementary antibody and (b) a  
CC second polypeptide sequence which is not an AIDS associated virus  
CC polypeptide. Also described are (1) a fusion polypeptide having a  
CC herpes simplex virus (HSV) gD signal peptide sequence fused in reading  
CC frame with a polypeptide sequence other than HSV gD, (2) a nucleic acid  
CC encoding a fusion polypeptide as in (1); (3) an expression vector  
CC comprising a nucleic acid as in (2); (4) a host comprising a vector as  
CC in (3). The AIDS-associated fusion polypeptides can be used in the  
CC detection of and vaccination against viral etiological agents of AIDS.  
CC They can also be administered as a pharmaceutical agent to inhibit  
CC infection by AIDS associated retrovirus or dissemination of such  
CC retrovirus in infected individuals.  
XX  
SQ Sequence 206 AA;  
  
Query Match 48.2%; Score 1092; DB 20; Length 206;  
Best Local Similarity 96.1%; Pred. No. 6.5e-95;  
Matches 198; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
  
QY 112 MGGKWSKSVVGVWPTVRERMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 171  
Db 11 mggkwsksvvgwptvrermtraepaahgvgaaaspdlkghaigtsntaatnaacawlea 60  
  
QY 172 QEEEVGFPTVPQVPLRPMYKAAVDLSHFLKEKGLGGLIHSQRQDILDWIYHTOGY 231  
Db 61 qeeevgfptvpqplrpmtykaavdlshflkekggleglihsqrqrqldilwihtggy 120

Query Match 44.78; Score 1011; DB 22; Length 216;

CC is increased by a factor of 50-100 compared with the use of a vector  
CC containing the SV40 early promoter.

XX  
SQ Sequence 210 AA;

Query Match 44.0%; Score 997; DB 19; Length 210;  
Best Local Similarity 85.2%; Pred. No. 6.4e-86;  
Matches 179; Conservative 16; Mismatches 11; Indels 4; Gaps 1;

QY 112 MGGKWSKSSVVGWPTVRMR---RAEPAADGVGAASRDLEKHGATSSNTAATNAACA 167  
DB 1 mggkwskrsmgwsairermraepaadvavsdlekhgaitssntaataadca 60  
QY 168 WLEAQEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKGGLGLHSQRQDILDWIYH 227  
DB 61 wleaqeeveevfpvpdpplrpmtykaaldishfkekgglegliwsgrrgeildlwiyh 120  
QY 228 TQGYFDPQNYTPGVRYPPLTFGCWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDDP 287  
DB 121 tqgyfdpqnytpgpylryplttfgwciklvpepveeeanegennsilhpmslhgmada 180  
QY 288 EREYLEWRFDSRLAFHHVARELHPEYFKNC 317  
DB 181 ekevlvwrfsdsklafhmarelhppeyykdc 210

RESULT 24  
AAAY77299  
ID AAY77299 standard; Protein: 210 AA.  
AC AAY77299;  
XX  
XX 22-MAY-2000 (first entry)  
DT  
DE HIV-1 (ATCC CRL 8597) ORF #3-encoded protein.  
KW HIV-1; immunoassay; antigen; pol fragment; p31; recombinant; antibody;  
KW detection.  
XX  
XX Human immunodeficiency virus type 1 'ATCC CRL 8597'.  
XX  
XX US6013432-A.  
XX  
XX 11-JAN-2000.  
XX  
XX 17-MAY-1995; 95US-0443434.  
XX  
XX 08-JUL-1993; 93US-0089407.  
XX 24-DEC-1987; 87US-0138894.  
XX 17-AUG-1992; 92US-0931154.  
XX 31-OCT-1984; 84US-0667501.  
XX 30-JAN-1985; 85US-0696534.  
XX 06-SEP-1985; 85US-0773447.  
XX (CHIR ) CHIRON CORP.  
XX  
XX Luciw PA, Dina D;  
XX  
XX WPI; 2000-170256/15.  
XX N-PSDB; AAZ90201.  
XX  
XX Immunoassay for antibodies against human immune deficiency virus, for  
XX diagnosing infection, uses an immunogenic fragment of the pol protein  
XX as antigen.  
XX  
XX Example 1; Fig 40-P; 99pp; English.  
XX  
XX The invention relates to the improvement of HIV-1 immunoassays by the  
XX use of an HIV-1 antigen comprising an immunogenic fragment of  
XX recombinant or synthetic HIV-1 pol, which is encoded by an approximately  
XX 9.7 kb sequence between a BstXI restriction site at position 3006 and an  
XX NdeI site at position 5131 of the genome (the proviral DNA sequence is

CC given in AAZ90201). The immunogenic pol fragment is not immunologically  
CC cross-reactive with human T cell lymphotropic viruses I or II. The  
CC invention also encompasses the use of p31 as an antigen. The recombinant  
CC antigens may be produced in *Escherichia coli*, *Saccharomyces cerevisiae* or  
CC in mammalian cells. Immunoassays using the recombinant HIV proteins may  
CC be used to diagnose and stage HIV-1 infections. Sequences  
CC AAY77294-Y77299 represent proteins encoded by the genome of HIV-1 (ATCC  
CC CRL 8597).

XX  
SQ Sequence 210 AA;

Query Match 44.0%; Score 997; DB 21; Length 210;  
Best Local Similarity 85.2%; Pred. No. 6.4e-86;  
Matches 179; Conservative 16; Mismatches 11; Indels 4; Gaps 1;

QY 112 MGGKWSKSSVVGWPTVRMR---RAEPAADGVGAASRDLEKHGATSSNTAATNAACA 167  
DB 1 mggkwskrsmgwsairermraepaadvavsdlekhgaitssntaataadca 60  
QY 168 WLEAQEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKGGLGLHSQRQDILDWIYH 227  
DB 61 wleaqeeveevfpvpdpplrpmtykaaldishfkekgglegliwsgrrgeildlwiyh 120  
QY 228 TQGYFDPQNYTPGVRYPPLTFGCWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDDP 287  
DB 121 tqgyfdpqnytpgpylryplttfgwciklvpepveeeanegennsilhpmslhgmada 180  
QY 288 EREYLEWRFDSRLAFHHVARELHPEYFKNC 317  
DB 181 ekevlvwrfsdsklafhmarelhppeyykdc 210

RESULT 25  
AAE04962  
ID AAE04962 standard; Protein: 217 AA.  
AC AAE04962;  
XX  
XX 10-SEP-2001 (first entry)  
DT  
DE HIV-1 jrf1 Nef (G2A, L1AA) mutant protein.  
KW DNA vaccine: codon optimisation; Nef protein; HIV infection; anti-HIV;  
KW cell mediated immune response; cytotoxic T lymphocyte; CTL;  
KW human immunodeficiency virus-1; HIV-1; jrf1 Nef; mutant; mutein.  
XX  
XX Human immunodeficiency virus type 1.  
XX Synthetic.  
XX  
XX OS  
XX OS  
XX  
XX Key Location/Qualifiers  
XX  
XX Misc-difference 2 /note= "Wild type myristylation site at Gly2 substituted  
XX with Ala"  
XX Misc-difference 174..175 /note= "Wild type dileucine motif (Leu-Leu) substituted  
XX with Ala-Ala"  
XX  
XX WO200143693-A2.  
XX  
XX 21-JUN-2001.  
XX  
XX 15-DEC-2000; 2000WO-US34162.  
XX  
XX 17-DEC-1999; 99US-0172442.  
XX (MERI ) MERCK & CO INC.  
XX  
XX Shiver JW, Liang X, Fu T;  
XX WPI; 2001-417878/44.  
XX DR  
XX N-PSDB; AAD09605.  
XX

PT Novel DNA vaccine useful for inducing cell mediated immune response  
PT against virulent strains of HIV, comprises DNA expression vector, and  
PT DNA containing codon optimized open reading frame encoding Nef protein  
XX  
PS Claim 29; Page 18; 84pp; English.

XX The present invention relates to a DNA vaccine comprising a DNA  
CC expression vector, and a DNA molecule containing a codon optimised open  
CC reading frame encoding a Nef protein or its immunogenic derivative. The  
CC Nef protein or its derivative is expressed and generates an immune  
CC response which provides a substantial level of protection against HIV  
CC infection, upon administration of to a host. The DNA vaccine is useful  
CC for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL)  
CC response against infection or disease caused by virulent strains of HIV,  
CC by administering the DNA vaccine into the tissue of the vertebrate host,  
CC preferably human. It is also useful for lowering transmission rate to  
CC previously uninfected individuals and/or for reducing levels of viral  
CC loads within an infected individual, so as to prolong the asymptomatic  
CC phase of HIV infection. The present sequence is human immunodeficiency  
CC virus-1 (HIV-1) jrf1 Nef (G2A, L2AA) mutant protein. The different nef  
CC constructs of the invention are used in the exemplification of the  
CC invention.

XX Sequence 217 AA;

Query Match 44.0%; Score 996; DB 22; Length 217;  
Best Local Similarity 82.0%; Pred. No. 8.4e-86;  
Matches 178; Conservative 16; Mismatches 13; Indels 10; Gaps 1;

QY 112 MGKWSKSVWGVPVTRMRRAEPAAD-----GVGAASRDLEKHGAISSNTAA 161  
DB 1 magkwsksrvgpwtvtrmrtraepadvrrtpaavvgavsvrdlekhgaitssntaa 60  
QY 162 TNACAWLEAQEEEEVGFPVTPQVPLRPMYKAAVDLSHFLKEKGLEGLIHSQRQDIL 221  
DB 61 tnadcaawleaqedeegvfpvtpqvlrmpntykgavdlshflkekggleglisqrqdl 120  
QY 222 DLWIVHTQGYFDWQNYTPGPGVRYPLTFGCWYKLVPEPDKVEEANKGENTSLHHPVSL 281  
DB 121 dlwvhtqgyfdwqnytpgpgvrypltfpgwcfklvpevekeveeaneenncaahpmsq 180  
QY 282 HGMDDPEREVLWRFDSRLAFHHVARELHPEYFKNC 318  
DB 181 hgiedpekevelewfdsrlafhhvarelhpeyfkncs 217

RESULT 26  
AA012262  
ID AAR12262 standard; Protein; 210 AA.  
XX  
AC AAR12262;  
XX  
DT 20-AUG-1991 (first entry)  
XX  
DE HIV-1 strain OYI open reading frame (ORF) F protein.  
XX  
KW HIV-1; AIDS; retroviruses.  
XX  
OS Homo sapiens.  
XX  
PN US5019510-A.  
XX  
PD 28-MAY-1991.  
XX  
PF 28-OCT-1987; 87US-0113655.  
XX  
PR 28-OCT-1987; 87US-0113655.  
XX  
PA (INSP ) INST PASTEUR.  
XX  
PI Wain-Hobson S, Huet T, Delaporte E, Brun-Vezinet F;

XX WPI; 1991-177518/24.  
XX Purified human retrovirus - is mutant of HIV-1 having  
PT characteristics of HIV-1 OYI, used in diagnosis of HIV infection  
XX  
PS Disclosure; fig 8; 23pp; English.

XX This sequence constitutes the ORF F protein constituent of a new  
CC strain of HIV-1 retrovirus, OYI. This mutant retroviral strain is  
CC useful in an assay for diagnosing HIV infection. See also AAO11943  
CC (OYI nucleotide sequence), AAR12255-61 (other HIV OYI constituent  
CC proteins).

XX Sequence 210 AA;

Query Match 43.4%; Score 983; DB 12; Length 210;  
Best Local Similarity 82.5%; Pred. No. 1.3e-84;  
Matches 174; Conservative 22; Mismatches 9; Indels 6; Gaps 2;

QY 112 MGKWSKSVWGVPVTRMRRA-----EPAADGVGAASRDLEKHGAISSNTAATNAAC 166  
DB 1 mgkwskskmgvptirermkraelqppepaagvgaasrdlekhgaitssntaataadnc 60  
QY 167 AWLEAQEEEEVGFPVTPQVPLRPMYKAAVDLSHFLKEKGLEGLIHSQRQDILDWIY 226  
DB 61 awleaqedeegvfpvtpqvlrmpntykgaldishflkekggleglisqrqgdild-wvy 119  
QY 227 HQQGYFPDQNYTPGPGVRYPLTFGCWYKLVPEPDKVEEANKGENTSLHHPVSLHGMDD 286  
DB 120 hqgyfpdqnytpgpgvrypltfgcwcfklvpmddpqqveeaneennsilhplshgmdd 179  
QY 287 PEREVLWRFDSRLAFHHVARELHPEYFKNC 317  
DB 180 pekevlwrfdsrlafhhvarelhpeyfkdc 210

RESULT 27

AA004961  
ID AAE04961 standard; Protein; 237 AA.

XX AAE04961;

XX 10-SEP-2001 (first entry)

XX Human tPA leader peptide-HIV-1 jrf1 Nef (opt tpanef) mutant protein.

XX DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV;  
KW cell mediated immune response; cytotoxic T lymphocyte; CTL;  
KW human immunodeficiency virus-1; HIV-1; human; jrf1 Nef; opt tpanef;  
KW tissue plasminogen activator; tPA; chimeric protein; mutant; mutein.

XX Chimeric - Human immunodeficiency virus type 1.

OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers  
FH Peptide 1..26  
FT /label= Leader\_peptide

FT /note= "Human tissue plasminogen activator (tPA)  
FT leader sequence"

FT Protein 27..237  
FT /note= "Mature HIV-1 Nef (6-216aa) protein"

FT Domain 195..196  
FT /label= Dileucine\_motif

XX WO200143693-A2.

XX 21-JUN-2001.

XX 15-DEC-2000; 2000WO-US34162.

XX 17-DEC-1999; 99US-0172442.

XX PA (MERI ) MERCK & CO INC.

XX PI Shiver JW, Liang X, Fu T;

XX FT WPI: 2001-417878/44.

XX DR N-PSDB; AAD09604.

XX PT Novel DNA vaccine useful for inducing cell mediated immune response

XX PT against virulent strains of HIV, comprises DNA expression vector, and

XX PT DNA containing codon optimized open reading frame encoding Nef protein

XX PT

XX PS Claim 29; Page 17; 84pp; English.

XX CC The present invention relates to a DNA vaccine comprising a DNA

XX CC expression vector, and a DNA molecule containing a codon optimised open

XX CC reading frame encoding a Nef protein or its immunogenic derivative. The

XX CC Nef protein or its derivative is expressed and generates an immune

XX CC response which provides a substantial level of protection against HIV

XX CC infection, upon administration of to a host. The DNA vaccine is useful

XX CC for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL)

XX CC response against infection or disease caused by virulent strains of HIV,

XX CC by administering the DNA vaccine into the tissue of the vertebrate host,

XX CC preferably human. It is also useful for lowering transmission rate to

XX CC previously uninfected individuals and/or for reducing levels of viral

XX CC loads within an infected individual, so as to prolong the asymptomatic

XX CC phase of HIV infection. The present sequence is human tissue plasminogen

XX CC activator (tPA) leader peptide-human immunodeficiency virus-1 (HIV-1)

XX CC jrlf Nef (Opt tpanef) chimeric mutant protein. The mutation include

XX CC deletion of the myristylation site (Gly2) in the HIV-1 jrlf Nef protein.

XX CC The different codon optimised nef constructs of the invention are used

XX CC in the exemplification of the invention.

XX PS Sequence 237 AA;

XX SQ

Query Match 43.2%; Score 978; DB 22; Length 237;

Best Local Similarity 83.4%; Pred. No. 4.8e-84;

Matches 176; Conservative 15; Mismatches 10; Indels 10; Gaps 1;

Qy 117 SKSSVVGWPTVRMRRAEPAAD-----GVGAASRDLEKKGALTSNTAATNAAC 166

Db 27 skrvpgwstvrmrtraepadrvttepaavgavsvrdlekghgaltssntaatnadc 86

Qy 167 AWLEAQEEVEEFGFVPTQVPLRPMTYKAADVLSHFLKKGGLGGLIHSQRDIDLWY 226

Db 87 awleaqedeegvfvrpqvprmpkykgavdlshfikekgleglihsqkrqdlldlwy 146

Qy 227 HTQGYFPDQWNTPGVRYPLTFGWCYKLVPEDPKVEEANKGENTSLHPVSLHGMD 286

Db 147 htqgyfpdqwnytpggrfpltfwgcfklvpvekeeanegenncilhpmsqhgied 206

Qy 287 PEREVLWRFDSRLAFHVARLHPEYFKNC 317

Db 207 pekevlwrfdsrlafhvarlhpeyfknc 237

RESULT 28

ID AAE04963

XX AAE04963 standard; Protein; 237 AA.

XX AC AAE04963;

XX DT 10-SEP-2001 (first entry)

XX DE Human tPA leader peptide-HIV-1 jrlf Nef (LLAA) mutant protein.

XX KW DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV;

XX KW cell mediated immune response; cytotoxic T lymphocyte; CTL;

XX KW human immunodeficiency virus-1; HIV-1; human; jrlf nef; Opt tpanef;

XX KW tissue plasminogen activator; tPA; chimeric protein; mutant; mutein.

OS OS Chimeric - Human immunodeficiency virus type 1.

XX OS Chimeric - Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..26

XX FT /label= "Leader peptide"

XX FT /note= "Human tissue plasminogen activator (tPA)

XX FT leader sequence"

XX FT Protein 27..237

XX FT /note= "Mature HIV-1 Nef (6-216aa) protein"

XX FT Misc-difference: 195..196

XX FT /note= "Wild type dileucine motif (Leu-Leu) substituted

XX FT with Ala-Ala"

XX PS WO200143693-A2.

XX PN 21-JUN-2001.

XX PD 15-DEC-2000; 2000WO-US34162.

XX PF 17-DEC-1999; 99US-0172442.

XX PR (MERI ) MERCK & CO INC.

XX PA Shiver JW, Liang X, Fu T;

XX PI WPI: 2001-417878/44.

XX PS N-PSDB; AAD09606.

XX PT Novel DNA vaccine useful for inducing cell mediated immune response

XX PT against virulent strains of HIV, comprises DNA expression vector, and

XX PT DNA containing codon optimized open reading frame encoding Nef protein

XX PT

XX PS Claim 29; Page 19; 84pp; English.

XX CC The present invention relates to a DNA vaccine comprising a DNA

XX CC expression vector, and a DNA molecule containing a codon optimised open

XX CC reading frame encoding a Nef protein or its immunogenic derivative. The

XX CC Nef protein or its derivative is expressed and generates an immune

XX CC response which provides a substantial level of protection against HIV

XX CC infection, upon administration of to a host. The DNA vaccine is useful

XX CC for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL)

XX CC response against infection or disease caused by virulent strains of HIV,

XX CC by administering the DNA vaccine into the tissue of the vertebrate host,

XX CC preferably human. It is also useful for lowering transmission rate to

XX CC previously uninfected individuals and/or for reducing levels of viral

XX CC loads within an infected individual, so as to prolong the asymptomatic

XX CC phase of HIV infection. The present sequence is human tissue plasminogen

XX CC activator (tPA) leader peptide-human immunodeficiency virus-1 (HIV-1)

XX CC jrlf Nef (LLAA) chimeric mutant protein. The different codon

XX CC optimised nef constructs of the invention are used in the exemplification

XX CC of the invention.

XX SQ Sequence 237 AA;

Query Match 42.8%; Score 968; DB 22; Length 237;

Best Local Similarity 82.5%; Pred. No. 4.2e-83;

Matches 174; Conservative 15; Mismatches 12; Indels 10; Gaps 1;

Qy 117 SKSSVVGWPTVRMRRAEPAAD-----GVGAASRDLEKKGALTSNTAATNAAC 166

Db 27 skrvpgwstvrmrtraepadrvttepaavgavsvrdlekghgaltssntaatnadc 86

Qy 167 AWLEAQEEVEEFGFVPTQVPLRPMTYKAADVLSHFLKKGGLGGLIHSQRDIDLWY 226

Db 87 awleaqedeegvfvrpqvprmpkykgavdlshfikekgleglihsqkrqdlldlwy 146

Qy 227 HTQGYFPDQWNTPGVRYPLTFGWCYKLVPEDPKVEEANKGENTSLHPVSLHGMD 286

Db 147 htqgyfpdqwnytpggrfpltfwgcfklvpvekeeanegenncilhpmsqhgied 206

```

QY 287 PEREVLWRFDSRLAFHVRHARELHPEYFKNC 317
Db 207 pekevlwrfdsrlafhvrharelhpeyykdc 237

RESULT 29
AAB69363
ID AAB69363 standard; Protein; 206 AA.
AC AAB69363;
XX
XX 20-APR-2001 (first entry)
XX
XX HIV-1 non-subtype B clone 962M651-8 nef protein.
XX
XX HIV-1; human immunodeficiency virus; non-subtype B; gag; pol; env;
KW vpr; vif; vpr; tat; rev; nef; vaccine.
XX
XX Human immunodeficiency virus type 1.
XX
XX WO200026416-A1.
XX
XX 11-MAY-2000.
XX
XX 25-OCT-1999; 99WO-US24837.
XX
XX 02-NOV-1998; 98US-0184418.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Hahn BH, Shaw GM, Gao F;
XX
XX WPI; 2000-365651/31.
XX
XX Novel genomic nucleic acids of non-subtype B human immunodeficiency
PT virus type 1 useful for detecting and treating AIDS comprises a
PT specific nucleotide sequence
XX
XX Claim 41; Fig 22; 131pp; English.
XX
XX The present invention provides the protein and coding sequences for a
CC number of human immunodeficiency virus (HIV) type 1 non-subtype B
CC isolates. The sequences shown include the near full-length coding
CC sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, tat,
CC rev and nef proteins. These can be used to detect the presence of HIV-1
CC in a sample and to produce antibodies against non-subtype B HIV-1 virus.
CC These antibodies can be used in vaccines to prevent and treat HIV
CC infection.
XX
XX Sequence 206 AA;

Query Match 42.0%; Score 952; DB 21; Length 206;
Best Local Similarity 81.1%; Pred. No. 1.1e-81;
Matches 167; Conservative 24; Mismatches 15; Indels 0; Gaps 0;

QY 112 MGKWKSSVGVGPTVVRMRRAEPADGVGAASRDLEKHGALTSSNTAATNACAWLEA 171
Db 1 mggkwsksivgvpavrrirrtetpaagvgavsdldkygaltssntttnaacawlea 60

QY 172 QEEEEVGFPTVPOVPLRPMYTKAAVDLSHFLKEKGGLEGILHSQRQDILDLYIHTQGY 231
Db 61 qeeeevfpvprpdpvplrmpmtkyaaavdlshflkekgglegilyskrqeldlwyhtqgf 120

QY 232 FPDQNYTTPGVRYPVPLTFGWCYKLVPEPDKVVEANKGENTSLHPVSLHGMDPPERV 291
Db 121 fpdqnytpgvrpyplttfgwcfklyvpdpgeveanegenncllhpsmqggmddhrev 180

QY 292 LEWRFDSRLAFHVRHARELHPEYFKNC 317
Db 181 lkwkfdshlahkhmarelhpeyykdc 206

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RESULT 30
AAB86169
ID AAB86169 standard; Protein; 3025 AA.
XX
XX AAB86169;
XX
XX 21-AUG-2001 (first entry)
XX
XX HIV-1 subtype C protein fragment #1.
XX
XX Infection; diagnosis; human; humoral immune response; antiviral;
KW cellular immune response; vaccine; treatment; gene therapy.
XX
XX Human immunodeficiency virus type 1.
XX
XX Key Location/Qualifiers
FT Misc-difference 1..3025
FT /label= Xaa
FT /note= "Xaa represents a stop codon"
XX
XX DE10056747-A1.
XX
XX 31-MAY-2001.
XX
XX 16-NOV-2000; 2000DE-1056747.
XX
XX 16-NOV-1999; 99DE-1055089.
XX
XX (SHAO/) SHAO Y.
XX (GENE-) GENEART GMBH GES ANGEWANDTE BIOTECHNOLOG.
XX
XX Wagner R, Wolf H, Shao Y, Graf M;
XX
XX WPI; 2001-336417/36.
XX
XX N-PSDB; AAH20870.
XX
XX New nucleic acid sequences from a human immune deficiency virus
PT intersubtype, useful for treatment, prevention and diagnosis of
PT infection
XX
XX Disclosure: Fig 8A-O; 48pp; German.
XX
XX This invention describes a novel polynucleotide isolated from human
CC immunodeficiency virus type 1 subtype C/B' which can be used for the
CC induction of specific humoral and cellular immune responses. (I) are
CC polypeptides (II) encoded by them, are useful in pharmaceuticals,
CC vaccines and diagnostic agents, particularly for treatment or prevention
CC of human immune deficiency virus-1 (HIV-1) infections, also for rational
CC design of test or therapeutic reagents, or gene therapy vectors.
CC Polypeptides, especially antibodies, specifically directed against (II)
CC are similarly useful as pharmaceutical and diagnostic agents. (I) are
CC specific for intersubtype C/B' of HIV-1 so are useful in regions
CC (particularly China and South-East Asia) where this subtype is prevalent.
CC The products of the invention have antiviral activity. This sequence
CC represents a protein encoded by the HIV-1 subtype C genome described in
CC the method of the invention.
XX
XX Sequence 3025 AA;

Query Match 41.9%; Score 948.5; DB 22; Length 3025;
Best Local Similarity 70.6%; Pred. No. 1.2e-79;
Matches 175; Conservative 22; Mismatches 42; Indels 9; Gaps 2;

QY 112 MGKWKSSVGVGPTVVRMRRAEPADGVGAASRDLEKHGALTSSNTAATNACAWLEA 171
Db 2723 mggkwsksivgvpairrrrtetpaagvgavsdldkygaltssntttnaacawlea 2782

QY 172 QEEEEVGFPTVPOVPLRPMYTKAAVDLSHFLKEKGGLEGILHSQRQDILDLYIHTQGY 231
Db 2783 qeeeevfpvprpdpvplrmpmtkyaaavdlshflkekgglegilyskrqeldlwyhtqgy 2842

QY 232 FPDQNYTTPGVRYPVPLTFGWCYKLVPEPDKVVEANKGENTSLHPVSLHGMDPPERV 291

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Db 2843 fpdwnytpgpgvrlptfgwcklvdpveeeanedncilhpvcqhgmedhrev 2902
QY 292 LEWREDSRLAFHHVARELHPEYFKNCTSEPVDPDR-----LEPWKHGSGPKTACTNCY 344
Db 2903 lkwkfdslahrhrarelhpefykdcxhrrdfprglstgafxews--ggtsgqpsnaa 2960
QY 345 CKKCFHC 352
Db 2961 ykqlifac 2968

```

Search completed: August 26, 2002, 08:12:30  
Job time: 239 sec



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OM protein - protein search, using sw model

Run on: August 26, 2002, 08:13:22 ; Search time 50.45 Seconds  
(without alignments)  
786.618 Million cell updates/sec

Title: US-09-509-239-21  
Perfect score: 2264  
Sequence: 1 WDPSSHSSNMANTQMSDKI.....QSRGDPGTGPKETSGHHHHH 413

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1130	49.9	206	1 ASLJFV	nef protein - huma
2	1115	49.2	205	2 S43467	nef protein - huma
3	1115	49.2	206	2 S03244	nef protein (clone
4	1114	49.2	206	1 ASLJYL	nef protein - huma
5	1108	48.9	206	1 ASLJ12	nef protein - huma
6	1097	48.5	206	2 JC5400	nef protein - huma
7	1096	48.4	206	2 S03245	nef protein (clone
8	1096	48.4	206	2 S33986	nef protein - huma
9	1081.5	47.8	205	1 ASLJH3	nef protein - huma
10	1019	45.0	204	2 S24985	nef protein - huma
11	1019	45.0	218	1 ASLJBR	nef protein - huma
12	1007	44.5	206	2 S25937	nef protein - huma
13	997	44.0	210	1 ASLJ02	nef protein - huma
14	991.5	43.8	214	1 I44001	nef protein - huma
15	987	43.6	182	2 S03247	nef protein (clone
16	987	43.6	204	2 S03246	nef protein (clone
17	911	40.2	212	1 QOLJ2R	nef protein - huma
18	903.5	39.9	207	1 QOLJND	nef protein - huma
19	837	37.0	205	1 B44963	nef protein - huma
20	834.5	36.9	209	2 T01673	nef protein - huma
21	832	36.7	205	1 ASLJIK	nef protein - simi
22	569.5	25.2	364	2 S59931	glycerophosphodies
23	569.5	25.2	364	2 S59932	glycerophosphodies
24	569.5	25.2	364	2 A43576	glycerophosphodies
25	569.5	25.2	364	2 S59934	glycerophosphodies
26	563.5	24.9	364	2 S59933	glycerophosphodies
27	553.5	24.4	364	2 G64086	glycerophosphodies
28	547.5	24.2	364	2 S59935	glycerophosphodies
29	486	21.5	86	2 S33982	trans-activating t

30	478	21.1	95	1 TNLJ12	trans-activating t
31	470	20.8	86	2 A25700	trans-activating t
32	443	19.6	226	2 S46353	nef protein - simi
33	439.5	19.4	97	2 S54385	nef protein - huma
34	437	19.3	101	2 T09446	tat protein - huma
35	434	19.2	101	1 E44001	trans-activating t
36	429.5	19.0	309	2 S07993	nef protein - simi
37	426.5	18.8	259	2 T11567	nef protein - simi
38	421.5	18.6	255	2 S53099	nef protein - huma
39	421	18.6	257	2 S12160	nef protein - huma
40	413	18.2	260	1 ASLJC2	nef protein - huma
41	411.5	18.2	263	2 T11556	nef protein - simi
42	411	18.2	86	2 JC5391	transactivator pro
43	409	18.1	250	2 S54851	nef protein - simi
44	408	18.0	86	2 S54381	tat protein - huma
45	405	17.9	86	1 TNLJ2R	trans-activating t

#### ALIGNMENTS

RESULT 1

ASLJFV  
nef protein - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A04008; S14609  
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.  
Cell 40, 9-17, 1985  
A:Title: Nucleotide sequence of the AIDS virus, LAV.  
A:Reference number: A90866; MUID:85099333  
A:Accession: A04008  
A:Molecule type: DNA  
A:Residues: 1-206 <WAI>  
A:Cross-references: GB:R02013; NID:9326417; PIDN:AB59752.1; PID:9326425  
A:Experimental source: Isolate LAV-1a  
R:Ciccarelli, R.B.  
submitted to the EMBL Data Library, March 1991  
A:Reference number: S14607  
A:Accession: S14609  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-206 <CIC>  
A:Cross-references: EMBL:X58780; NID:960113; PIDN:CAA1585.1; PID:960114  
C:Genetics:  
A:Gene: nef; 3'-orf; orf-F  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; immunodeficiency; phosphoprotein

Query Match 49.9% Score 1130; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. 2.2e-80;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	112	MGKKWSKSVVGVPTVPRMRRAEPAADGVGAASRDLEKKGALTSSTNTAATNAACAWLEA	171
Db	1	MGKKWSKSVVGVPTVPRMRRAEPAADGVGAASRDLEKKGALTSSTNTAATNAACAWLEA	60
Qy	172	QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLIHSQRRODLDLWIYHTQGY	231
Db	61	QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLIHSQRRODLDLWIYHTQGY	120
Qy	232	FPDMQNYTPGCVRYPLTFGCYKLVVPDPKVEEANKGENTSLHPVSLHGMDDPEREV	291
Db	121	FPDMQNYTPGCVRYPLTFGCYKLVVPDPKVEEANKGENTSLHPVSLHGMDDPEREV	180
Qy	292	LEWRDSSLAPHHVARELHPEYFKNC	317
Db	181	LEWRDSSLAPHHVARELHPEYFKNC	206

RESULT 2  
S43467

nef protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 20-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
C:Accession: S43467  
Eur. J. Biochem. 221, 811-819, 1994.  
R:Freund, J.; Kellner, R.; Houthaeve, T.; Kalbitzer, H.R.  
A:Title: Stability and proteolytic domains of Nef protein from human immunodeficiency virus type 1  
A:Reference number: S43467; MUID:94229079  
A:Accession: S43467  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-205 <PRE>  
C:Superfamily: AIDS nef protein

Query Match 49.2%; Score 1115; DB 2; Length 205;  
Best Local Similarity 99.0%; Pred. No. 3.2e-79;  
Matches 203; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 113 GKKWSKSSVVGWPTVRRMRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEAQ 172

Db 1 GKKWSKSSVVGWPAVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEAQ 60

Qy 173 EEEVGGFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLHSQRQDILDLDWIYHTOGYF 232

Db 61 EEEVGGFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLHSQRQDILDLDWIYHTOGYF 120

Qy 233 PDWQNTYTPGCVRYPLTFGWCYKLVPEPDKVEEANKGENTSLLRHPSVSLHGMDPDERVL 292

Db 121 PDWQNTYTPGCVRYPLTFGWCYKLVPEPDKVEEANKGENTSLLRHPSVSLHGMDPDERVL 180

Qy 293 EWRFDLSRLAFHHVARELHPEYFKNC 317

Db 181 EWRFDLSRLAFHHVARELHPEYFKNC 205

RESULT 3  
S03244

nef protein (clone HXB2) - human immunodeficiency virus type 1  
N:Alternate names: 3'-orf protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 30-Sep-1993  
C:Accession: S03244  
R:Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettawa  
Nucleic Acids Res. 13, 8219-8229, 1985  
A:Title: Polymorphism of the 3' open reading frame of the virus associated with the acqu  
A:Reference number: S03244; MUID:86067228  
A:Accession: S03244  
A:Molecule type: DNA  
A:Residues: 1-206 <RAT>  
A:Cross-references: EMBL:X03187  
A:Note: the in-frame stop codon at residue 124, shown as 'X', may be suppressed  
C:Genetics:  
A:Gene: nef; 3'-orf; Orf-F  
C:Superfamily: AIDS nef protein

Query Match 49.2%; Score 1115; DB 2; Length 206;  
Best Local Similarity 98.5%; Pred. No. 3.3e-79;  
Matches 203; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRRMRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 171

Db 1 MGGKWSKSSVIGWPAVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60

Qy 172 QEEVGGFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLHSQRQDILDLDWIYHTOGY 231

Db 61 QEEVGGFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLHSQRQDILDLDWIYHTOGY 120

Qy 232 FPDWQNTYTPGCVRYPLTFGWCYKLVPEPDKVEEANKGENTSLLRHPSVSLHGMDPDERV 291

Db 121 FPDWQNTYTPGCVRYPLTFGWCYKLVPEPDKVEEANKGENTSLLRHPSVSLHGMDPDERV 180

Db 121 FPDQNTYTPGCVRYPLTFGWCYKLVPEPDKVEEANKGENTSLLRHPSVSLHGMDPDERV 180

Qy 292 LEWRFDLSRLAFHHVARELHPEYFKNC 317

Db 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206

RESULT 4  
ASLJVL

nef protein - human immunodeficiency virus type 1 (isolate LV)  
N:Alternate names: 3'-orf protein; Orf-F protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A04007  
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.;  
Nature 313, 450-458, 1985  
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy reti  
A:Reference number: A93355; MUID:85111157  
A:Accession: A04007  
A:Molecule type: DNA  
A:Residues: 1-206 <MUE>  
A:Cross-references: GB:K02083; NID:9555008; PIDN:AAB59874.1; PID:g328560  
C:Genetics:  
A:Gene: nef; 3'-orf; Orf-F  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; immunodeficiency

Query Match 49.2%; Score 1114; DB 1; Length 206;  
Best Local Similarity 97.6%; Pred. No. 3.9e-79;  
Matches 201; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRRMRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 171

Db 1 MGGKWSKSSVIGWPAVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60

Qy 172 QEEVGGFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLHSQRQDILDLDWIYHTOGY 231

Db 61 QEEVGGFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLHSQRQDILDLDWIYHTOGY 120

Qy 232 FPDWQNTYTPGCVRYPLTFGWCYKLVPEPDKVEEANKGENTSLLRHPSVSLHGMDPDERV 291

Db 121 FPDWQNTYTPGCVRYPLTFGWCYKLVPEPDKVEEANKGENTSLLRHPSVSLHGMDPDERV 180

Qy 292 LEWRFDLSRLAFHHVARELHPEYFKNC 317

Db 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206

RESULT 5  
ASLJL2

nef protein - human immunodeficiency virus type 1 (isolate HTLV-III, 12)  
N:Alternate names: 3'-orf protein; Orf-F protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 04-Dec-1986 #sequence\_revision 31-Dec-1991 #text\_change 16-Jul-1999  
C:Accession: A04006  
R:Arya, S.K.; Gallo, R.C.  
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986  
A:Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity  
A:Reference number: A94093; MUID:86177573  
A:Accession: A04006  
A:Molecule type: DNA  
A:Residues: 1-206 <ARY>  
A:Cross-references: EMBL:M11840; NID:g328453; PIDN:AAK45001.1; PID:g328458  
C:Genetics:  
A:Gene: nef; 3'-orf; Orf-F  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; immunodeficiency

Query Match 48.9%; Score 1108; DB 1; Length 206;  
Best Local Similarity 97.1%; Pred. No. 1.1e-78;

Matches 200; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGGLIHSQRRQDILDLWIYHTQGY 171  
 Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGGLIHSQRRQDILDLWIYHTQGY 60

Qy 172 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLIHSQRRQDILDLWIYHTQGY 231  
 Db 61 QEEKVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLIHSQRRQDILDLWIYHTQGY 120

Qy 232 FPDQNYTPGCGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 291  
 Db 121 FPDQNYTPGCGIRYPLTFGWCYKLVPEPEKLEEANKGENTSLHHPVSLHGMDDPEREV 180

Qy 292 LEWRDLSRLAFHHVARELHPEYFKNC 317  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

RESULT 6  
 JC5400  
 nef protein - Human immunodeficiency virus type 1, HIV-1  
 C:Species: Human immunodeficiency virus type 1, HIV-1  
 C:Date: 07-Jul-1997 #sequence\_revision 18-Jul-1997 #text\_change 31-Oct-1997  
 C:Accession: JC5400  
 R:Macreadie, I.G.; Love, M.G.; Curtain, C.C.; Hewish, D.; Azad, A.A.  
 Biochem. Biophys. Res. Commun. 232, 707-711, 1997  
 A:Title: Cytotoxicity resulting from addition of HIV-1 Nef N-terminal peptides to yeast  
 A:Reference number: JC5400; MUID:97271389  
 A:Accession: JC5400  
 A:Molecule type: protein  
 A:Residues: 1-206 <MAC>  
 C:Comment: The amino-terminal part possesses membrane-perturbing and fusogenic activities.  
 C:Superfamily: AIDS nef protein  
 F:2-206/Product: nef protein #status predicted <MAT>

Query Match 48.5%; Score 1097; DB 2; Length 206;  
 Best Local Similarity 97.1%; Pred. No. 8.1e-78;  
 Matches 200; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGGLIHSQRRQDILDLWIYHTQGY 171  
 Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGGLIHSQRRQDILDLWIYHTQGY 60

Qy 172 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLIHSQRRQDILDLWIYHTQGY 231  
 Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLIHSQRRQDILDLWIYHTQGY 120

Qy 232 FPDQNYTPGCGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 291  
 Db 121 FPDQNYTPGCGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 180

Qy 292 LEWRDLSRLAFHHVARELHPEYFKNC 317  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

RESULT 7  
 S03245  
 nef protein (clone HXB3) - human immunodeficiency virus type 1  
 N:Alternate names: 3'-orf protein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 20-Sep-1999  
 C:Accession: S03245  
 R:Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettawa  
 Nucleic Acids Res. 13, 8219-8229, 1985  
 A:Title: Polymorphism of the 3' open reading frame of the virus associated with the acqu  
 A:Reference number: S03244; MUID:86067228  
 A:Accession: S03245  
 A:Molecule type: DNA  
 A:Residues: 1-206 <RAT>

A:Cross-references: EMBL:X03188; NID:g61556; PIDN:CAA26947.1; PID:g61557  
 C:Genetics:  
 A:Gene: nef; 3'-orf; Orf-F  
 C:Superfamily: AIDS nef protein

Query Match 48.4%; Score 1096; DB 2; Length 206;  
 Best Local Similarity 96.6%; Pred. No. 9.7e-78;  
 Matches 199; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGGLIHSQRRQDILDLWIYHTQGY 171  
 Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGGLIHSQRRQDILDLWIYHTQGY 60

Qy 172 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLIHSQRRQDILDLWIYHTQGY 231  
 Db 61 QEEKVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLIHSQRRQDILDLWIYHTQGY 120

Qy 232 FPDQNYTPGCGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 291  
 Db 121 FPDQNYTPGCGIRYPLTFGWCYKLVPEPEKLEEANKGENTSLHHPVSLHGMDDPEREV 180

Qy 292 LEWRDLSRLAFHHVARELHPEYFKNC 317  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

RESULT 8  
 S33986  
 nef protein - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Sep-1999  
 C:Accession: S33986  
 R:Carlini, F.  
 submitted to the EMBL Data Library, November 1991  
 A:Reference number: S33979  
 A:Accession: S33986  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-206 <CAR>  
 A:Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77629.1; PID:g60200  
 C:Superfamily: AIDS nef protein

Query Match 48.4%; Score 1096; DB 2; Length 206;  
 Best Local Similarity 96.6%; Pred. No. 9.7e-78;  
 Matches 199; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGGLIHSQRRQDILDLWIYHTQGY 171  
 Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGGLIHSQRRQDILDLWIYHTQGY 60

Qy 172 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLIHSQRRQDILDLWIYHTQGY 231  
 Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLIHSQRRQDILDLWIYHTQGY 120

Qy 232 FPDQNYTPGCGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 291  
 Db 121 FPDQNYTPGCGIRYPLTFGWCYKLVPEPEKLEEANKGENTSLHHPVSLHGMDDPEREV 180

Qy 292 LEWRDLSRLAFHHVARELHPEYFKNC 317  
 Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

RESULT 9  
 ASLJH3  
 nef protein - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)  
 N:Alternate names: 3'-orf protein; orf-F protein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 31-Jan-1997  
 C:Accession: A04005

R: Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doria-Rivera, J.A.; Papas, T.S.; Grayer, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.; Nature 313, 277-284, 1985

A: Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.

C: Reference number: A93353; MUID: 85111123

A: Accession: A04005

A: Molecule type: DNA

A: Residues: 1-205 <RAT>

C: Genetics:

A: Gene: nef; 3'-orf; orf-F

C: Superfamily: AIDS nef protein

C: Keywords: AIDS; immunodeficiency

Query Match 47.8%; Score 1081.5; DB 1; Length 205;  
Best Local Similarity 96.1%; Pred. No. 1.3e-76;  
Matches 198; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

Qy 112 MGGKWSKSSVVGWPTVRRMRRAEPAADGCGAASRDLEKKGAISSNTAATNAACAWLEA 171

Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGCGAASRDLEKKGAISSNTAANACAWLEA 60

Qy 172 QEEVEGVFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLHSORRQDILDWYHTQGY 231

Db 61 QEEVEGVFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLHSORRQDILDWYHTQGY 120

Qy 232 FPDQNTPGGVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDDPREV 291

Db 121 FPD-QNTPGGVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDDPREV 179

Qy 292 LEWRDLSRLAFHHVARELHPEYFKNC 317

Db 180 LEWRDLSRLAFHHVARELHPEYFKNC 205

#### RESULT 10

S24985

nef protein - human immunodeficiency virus type 1

C: Species: human immunodeficiency virus type 1, HIV-1

C: Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Sep-1999

C: Accession: S24985

R: Harris, M.; Hislop, S.; Patsillinos, P.; Neil, J.C.

A: Description: In vivo derived HIV-1 NEF genes are heterogeneous and lack detectable nuc

A: Reference number: S24985

A: Accession: S24985

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-204 <HAR>

A: Cross-references: EMBL:X63044; NID:G60123; PIDN:CAA44770.1; PID:G60124

C: Superfamily: AIDS nef protein

Query Match 45.0%; Score 1019; DB 2; Length 204;  
Best Local Similarity 89.8%; Pred. No. 9.1e-72;  
Matches 185; Conservative 10; Mismatches 9; Indels 2; Gaps 1;

Qy 112 MGGKWSKSSVVGWPTVRRMRRAEPAADGCGAASRDLEKKGAISSNTAATNAACAWLEA 171

Db 1 MGGKWSK--LGGWPTVRRMRRAEPAADGCGAASRDLEKKGAISSNTAATNAACAWLEA 58

Qy 172 QEEVEGVFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLHSORRQDILDWYHTQGY 231

Db 59 QEEVEGVFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLHSORRQDILDWYHTQGY 118

Qy 232 FPDQNTPGGVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDDPREV 291

Db 119 FPDQNTPGGVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDDPREV 178

Qy 292 LEWRDLSRLAFHHVARELHPEYFKNC 317

Db 179 LEWRDLSRLAFHHVARELHPEYFKNC 204

#### RESULT 11

ASLJBR

nef protein - human immunodeficiency virus type 1 (isolate BR)

N: Alternate names: 3'-orf protein; orf-F protein

C: Species: human immunodeficiency virus type 1, HIV-1

A: Note: host Homo sapiens (man)

C: Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 16-Jul-1999

C: Accession: D31667; S21993; S21995; S21997; S21999; S21991

R: Anand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar

Virolgy 168, 79-89, 1989

A: Title: Biological and molecular characterization of human immunodeficiency virus (I

A: Reference number: A94389; MUID: 89085613

A: Accession: D31667

A: Molecule type: DNA

A: Residues: 1-218 <ANA>

A: Cross-references: GB:M21098; NID:G326426; PIDN:AAA44222.1; PID:G326431

R: Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A: Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as det

A: Reference number: S21990

A: Accession: S21993

A: Molecule type: DNA

A: Residues: 1-7 <STE>

A: Cross-references: EMBL:X61358; NID:G60177; PIDN:CAA43629.1; PID:G584027; EMBL:X613

A: Accession: S21995

A: Molecule type: DNA

A: Residues: 1-7 <ST2>

A: Cross-references: EMBL:X61355; NID:G60179; PIDN:CAA43623.1; PID:G584028; EMBL:X613

A: Accession: S21997

A: Molecule type: DNA

A: Residues: 1-7 <ST3>

A: Cross-references: EMBL:X61356; NID:G60181; PIDN:CAA43625.1; PID:G1129140; EMBL:X61

A: Accession: S21999

A: Molecule type: DNA

A: Residues: 1-7 <ST4>

A: Cross-references: EMBL:X61359; NID:G60182; PIDN:CAA43631.1; PID:G584030

C: Genetics:

A: Gene: nef; 3'-orf; orf-F

C: Superfamily: AIDS nef protein

C: Keywords: AIDS; immunodeficiency

Query Match 45.0%; Score 1019; DB 1; Length 218;

Best Local Similarity 84.1%; Pred. No. 9.9e-72;

Matches 185; Conservative 12; Mismatches 7; Indels 16; Gaps 2;

Qy 112 MGGKWSKSSVVGWPTVRRMR-----RAEPAADGCGAASRDLEKKGAISS 157

Db 1 MGGKWSK--MAGWSTVRRMRRAEPAEPAADGCGAASRDLEKKGAISS 58

Qy 158 NTAATNAACAWLEAQEEVEGVFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLHSORR 217

Db 59 NTAATNADCAWLEAQEEVEGVFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLHSORR 118

Qy 218 QDILDWYHTQGYPPDQNTPGGVRYPLTFGCYKLVPEPKVEANKGENTSLH 277

Db 119 QDILDWYHTQGYPPDQNTPGGVRYPLTFGCYKLVPEPKVEANKGENTSLH 178

Qy 278 PVSLSHGMDPREVLEWRDLSRLAFHHVARELHPEYFKNC 317

Db 179 PMSQHGMDPREVLEWRDLSRLAFHHVARELHPEYFKNC 218

#### RESULT 12

S25937

nef protein - human immunodeficiency virus type 1

C: Species: human immunodeficiency virus type 1, HIV-1

C: Date: 25-Feb-1994 #sequence\_revision 01-Dec-1995 #text\_change 20-Sep-1999

C: Accession: S25937

R: Guo, H.G.; Chermann, J.C.; Waters, D.; Hall, L.; Louie, A.; Gallo, R.C.; Streicher

Nature 349, 745-746, 1991

A: Title: Sequence analysis of original HIV-1.

A:Reference number: S25937; MUID:91156044  
A:Accession: S25937  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: nucleic acid  
A:Residues: 1-206 <GU>  
A:Cross-references: EMBL:X57465; NID:g60217; PIDN:CRAA0702.1; PID:g60218  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1991  
C:Superfamily: AIDS nef protein

Query Match 44.5%; Score 1007; DB 2; Length 206;  
Best Local Similarity 85.9%; Pred. No. 7.9e-71;  
Matches 177; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

QY 112 MGKSKSSVGVGPTVRRMRRAEPAADGGAASRDLEKKGALTSSTNTAATNAACAWLEA 171  
Db 1 MGKSKSSVGVGPTVRRMRRAEPAADGGAASRDLEKKGALTSSTNTAATNAACAWLEA 60

QY 172 QEEEEVGFVTPQVPLRPMYTKAAVDLSHFLKKEGGLIHSQRQDILDLMWYHTQGY 231  
Db 61 QEEKVGFPVTPQVPLRPMYTKGALDLSHFLKKGGLIYSQKQDILDLMWYHTQGY 120

QY 232 FPDQWNTPGGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 291  
Db 121 FPDQWNTPGGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180

QY 292 LEWRFDRLAFHVAHRELHPEYFKNC 317  
Db 181 LEWRFDRLAFHVAHRELHPEYFKNC 206

RESULT 13  
ASLJ02  
nef protein - human immunodeficiency virus type 1 (isolate ARV-2)  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C>Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A04009  
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempfen, M.M.; Brown-SH  
Science 227, 484-492, 1985  
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
A:Reference number: A04003; MUID:85090453  
A:Accession: A04009  
A:Molecule type: DNA  
A:Residues: 1-210 <S>  
A:Cross-references: GB:K02007; NID:g328658; PIDN:AAB59883.1; PID:g328667  
C:Genetics:  
A:Gene: nef; 3'-orf; orf-F  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; immunodeficiency

Query Match 44.0%; Score 997; DB 1; Length 210;  
Best Local Similarity 85.2%; Pred. No. 4.8e-70;  
Matches 179; Conservative 16; Mismatches 11; Indels 4; Gaps 1;

QY 112 MGKSKSSVGVGPTVRRMR-----RAEPAADGGAASRDLEKKGALTSSTNTAATNAACA 167  
Db 1 MGKSKSSVGVGPTVRRMRRAEPAADGGAASRDLEKKGALTSSTNTAATNAACA 60

QY 168 WLEAQEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKKEGGLIHSQRQDILDLMWYH 227  
Db 61 WLEAQEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKKEGGLIHSQRQDILDLMWYH 120

QY 228 TQGYFPDQWNTPGGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDP 287  
Db 121 TQGYFPDQWNTPGGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDP 180

QY 288 EREVLWRFDRLAFHVAHRELHPEYFKNC 317  
Db 181 EREVLWRFDRLAFHVAHRELHPEYFKNC 210

RESULT 14  
I44001  
nef protein - human immunodeficiency virus type 1 (strain YU-2)  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 23-Feb-1997  
C:Accession: I44001  
R:Li, Y.; Hul, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.  
J. Virol. 66, 6587-6600, 1992  
A:Title: Complete nucleotide sequence, genome organization, and biological properties  
A:Reference number: A44001; MUID:93021387  
A:Accession: I44001  
A:Molecule type: DNA  
A:Residues: 1-214 <LIY>  
A:Cross-references: GB:M93258  
C:Genetics:  
A:Gene: nef; 3'-orf; orf-F  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; immunodeficiency

Query Match 43.8%; Score 991.5; DB 1; Length 214;  
Best Local Similarity 84.2%; Pred. No. 1.3e-69;  
Matches 181; Conservative 12; Mismatches 11; Indels 11; Gaps 2;

QY 112 MGKSKSSVGVGPTVTR-----ERMRAEPAADGGAASRDLEKKGALTSSTNTAA 161  
Db 1 MGKSKSSVGVGPTVTRERMRAEPAADGGAASRDLEKKGALTSSTNTAA 60

QY 162 TNACAWLEAQEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKKEGGLIHSQRQDIL 221  
Db 61 TNACAWLEAQEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKKEGGLIHSQRQDIL 120

QY 222 DLWYHTQGYFPDQWNTPGGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSL 281  
Db 121 DLWYHTQGYFPDQWNTPG-GTRWPLTFGWCYKLVPEPKVEEANKGENTSLHPVSL 179

QY 282 HGMDDPEREVLWRFDRLAFHVAHRELHPEYFKN 316  
Db 180 HGMDDPEREVLWRFDRLAFHVAHRELHPEYFKN 214

RESULT 15  
S03247  
nef protein (clone C15) - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: 3'-orf protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 20-Jun-2000  
C:Accession: S03247  
R:Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pett  
Nucleic Acids Res. 13, 8219-8229, 1985  
A:Title: Polymorphism of the 3' open reading frame of the virus associated with the a  
A:Reference number: S03244; MUID:86067228  
A:Accession: S03247  
A:Molecule type: mRNA  
A:Residues: 1-182 <RAT>  
A:Cross-references: EMBL:X03189; NID:g61552; PIDN:CAA26948.1; PID:g1335562  
C:Genetics:  
A:Gene: nef; 3'-orf; orf-F  
C:Superfamily: AIDS nef protein

Query Match 43.6%; Score 987; DB 2; Length 182;  
Best Local Similarity 98.4%; Pred. No. 2.4e-69;  
Matches 179; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 136 PAADGGAASRDLEKKGALTSSTNTAATNAACAWLEAQEEVEGFPVTPQVPLRPMYTKAA 195  
Db 1 PAADGGAASRDLEKKGALTSSTNTAATNAACAWLEAQEEVEGFPVTPQVPLRPMYTKAA 60

QY 196 VDLSHFLKKEGGLIHSQRQDILDLMWYHTQGYFPDQWNTPGGVRYPLTFGWCYK 255

|||||  
Db 61 VDSLFLKEKGLGLHSQRQDLDLWYHTGYFPDMQNYTPGCVRIPLTFGWCYK 120  
QY 256 LVPVEPKVEANKGENTSLLRHPSVLSHGMDPEREVLEWFRDSRLAFHHVARELHPYFK 315  
|||||  
Db 121 LVPVEPKVEANKGENTSLLRHPSVLSHGMDPEREVLEWFRDSRLAFHHVARELHPYFK 180  
QY 316 NC 317  
||  
Db 181 NC 182

RESULT 16  
S03246  
nef protein (clone HAT3) - human immunodeficiency virus type 1  
N:Alternate names: 3'-orf protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 20-Sep-1999  
A:Title: Polymorphism of the 3' open reading frame of the virus associated with the acquisition of AIDS  
R:Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Petteway  
Nucleic Acids Res. 13, 8219-8229, 1985  
A:Reference number: S03244; MUID:86067228  
A:Accession: S03246  
A:Molecule type: DNA  
A:Residues: 1-204 <RAT>  
A:Cross-references: EMBL:X03190; NID:g61550; PIDN:CAA26949.1; PID:g61551  
A:Note: the authors translated the codon AGT for residue 11 as Gly  
C:Genetics:  
A:Gene: nef; 3'-orf; orf-F  
C:Superfamily: AIDS nef protein

Query Match 43.6%; Score 987; DB 2; Length 204;  
Best Local Similarity 84.5%; Pred. No. 2.8e-69;  
Matches 174; Conservative 16; Mismatches 14; Indels 2; Gaps 1;  
QY 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGALTSNTAATNAACAWLEA 171  
|||  
Db 1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGALTSNTAATNAACAWLEA 58  
QY 172 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDLDLWYHTGY 231  
|||  
Db 59 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDLDLWYHTGY 118  
QY 232 FPDQNYTPGCVRIPLTFGWCYKLVPEPKVEANKGENTSLLRHPSVLSHGMDPEREV 291  
|||  
Db 119 FPDQNYTPGCVRIPLTFGWCYKLVPEPKVEANKGENTSLLRHPSVLSHGMDPEREV 178  
QY 292 LEWFRDSRLAFHHVARELHPYFKNC 317  
|||  
Db 179 LVWKFDLSRLAFHHVARELHPYFKNC 204

RESULT 17  
Q0LJ2R  
nef protein - human immunodeficiency virus 2r-6  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: human immunodeficiency virus 2r-6  
C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999  
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotide sequence of the 3' open reading frame  
R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu  
Gene 52, 71-82, 1987  
A:Reference number: A36192; MUID:87248097  
A:Accession: F26192  
A:Molecule type: DNA  
A:Residues: 1-212 <SRI>  
A:Cross-references: GB:K03458; GB:M16322; NID:g29398; PIDN:AAA45381.1; PID:g29404  
C:Genetics:  
A:Gene: nef; 3'-orf; orf-F  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; immunodeficiency

Query Match 40.2%; Score 911; DB 1; Length 212;  
Best Local Similarity 77.4%; Pred. No. 2.3e-63;  
Matches 164; Conservative 23; Mismatches 19; Indels 6; Gaps 2;

QY 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGALTSNTAATNAAC 166  
|||  
Db 1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGALTSNTAATNAAC 60  
QY 167 AWLEAQEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDLDLWY 225  
|||  
Db 61 AWLEAQEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDLDLWY 120  
QY 226 YHTGYFPDMQNYTPGCVRIPLTFGWCYKLVPEPKVEANKGENTSLLRHPSVLSHGMD 285  
|||  
Db 121 YHTGYFPDMQNYTPGCVRIPLTFGWCYKLVPEPKVEANKGENTSLLRHPSVLSHGMD 180  
QY 286 DPEREVLEWFRDSRLAFHHVARELHPYFKNC 317  
|||  
Db 181 DPEREVLEWFRDSRLAFHHVARELHPYFKNC 212

RESULT 18  
Q0LJND  
nef protein - human immunodeficiency virus type 1 (isolate NDK)  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999  
A:Accession: J00068  
R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe,  
Gene 81, 275-284, 1989  
A:Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human im  
A:Reference number: J00065; MUID:90034200  
A:Accession: J00068  
A:Molecule type: DNA  
A:Residues: 1-207 <SRI>  
A:Cross-references: GB:M27323; NID:g328154; PIDN:AAA44874.1; PID:g328163  
C:Genetics:  
A:Gene: nef  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; immunodeficiency

Query Match 39.9%; Score 903.5; DB 1; Length 207;  
Best Local Similarity 77.3%; Pred. No. 8.6e-63;  
Matches 160; Conservative 25; Mismatches 21; Indels 1; Gaps 1;  
QY 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGALTSNTAATNAACAWLEA 171  
|||  
Db 1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGALTSNTAATNAACAWLEA 60  
QY 172 QEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDLDLWYHTGY 230  
|||  
Db 61 QEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLHSQRQDLDLWYHTGY 120  
QY 231 YFPDMQNYTPGCVRIPLTFGWCYKLVPEPKVEANKGENTSLLRHPSVLSHGMDPERE 290  
|||  
Db 121 YFPDMQNYTPGCVRIPLTFGWCYKLVPEPKVEANKGENTSLLRHPSVLSHGMDPERE 180  
QY 291 VLEWFRDSRLAFHHVARELHPYFKNC 317  
|||  
Db 181 VLEWFRDSRLAFHHVARELHPYFKNC 207

RESULT 19  
B44903  
nef protein - human immunodeficiency virus type 1 (isolate 2321)  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 28-May-1999

C:Accession: B44963  
R:Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J.  
AIDS Res. Hum. Retroviruses 5, 121-129, 1989  
A:Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nu  
A:Reference number: A44963; MUID:89228766  
A:Accession: B44963  
A:Molecule type: DNA  
A:Residues: 1-205 <SRI>  
A:Cross-references: GB:M15896; NID:g329392; PIDN:AAB53951.1; PID:g329397  
C:Genetics:  
A:Gene: nef; 3'-orf; orf-F  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; Immunodeficiency

Query Match 37.0%; Score 837; DB 1; Length 205;  
Best Local Similarity 73.2%; Pred. No. 1.2e-57;  
Matches 153; Conservative 23; Mismatches 25; Indels 8; Gaps 3;

QY 112 MGGKWSKSSVVGWPTVRMR---AEPADGVGAASRDLEKHGAISSNTAATNAACAW 168  
DB 1 MGNKSK-----GWPVREIRQTPTPAPPAEAGVGAASQDLAKHGAISSNTATNPDCAW 56

QY 169 LEAQEE-EVGFPPVTPQVPLRPMYKAAVDLSHFLKEKGLGLIHSORRQDILDWYH 227  
DB 57 LEAQEESEVGFPPVTPQVPLRPMYKAAVDLSHFLKEKGLGLIYSKKRQDILDWYH 116

QY 228 TQGYFPDQWNTPGVVRPLTFGCWYKLVPEPDKVEANKGENTSLLHPVSLHGMDP 287  
DB 117 TQGYFPDQWNTPGVVRPLTFGCWYKLVPEPDKVEANKGENTSLLHPVSLHGMDP 287

QY 288 EREVLEWFRDLSRALFHVARELHPEYFKN 316  
DB 177 EREVLEWFRDLSRALFHVARELHPEYFKN 205

RESULT 20  
T01673  
nef protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 21-Jul-2000  
C:Accession: T01673  
R:Alizon, M.; Main-Hobson, S.; Gluckman, J.C.; Sonigo, P.  
Cell 46, 63-74, 1986  
A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol  
A:Reference number: Z14389; MUID:86245056  
A:Accession: T01673  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-209 <ALI>  
A:Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28017.1; PID:g60235  
C:Superfamily: AIDS nef protein

Query Match 36.9%; Score 834.5; DB 2; Length 209;  
Best Local Similarity 70.1%; Pred. No. 2e-57;  
Matches 148; Conservative 26; Mismatches 30; Indels 7; Gaps 2;

QY 112 MGGKWSKSSVVGWPTVRMRRAEPADGVG-----AASRDLEKHGAISSNTAATNAAC 166  
DB 1 MGGKWSKSSVVGWPKIRIRIRTPPTETGVGAVSQDLDKCGAAASSSSPAANNASC 60

QY 167 AWLEAOEEVGFPPVTPQVPLRPMYKAAVDLSHFLKEKGLGLIHSORRQDILDWY 226  
DB 61 E--PPEEVEVGFPPVTPQVPLRPMYKAAVDLSHFLKEKGLGLIHSORRQDILDWY 118

QY 227 HTQGYFPDQWNTPGVVRPLTFGCWYKLVPEPDKVEANKGENTSLLHPVSLHGMD 286  
DB 119 HTQGYFPDQWNTPGVVRPLTFGCWYKLVPEPDKVEANKGENTSLLHPVSLHGMD 178

QY 287 PEREVLEWFRDLSRALFHVARELHPEYFKN 317  
DB 179 AEREVLKWKFDSSALRHRAHQHPEYFKN 209

RESULT 21  
ASLJK  
nef protein - simian immunodeficiency virus SIVcpz  
N:Alternate names: 3'-orf protein; orf-F protein  
C:Species: simian immunodeficiency virus SIVcpz  
A:Note: host Pan troglodytes (chimpanzee)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999  
C:Accession: S09991  
R:Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.  
Nature 345, 356-359, 1990  
A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.  
A:Reference number: S09983; MUID:90259077  
A:Accession: S09991  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-205 <HUE>  
A:Cross-references: EMBL:X52154; NID:g58866; PIDN:CAA36408.1; PID:g58877  
C:Genetics:  
A:Gene: nef  
C:Superfamily: AIDS nef protein  
C:Keywords: AIDS; Immunodeficiency

Query Match 36.7%; Score 832; DB 1; Length 205;  
Best Local Similarity 70.2%; Pred. No. 3e-57;  
Matches 144; Conservative 27; Mismatches 34; Indels 0; Gaps 0;

QY 112 MGGKWSKSSVVGWPTVRMRRAEPADGVGAASRDLEKHGAISSNTAATNAACAWLEA 171  
DB 1 MGTKWSKSLVGVPEVRRIRREAPTAAGVGEVSKOLERHGAITSRTPTNQTALWEE 60

QY 172 QEEVEVGFPPVTPQVPLRPMYKAAVDLSHFLKEKGLGLIHSORRQDILDWYHTQGY 231  
DB 61 MDNEEVGFPPVTPQVPLRPMYKAAVDLSHFLKEKGLGLIHSORRQDILDWYHTQGY 120

QY 232 FPDQWNTPGVVRPLTFGCWYKLVPEPDKVEANKGENTSLLHPVSLHGMDPEREV 291  
DB 121 FPDQWNTPGVVRPLTFGCWYKLVPEPDKVEANKGENTSLLHPVSLHGMDPEREV 180

QY 292 LEWRFDSRLAHLHRAHQHPEYFKN 316  
DB 181 LEWRFDSRLAHLHRAHQHPEYFKN 205

RESULT 22  
S59931  
glycerophosphodiester phosphodiesterase (EC 3.1.1.4.46) - Haemophilus influenzae (strai  
N:Alternate names: Igd-binding protein; protein D  
C:Species: Haemophilus influenzae  
A:Variety: strain 3639  
C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999  
C:Accession: S59931; S47333  
R:Song, X.M.; Forsgren, A.; Jansson, H.  
Infect. Immun. 63, 696-699, 1995  
A:Title: The gene encoding protein D (hpd) is highly conserved among Haemophilus Infl  
A:Reference number: S59931; MUID:95122210  
A:Accession: S59931  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-364 <SON>  
A:Cross-references: EMBL:Z35656; NID:g525213; PIDN:CAA84715.1; PID:g525214  
A:Experimental source: strain 3639  
C:Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen

Query Match 25.2%; Score 569.5; DB 2; Length 364;  
Best Local Similarity 46.9%; Pred. No. 1.4e-36;  
Matches 144; Conservative 19; Mismatches 71; Indels 73; Gaps 11;

QY 4 SSHSSNNANTQMSDKIIIAHRCAGSYLPHTLESKALFAQQAQDYLEQDLAMTKDGLV 63  
|||||





F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-364/Product: protein D #status predicted <MAT>

Query Match 25.2%; Score 569.5; DB 2: Length 364;  
Best Local Similarity 46.9%; Pred. No. 1.4e-36;  
Matches 144; Conservative 19; Mismatches 71; Indels 73; Gaps 11;

QY 4 SSHSSNNANTOMKSKIIIAHAGASYLPPEHTLESKALAFQAQADYLEODLMTKDGRLV 63  
DB 20 SSHSSNNANTOMKSKIIIAHAGASYLPPEHTLESKALAFQAQADYLEODLMTKDGRLV 79  
QY 64 VIHDFLDGLTDVAKKFPFHRKDGYYVIDFTLKEIQSLEMTENFETMGKK----- 115  
DB 80 VIHDFLDGLTDVAKKFPFHRKDGYYVIDFTLKEIQSLEMTENFETMGKKQAQVYVNR 139  
QY 116 -----W-----SKSSVVG-WPTVVRMRRAEPAADGVGAASRDLEK 150  
DB 140 FPLWQSHFRHTFDEIEFIQGLEKSTGRKGVYPEIKAPWFHONGKDIAAETLKVKK 199  
QY 151 HGAITSNTAATNAACAWLEAEQEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLG 210  
DB 200 YGVYDKKTD-----MVLQTFDFNELKRIKTELLPQMGMDLK-LVQLIAYTDWK----- 246  
QY 211 LIHSORRQDILDLIYHTOGYFPDQW-----NYTPGQVRYPLTFGWCYKLPVPE 260  
DB 247 ---ETOEKDPKGVW----NINYDMWFKPGMAEVVYKADGVGP-----GW-YMLVNKE 292  
QY 261 ---PDKV 264  
DB 293 ESKPDNI 299

RESULT 26  
S59933  
glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenzae (strain 6  
N:Alternate names: immunoglobulin D-binding protein; protein D  
C:Species: Haemophilus influenzae  
A:Variety: strain 6-7626  
C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999  
C:Accession: S59933; S47335  
R:Song, X.M.; Forsgren, A.; Janson, H.  
Infect. Immun. 63, 696-699, 1995  
A:Title: The gene encoding protein D (hpd) is highly conserved among Haemophilus influen  
A:Reference number: S59931; MUID:95122210  
A:Accession: S59933  
A:Molecule type: DNA  
A:Residues: 1-364 <TIGR>  
A:Cross-references: EMBL:235658; NID:9525217; PIDN:CAA84717.1; PID:9525218  
A:Experimental source: strain 6-7626  
C:Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen

Query Match 24.9%; Score 563.5; DB 2: Length 364;  
Best Local Similarity 46.6%; Pred. No. 4.2e-36;  
Matches 143; Conservative 19; Mismatches 72; Indels 73; Gaps 11;

QY 4 SSHSSNNANTOMKSKIIIAHAGASYLPPEHTLESKALAFQAQADYLEODLMTKDGRLV 63  
DB 20 SSHSSNNANTOMKSKIIIAHAGASYLPPEHTLESKALAFQAQADYLEODLMTKDGRLV 79  
QY 64 VIHDFLDGLTDVAKKFPFHRKDGYYVIDFTLKEIQSLEMTENFETMGKK----- 115  
DB 80 VIHDFLDGLTDVAKKFPFHRKDGYYVIDFTLKEIQSLEMTENFETMGKKQAQVYVNR 139  
QY 116 -----W-----SKSSVVG-WPTVVRMRRAEPAADGVGAASRDLEK 150  
DB 140 FPLWQSHFRHTFDEIEFIQGLEKSTGRKGVYPEIKAPWFHONGKDIAAETLKVKK 199  
QY 151 HGAITSNTAATNAACAWLEAEQEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLG 210  
DB 200 YGVYDKKTD-----MVLQTFDFNELKRIKTELLPQMGMDLK-LVQLIAYTDWK----- 246

QY 211 LIHSORRQDILDLIYHTOGYFPDQW-----NYTPGQVRYPLTFGWCYKLPVPE 260  
DB 247 ---ETOEKDPKGVW----NINYDMWFKPGMAEVVYKADGVGP-----GW-YMLVNKE 292  
QY 261 ---PDKV 264  
DB 293 ESKPDNI 299

RESULT 27  
G64086  
glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenzae (strai  
N:Alternate names: Igp-binding protein; protein D  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 21-Jul-2000  
C:Accession: G64086  
R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: G64086  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-364 <TIGR>  
A:Cross-references: GB:U32751; GB:L42023; NID:g3312200; PIDN:AAC22348.1; PID:g1573690  
A:Experimental source: strain Rd KW20  
C:Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen

Query Match 24.4%; Score 553.5; DB 2: Length 364;  
Best Local Similarity 45.9%; Pred. No. 2.5e-35;  
Matches 141; Conservative 21; Mismatches 72; Indels 73; Gaps 11;

QY 4 SSHSSNNANTOMKSKIIIAHAGASYLPPEHTLESKALAFQAQADYLEODLMTKDGRLV 63  
DB 20 SSHSSNNANTOMKSKIIIAHAGASYLPPEHTLESKALAFQAQADYLEODLMTKDGRLV 79  
QY 64 VIHDFLDGLTDVAKKFPFHRKDGYYVIDFTLKEIQSLEMTENFETMGKK----- 115  
DB 80 VIHDFLDGLTDVAKKFPFHRKDGYYVIDFTLKEIQSLEMTENFETMGKKQAQVYVNR 139  
QY 116 -----W-----SKSSVVG-WPTVVRMRRAEPAADGVGAASRDLEK 150  
DB 140 FPLWQSHFRHTFDEIEFIQGLEKSTGRKGVYPEIKAPWFHONGKDIAAETLKVKK 199  
QY 151 HGAITSNTAATNAACAWLEAEQEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLG 210  
DB 200 YGVYDKKTD-----MVLQTFDFNELKRIKTELLPQMGMDLK-LVQLIAYTDWK----- 246  
QY 211 LIHSORRQDILDLIYHTOGYFPDQW-----NYTPGQVRYPLTFGWCYKLPVPE 260  
DB 247 ---ETOEKDPKGVW----NINYDMWFKPGMAEVVYKADGVGP-----GW-YMLVNKE 292  
QY 261 ---PDKV 264  
DB 293 ESKPDNI 299

RESULT 28  
S59936  
glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenzae (strai  
N:Alternate names: Igp-binding protein; protein D  
C:Species: Haemophilus influenzae  
A:Variety: strain NCTC 8468  
C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999  
C:Accession: S59936; S47338  
R:Song, X.M.; Forsgren, A.; Janson, H.  
Infect. Immun. 63, 696-699, 1995  
A:Title: The gene encoding protein D (hpd) is highly conserved among Haemophilus infl  
A:Reference number: S59931; MUID:95122210

2 EFVDFENEFNAHFUSQFPAIACINCICAKKCCFACQVCFIINATGTSIGRAKRRQRKRRPPQG 61

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2002, 08:10:40 ; Search time 38.46 Seconds  
(without-alignments)  
262.293 Million cell updates/sec

Title: US-09-509-239-21  
Perfect score: 2264  
Sequence: 1 MDPSSSSNWMANTQMSDKI.....QSRGDTGPKETSGHHHHH 413

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A-COMB.pap.\*  
2: /cgn2\_6/ptodata/2/1aa/5B-COMB.pap.\*  
3: /cgn2\_6/ptodata/2/1aa/6A-COMB.pap.\*  
4: /cgn2\_6/ptodata/2/1aa/6B-COMB.pap.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS-COMB.pap.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1138	50.3	239	4	US-08-679-493A-76
2	1115	49.2	239	4	US-08-388-353-644
3	1115	49.2	206	3	US-08-488-551B-644
4	971	42.9	206	4	US-08-679-493A-75
5	638	28.2	123	4	US-09-124-900-10
6	603.5	26.7	278	4	US-09-485-885-21
7	597	26.4	383	4	US-09-485-885-23
8	594	26.2	220	4	US-09-485-885-8
9	593	26.2	220	4	US-09-485-885-1
10	590	26.1	227	4	US-09-485-885-16
11	590	26.1	371	4	US-09-485-885-6
12	587	25.9	227	4	US-09-485-885-19
13	582	25.7	273	4	US-09-485-885-4
14	498.5	22.0	151	4	US-08-679-493A-74
15	486	21.5	86	1	US-08-450-237-1
16	486	21.5	86	1	US-08-450-246-1
17	486	21.5	86	1	US-08-450-098-1
18	486	21.5	86	1	US-08-451-233-1
19	486	21.5	86	1	US-08-450-236-1
20	486	21.5	86	3	US-07-808-452-1
21	486	21.5	86	3	US-09-030-613-19
22	486	21.5	86	4	US-09-124-900-6
23	486	21.5	86	4	US-09-451-905-19
24	486	21.5	86	4	US-08-235-403-1
25	486	21.5	86	5	PCT-US92-10770-1
26	486	21.5	86	5	PCT-US95-06077-2
27	478.5	21.1	266	3	US-08-815-809-5

28	478.5	21.1	280	2	US-08-816-155B-43	Sequence 43, Appl
29	478.5	21.1	280	4	US-09-079-587-43	Sequence 43, Appl
30	470	20.8	86	2	US-08-505-210-1	Sequence 1, Appl
31	470	20.8	86	4	US-09-099-333-1	Sequence 1, Appl
32	466	20.6	83	2	US-08-417-210A-96	Sequence 96, Appl
33	455	20.1	82	1	US-08-053-079A-15	Sequence 15, Appl
34	439	19.4	253	2	US-08-659-251-4	Sequence 4, Appl
35	439	19.4	253	4	US-09-256-490-4	Sequence 4, Appl
36	439	19.4	253	5	PCT-US96-11445-4	Sequence 4, Appl
37	409	18.1	72	3	US-09-030-613-17	Sequence 17, Appl
38	409	18.1	72	4	US-09-451-905-17	Sequence 17, Appl
39	385	17.0	72	2	US-08-893-853-1	Sequence 1, Appl
40	385	17.0	72	4	US-09-113-921-1	Sequence 1, Appl
41	372	16.4	122	6	5304466-3	Patent No. 5304466
42	365.5	16.1	312	1	US-08-094-128A-27	Sequence 27, Appl
43	365.5	16.1	312	1	US-08-455-674-27	Sequence 27, Appl
44	365.5	16.1	312	1	US-08-455-992-27	Sequence 27, Appl
45	365.5	16.1	312	1	US-08-455-972-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1  
US-08-679-493A-76  
; Sequence 76, Application US/08679493A  
; Patent No. 6303295  
; GENERAL INFORMATION:  
; APPLICANT: Taylor, Ethan W.  
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
; FILE REFERENCE: 55-95  
; CURRENT APPLICATION NUMBER: US/08/679,493A  
; CURRENT FILING DATE: 1996-07-12  
; PRIOR APPLICATION NUMBER: 60/001203  
; PRIOR FILING DATE: 1995-07-14  
; PRIOR APPLICATION NUMBER: 60/003,112  
; PRIOR FILING DATE: 1995-09-01  
; NUMBER OF SEQ ID NOS: 216  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 76  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)..(239)  
; OTHER INFORMATION: X os selenocysteine.  
US-08-679-493A-76

Query Match	50.3%	Score 1138;	DB 4;	Length 239;
Best Local Similarity	88.7%	Pred. No. 5e-107;		
Matches 211;	Conservative	2;	Mismatches 25;	Indels 0;
Gaps	0;			
QY	112	MGGKSKSVVWGPVTRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA	171	
DB	1	MGGKSKSVVWGPVTRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA	60	
QY	172	QEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKEKGLIHSORRQDILDWVHTQGY	231	
DB	61	QEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKEKGLIHSORRQDILDWVHTQGY	120	
QY	232	FPDWNQYTPGCVRYPLTFGWCYKLVVPDPKVEEANKGENTSLHPVSLHGMDDPEREV	291	
DB	121	FPDWNQYTPGCVRYPLTFGWCYKLVVPDPKVEEANKGENTSLHPVSLHGMDDPEREV	180	
QY	292	LEWRDSDRLAFHHVARELHPEYFKNCTSEPVDPRLPEWKHPGSPKTACTNCKYKCC	349	
DB	181	LEWRDSDRLAFHHVARELHPEYFKNCTSEPVDPRLPEWKHPGSPKTACTNCKYKCC	238	

RESULT 2  
US-08-388-353-644

; Sequence 644, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 644:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 206 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-388-353-644

Query Match 49.28; Score 1115; DB 3; Length 206;  
Best Local Similarity 98.18; Pred. No. 8.5e-105;  
Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGGLIHSORRQDILDIWIYHTQY 171  
Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGGLIHSORRQDILDIWIYHTQY 60  
Qy 172 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRQDILDIWIYHTQY 231  
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRQDILDIWIYHTQY 120  
Qy 232 FPDQNYTPGCVRYPLTFGCYKLVPEPKVVEANKGENTSLHPVSLHGMDDPEREV 291  
Db 121 FPDQNYTPGCVRYPLTFGCYKLVPEPKVVEANKGENTSLHPVSLHGMDDPEREV 180  
Qy 292 LEWRFDLSRLAFHHVARELHPEYFKNC 317  
Db 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206

RESULT 3  
US-08-488-551B-644  
; Sequence 644, Application US/08488551B  
; Patent No. 6015661  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Deacon  
; APPLICANT: Dale A. McPhee  
; APPLICANT: David Cooper

; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 841  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 GARDEN CITY PLAZA  
; CITY: GARDEN CITY  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 11530-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,551B  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PM3864 (AU)  
; FILING DATE: 14-FEB-1994  
; APPLICATION NUMBER: PM4002 (AU)  
; FILING DATE: 21-FEB-1994  
; APPLICATION NUMBER: PM0284 (AU)  
; FILING DATE: 23-DEC-1994  
; APPLICATION NUMBER: US 08/388,353  
; FILING DATE: 14-FEB-1995  
; APPLICATION NUMBER: PM3021/95  
; FILING DATE: 17-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FRANK S. DIGIGLIO  
; REFERENCE/DOCKET NUMBER: 96062  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; INFORMATION FOR SEQ ID NO: 644:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 206 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-488-551B-644

Query Match 49.28; Score 1115; DB 3; Length 206;  
Best Local Similarity 98.18; Pred. No. 8.5e-105;  
Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGGLIHSORRQDILDIWIYHTQY 171  
Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGGLIHSORRQDILDIWIYHTQY 60  
Qy 172 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRQDILDIWIYHTQY 231  
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRQDILDIWIYHTQY 120  
Qy 232 FPDQNYTPGCVRYPLTFGCYKLVPEPKVVEANKGENTSLHPVSLHGMDDPEREV 291  
Db 121 FPDQNYTPGCVRYPLTFGCYKLVPEPKVVEANKGENTSLHPVSLHGMDDPEREV 180  
Qy 292 LEWRFDLSRLAFHHVARELHPEYFKNC 317  
Db 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206

RESULT 4  
US-08-679-493A-75  
; Sequence 75, Application US/08679493A  
; Patent No. 6303295  
; GENERAL INFORMATION:  
; APPLICANT: Taylor, Ethan W.  
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
; FILE REFERENCE: 55-95

; CURRENT APPLICATION NUMBER: US/08/679,493A  
; CURRENT FILING DATE: 1996-07-12  
; PRIOR APPLICATION NUMBER: 60/001203  
; PRIOR FILING DATE: 1995-07-14  
; PRIOR APPLICATION NUMBER: 60/003,112  
; PRIOR FILING DATE: 1995-09-01  
; NUMBER OF SEQ ID NOS: 216  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 75  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; NAME/KEY: VARIANT  
; FEATURE:  
; LOCATION: (1)..(206)  
; OTHER INFORMATION: X is selenocysteine.  
US-08-679-493A-75

Query Match 42.9%; Score 971; DB 4; Length 206;  
Best Local Similarity 89.0%; Pred. No. 3e-90; Mismatches 15; Indels 6; Gaps 3;  
Matches 186; Conservative 2; Mismatches 15; Indels 6; Gaps 3;  
Qy 112 MGGKWSKSSVVGWPTVRRMRRAEPAADVGGAASRDLEKHGAITSNTAATNAACAWLEA 171  
Db 1 MGGKWSKSSVVGWPTVRRMRRAEPAADVGGAASRDLEKHGAITSNTAATNAACAWLEA 60  
Qy 172 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGG---LEGLIHSQRQDILDWIYHT 228  
Db 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKRGKGTGRANSLPTKTPYXSVDL--PHT 118  
Qy 229 QCYFDMQNYTPGQVRYPLTFGWCKYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPE 288  
Db 119 R-LLPDMQNYTPGQVRYPLTFGWCKYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPE 177  
Qy 289 REVLEWRDLSRLAFHFAHVAHELHPEYFKNC 317  
Db 178 REVLEWRDLSRLAFHFAHVAHELHPEYFKNC 206

RESULT 5  
US-09-124-900-10  
; Sequence 10, Application US/09124900  
; Patent No. 6268484  
; GENERAL INFORMATION:  
; APPLICANT: KATINGER, Hermann  
; APPLICANT: BUCHACHER, Andrea  
; APPLICANT: ERNST, Wolfgang  
; APPLICANT: BALLAUN, Claudia  
; APPLICANT: PURTSCHER, Martin  
; APPLICANT: TRKOLA, Alexandra  
; APPLICANT: FREDL, Renate  
; APPLICANT: SCHMATZ, Christine  
; APPLICANT: KLINA, Annelies  
; APPLICANT: STEINDL, Franz  
; APPLICANT: MUSTER, Thomas  
; TITLE OF INVENTION: HIV-vaccines  
; FILE REFERENCE: 1939-112P  
; CURRENT APPLICATION NUMBER: US/09/124,900  
; CURRENT FILING DATE: 1998-07-30  
; PRIOR APPLICATION NUMBER: PCT/EP95/01481  
; PRIOR FILING DATE: 1995-04-19  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-124-900-10

Query Match 28.2%; Score 638; DB 4; Length 123;  
Best Local Similarity 97.6%; Pred. No. 6.5e-57;

Matches 120; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 112 MGGKWSKSSVVGWPTVRRMRRAEPAADVGGAASRDLEKHGAITSNTAATNAACAWLEA 171  
Db 1 MGGKWSKSSVVGWPTVRRMRRAEPAADVGGAASRDLEKHGAITSNTAATNAACAWLEA 60  
Qy 172 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTQY 231  
Db 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTQY 120  
Qy 232 FPD 234  
Db 121 FPD 123

RESULT 6  
US-09-485-885-21  
; Sequence 21, Application US/09485885  
; Patent No. 6342224  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/09/485,885  
; CURRENT FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 278  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-485-885-21

Query Match 26.7%; Score 603.5; DB 4; Length 278;  
Best Local Similarity 36.4%; Pred. No. 6.7e-53;  
Matches 158; Conservative 26; Mismatches 73; Indels 177; Gaps 12;  
Qy 1 MDPSSSHSNMANTQMSDKIIIAHRGASGLPEHTLESKALAFQAQADYLEODLMTKDG 60  
Db 1 MDPSSSHSNMANTQMSDKIIIAHRGASGLPEHTLESKALAFQAQADYLEODLMTKDG 60  
Qy 61 RLWVIHDFLGLTQVAKKFPHRHRKDGYYVIDFTLKEIQSLEMTENPFTMGKWSKSS 120  
Db 61 RLWVIHDFLGLTQVAKKFPHRHRKDGYYVIDFTLKEIQSLEMTENPFTMA----- 113  
Qy 121 VVGWPTVRRMRRAEPAADVGGAASRDLEKHGAITSNTAATN--AACAW----LEAOEE 174  
Db 114 -----RFEDP-----TRPYKLPDLCTELNTSLQDIEITCVYKTVLLETEV 155  
Qy 175 EEEVFPVTPQVPLRPMYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTQGYFPD 234  
Db 156 REFAFK-----DLFVVY----- 167  
Qy 235 WONYTPGQVRYPLTFGWCKYKLV-----PVEPDKVEE-ANKGENTSLHPV 279  
Db 168 -----RDSIPHAACHKCIDFYSRIRELRHYSDSYGDTLEKLTNTGLYNLLIRCL 217  
Qy 280 SLHGMDPEREVLEWRDLSRLAFHFAHVAHELHPEYFKNCTSEPDPRLEPKHPPGQPKTA 339  
Db 218 RCQKPLNPAEKL--HLNEKRRFHNIAGHYRCQ----- 248  
Qy 340 CTNICYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQSGQTHVSLKQPTSQSGDP 399  
Db 249 -----CHSCC-----NRQRERLQRRRETQ----- 268

QY 400 TGPKESTGHHHHH 413  
Db 269 -----VTSGHHHHH 278

## RESULT 7

US-09-485-885-23  
; Sequence 23 Application US/09485885  
; Patent No. 6342224  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/09/485.885  
; CURRENT FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 23  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-485-885-23

Query Match 26.4%; Score 597; DB 4; Length 383;  
Best Local Similarity 34.9%; Pred. No. 4.8e-52;  
Matches 170; Conservative 21; Mismatches 118; Indels 178; Gaps 11;  
QY 1 MDPSSSHSNMANTOMKSKIIIAHAGSGYLPEHTLESKALAFQAQADYLEODLMTKDG 60  
Db 1 MDPSSSHSNMANTOMKSKIIIAHAGSGYLPEHTLESKALAFQAQADYLEODLMTKDG 60  
QY 61 RLWVIHDFLDGLTDVAKKFPHRHRKDGYYVIDFTLKEIOSLEMTENFETMGGKSS 114  
Db 61 RLWVIHDFLDGLTDVAKKFPHRHRKDGYYVIDFTLKEIOSLEMTENFETMAREDPTR 120  
QY 115 -----KWSKSSVGVWPTVRRMRRAEPAADGVGAASRDLEKKGAIITS-- 156  
Db 121 RPKLPDLCTELNTSLQDIEITCVCKTVLETFEFAFKDLFVYVYRDSIPHAACHKCI 180  
QY 157 -----SNTAATNAACAWLEAQEEEEVGFVTPQVPLRPMTY 192  
Db 181 DFYSRIRELRHYSDVYGDTEKLTNTGLYNLLIRLCRCQK-----PLNPAEKLRLHNE 234  
QY 193 KAADVLSHFLKEKGGLEGILHS---QRRQDILDLWIYHTQGYFPDQWQNYTPGPGVRYPLT 249  
Db 235 K-----RRFNTIAGHYRGQCHSCCNRAQ----- 258  
QY 250 FGWCYKLPVPEPKVEEANKGENTSLLH-----PVSL---HGMDDP 287  
Db 259 -----ERLQRRRETQVMHGPKATLDQIVLHLEPQNEIPVDLLCHEQLSDS 303  
QY 288 EREVLWEFRDSRLAPHVARELHPE-YFKNCTSEPVDRLEPWKHPGSOPTACTNCYCK 346  
Db 304 EGENDE--IDGVNHOHLPARREPORHTMLCMCCKEARIELVWESSADDLRAFOQLFN 361  
QY 347 KCCFCQVCQFITKALGISYGRKKRRRRRPPQSGQTHOVSLSKQPTOSRGDPTGPKETS 406  
Db 362 TLSFVCPWC-----ASQOTS 376  
QY 407 GHHHHHH 413  
Db 377 GHHHHHH 383

## RESULT 8

US-09-485-885-8  
; Sequence 8 Application US/09485885  
; Patent No. 6342224  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/09/485.885  
; CURRENT FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-485-885-8

Query Match 26.2%; Score 594; DB 4; Length 220;  
Best Local Similarity 67.0%; Pred. No. 4.3e-52;  
Matches 126; Conservative 9; Mismatches 27; Indels 26; Gaps 3;  
QY 1 MDPSSSHSNMANTOMKSKIIIAHAGSGYLPEHTLESKALAFQAQADYLEODLMTKDG 60  
Db 1 MDPSSSHSNMANTOMKSKIIIAHAGSGYLPEHTLESKALAFQAQADYLEODLMTKDG 60  
QY 61 RLWVIHDFLDGLTDVAKKFPHRHRKDGYYVIDFTLKEIOSLEMTENFETMGGKSS 120  
Db 61 RLWVIHDFLDGLTDVAKKFPHRHRKDGYYVIDFTLKEIOSLEMTENFETMAMHGT-- 118  
QY 121 VVGWPTVRRMRRAEPAADGVGAASRDLEKKGAIITSNTAATNAACAWLEAQEEEEVGF 180  
Db 119 ----PTLHEYMLDLP-----ETDLYGYQLNDS-----SEEEDEIDGP 154  
QY 181 VTPQVPLR 188  
Db 155 AQAEPR 162  
RESULT 9  
US-09-485-885-1  
; Sequence 1 Application US/09485885  
; Patent No. 6342224  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/09/485.885  
; CURRENT FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: Homo sapien

US-09-485-885-1

Query Match 26.2%; Score 593; DB 4; Length 220;  
Best Local Similarity 67.0%; Pred. No. 5.4e-52;  
Matches 126; Conservative 9; Mismatches 27; Indels 26; Gaps 3;

QY 1 MDPSSSHSNANTQMSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEODLAWTKDG 60  
DB 1 MDPSSSHSNANTQMSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEODLAWTKDG 60

QY 61 RLWVIHDFDLGLTDVAKKFPFHRKRDGRYYVIDFTLKEIQSLQLENTFETMGGKWSKSS 120  
DB 61 RLWVIHDFDLGLTDVAKKFPFHRKRDGRYYVIDFTLKEIQSLQLENTFETMGGKWSKSS 118

QY 121 VVGWPTVRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEAQEEVEVGP 180  
DB 119 ----PTLHEYMLDLP-----ETDLYCYEQLNDS-----SEEEDEIDGP 154

QY 181 VTPOVPLR 188  
DB 155 AGQAEPR 162

RESULT 10

US-09-485-885-16  
; Sequence 16, Application US/09485885  
; Patent No. 6342224  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezón Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/09/485,885  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 227  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-485-885-16

Query Match 26.1%; Score 590; DB 4; Length 227;  
Best Local Similarity 37.0%; Pred. No. 1.1e-51;  
Matches 153; Conservative 14; Mismatches 59; Indels 188; Gaps 10;

QY 1 MDPSSSHSNANTQMSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEODLAWTKDG 60  
DB 1 MDPSSSHSNANTQMSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEODLAWTKDG 60

QY 61 RLWVIHDFDLGLTDVAKKFPFHRKRDGRYYVIDFTLKEIQSLQLENTFETMGGKWSKSS 120  
DB 61 RLWVIHDFDLGLTDVAKKFPFHRKRDGRYYVIDFTLKEIQSLQLENTFETM 112

QY 121 VVGWPTVRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEAQEEVEVGP 180  
DB 113 -----AMHGPKATLQDIVLH-----LEPQNE----- 133

QY 181 VTPOVPLRMTYKAAVDLSHFLKEGGLHSHLTHSRRQDILDLWIYHTGYPDQNYTP 240  
DB 134 ----IP-----VDL-----LCHQLSDS----- 147

QY 241 GPCVRYPLTFGWCYKLVPPVEPKVEEANKGENTSLHHPVSLHGMDDPERVLEWRFDSRL 300

Db 148 -----EEENDEIDEVN-----HQ----- 160

QY 301 AFHHVARELHPE-YFKNCTSEPVDPRLPEWKPUGSOPKTACTNCTCYCKKCCFHCQVCFTK 359  
DB 161 --HLPARRAEPQRHTMLCWCCKEARIELVSSADDLRAFOOLFNTLSFVCPWC----- 214

QY 360 ALGISYGRKKRRQRRRPPGOSQTHOVSLSKOPTSQSRGDPGPKTSGHHHHH 413  
DB 215 -----ASQQTSGHHHHH 227

RESULT 11  
US-09-485-885-6  
; Sequence 6, Application US/09485885  
; Patent No. 6342224  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezón Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/09/485,885  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 371  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-485-885-6

Query Match 26.1%; Score 590; DB 4; Length 371;  
Best Local Similarity 34.9%; Pred. No. 2.4e-51;  
Matches 167; Conservative 27; Mismatches 112; Indels 172; Gaps 14;

QY 1 MDPSSSHSNANTQMSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEODLAWTKDG 60  
DB 1 MDPSSSHSNANTQMSDKIIIAHRCAGSYLPEHTLESKALAFQAQADYLEODLAWTKDG 60

QY 61 RLWVIHDFDLGLTDVAKKFPFHRKRDGRYYVIDFTLKEIQSLQLENTFETMGGKWSKSS 120  
DB 61 RLWVIHDFDLGLTDVAKKFPFHRKRDGRYYVIDFTLKEIQSLQLENTFETM 112

QY 121 VVGWPTVRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEAQEEVEVGP 180  
DB 113 -AMFQDPOERPKLPOLCTELQTTIHI-----ILECVYCKQ----- 149

QY 181 VTPOVPLRMTYKAAVDLSHFLKEGGLHSHLTHSRRQDILDLWIYHTG----- 230

DB 150 -----LLREVYDFA-----FRDLCTVYRDGNPYAVCDKGL 180

QY 231 -YFPDQNYTPGPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPER 289  
DB 181 KEYSKISEYR-----HYCISLVGTTLE--QOYKPLCDLLIRCINQCKPLCPDE 227

QY 290 EYLEWRFDSRLAFHHVARELHPEYFNCTSEPVDPRL-----PMKHP---GSQPKTAC 340  
DB 228 K--QRHLDKKQRFHNIIRGRWTCRCMCCSSRTRRETQLMHGDTPTLHEYMLDLPETD 285

QY 341 TNCY-----CKKCCFHCQVC----- 355

DB 286 LYCYEQLNDSSEEDIDGPAQAEPRAHYNIIVTFCKCDSTLRLCVQSTHVDITLED 345

QY 356 FTTKALGISYGRKKRRQRRRPPGOSQTHOVSLSKOPTSQSRGDPGPKTSGHHHHH 413  
DB 346 LLMGTLGIVC-----PICSQ-----KPTSGHHHHH 371

RESULT 12  
US-09-485-885-19  
; Sequence 19, Application US/09485885  
; Patent No. 6342224  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/09/485,885  
; CURRENT FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 227  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-485-885-19

Query Match 25,9% Score 587; DB 4; Length 227;  
Best Local Similarity 36.7%; Pred. No. 2.3e-51;  
Matches 152; Conservative 15; Mismatches 59; Indels 188; Gaps 9;  
Qy 1 MDPSSSHSNMANTOMKSDKIIIAHAGSYLPHTLESKALAFQAQADYLEQDLAMTKDG 60  
Db 1 MDPSSSHSNMANTOMKSDKIIIAHAGSYLPHTLESKALAFQAQADYLEQDLAMTKDG 60  
Qy 61 RLVIHDFHGLDGLTVAKKPPHRRKDGYYVIDFTLKEIOSLENTFETMGKWSKSS 120  
Db 61 RLVIHDFHGLDGLTVAKKPPHRRKDGYYVIDFTLKEIOSLENTFETM----- 112  
Qy 121 VVGWPTVRMRRAEPAADGVGAASRDLEKKGAITSSNTAATNACAWLEAQEEEEVGFP 180  
Db 113 -----AHGFKATLQDVLH-----LEPQNE----- 133  
Qy 181 VTPQVPLRPMTYKAADVLSHFLKEKGGLEGLHSORRODILDLYHTQGYFPDQWNTY 240  
Db 134 ---IP-----VDLL-----GHQQLSDSEENDEID----- 155  
Qy 241 GPGVRYPLTFGCWYKLVPEPDKVEANKGENTSLHHPVSLHGMDDPEREVLWRFDRL 300  
Db 156 --GVNHQ----- 160  
Qy 301 AFHVARELHPE-YFKNCTSEPDVRLPEPKHPGSPQKPTACTNVCYKCCFHCQVCFTK 359  
Db 161 --HLPARAEPOHMTLMCCCKEARIELVVESSADDLRAFOQLNLTLFSVCPWC----- 214  
Qy 360 ALGISYGRKKRRRRPPQGSQTHOVSLSKPTOSRSDGPTGPKETSGHHHHH 413  
Db 215 -----ASQTSQSGHHHHH 227

RESULT 13  
US-09-485-885-4  
; Sequence 4, Application US/09485885  
; Patent No. 6342224  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabezon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine

; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/09/485,885  
; CURRENT FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 273  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-485-885-4

Query Match 25,7% Score 582; DB 4; Length 273;  
Best Local Similarity 36.3%; Pred. No. 9.7e-51;  
Matches 154; Conservative 24; Mismatches 84; Indels 162; Gaps 12;  
Qy 1 MDPSSSHSNMANTOMKSDKIIIAHAGSYLPHTLESKALAFQAQADYLEQDLAMTKDG 60  
Db 1 MDPSSSHSNMANTOMKSDKIIIAHAGSYLPHTLESKALAFQAQADYLEQDLAMTKDG 60  
Qy 61 RLVIHDFHGLDGLTVAKKPPHRRKDGYYVIDFTLKEIOSLENTFETMGKWSKSS 120  
Db 61 RLVIHDFHGLDGLTVAKKPPHRRKDGYYVIDFTLKEIOSLENTFETM----- 112  
Qy 121 VVGWPTVRMRRAEPAADGVGAASRDLEKKGAITSSNTAATNACAWLEAQEEEEVGFP 180  
Db 113 -AMQDQPERPKLPOLCTELQTTIHI-----ILECVYCKQ----- 149  
Qy 181 VTPQVPLRPMTYKAADVLSHFLKEKGGLEGLHSORRODILDLYHTQ----- 230  
Db 150 -----LLRREYDFA-----FRDLGIVYRDGNPYAVCDKCL 180  
Qy 231 -YEPDQWNTYPCGVRYPLTFGCWYKLVPEPDKVEANKGENTSLHHPVSLHGMDDPER 289  
Db 181 KFYKISEYR-----HYCVSLYGTLE--QQYNKPLCOLLIRINCQKPLCPPEE 227  
Qy 290 EVLEWRFDRLAFHVARLHPEYFKNCTSEPDVRLPEPKHPGSPQKPTACTNVCYKCC 349  
Db 228 K-QRHLDKKQRFHNR-----W-----TGRCMSCC 253  
Qy 350 FHCQVCFITKALGISYGRKKRRRRPPQGSQTHOVSLSKPTOSRSDGPTGPKETSGHH 409  
Db 254 -----RSSRTRRE-----TQLTSGHH 269  
Qy 410 HHHH 413  
Db 270 HHHH 273

RESULT 14  
US-08-679-493A-74  
; Sequence 74, Application US/08679493A  
; Patent No. 6303295  
; GENERAL INFORMATION:  
; APPLICANT: Taylor, Ethan W.  
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
; FILE REFERENCE: 55-95  
; CURRENT APPLICATION NUMBER: US/08/679,493A  
; CURRENT FILING DATE: 1996-07-12  
; PRIOR APPLICATION NUMBER: 60/001203  
; PRIOR FILING DATE: 1995-07-14  
; PRIOR APPLICATION NUMBER: 60/003,112  
; PRIOR FILING DATE: 1995-09-01  
; NUMBER OF SEQ ID NOS: 216  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 74  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1



FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)...(151)  
OTHER INFORMATION: X is selenocysteine.  
US-08-679-493A-74

Query Match 22.0%; Score 498.5; DB 4; Length 151;  
Best Local Similarity 73.0%; Pred. No. 1.1e-42;  
Matches 103; Conservative 4; Mismatches 7; Indels 27; Gaps 3;  
QY 112 MGKSKSSVGVNPTVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171  
DB 1 MGKSKSSVGVNPTVRMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60  
QY 172 QEEVEGVFPVTPQVPLRPMTYKAADVLSHFLKEKGG----- 207  
DB 61 QEEVEGVFPVTPQVPLRPMTYKAADVLSHFLKEKGGTGRANSLPTKTRYPXSVLDLPHTRL 120  
QY 208 LEGL--IHSORQDI-LDLWI 225  
DB 121 LPXLAEHLTRARGIGSTDLWM 141

RESULT 15  
US-08-450-257-1

; Sequence 1, Application US/08450257  
; Patent No. 5652122  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: PABO, Carl  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: FAWELL, Stephen E.  
; APPLICANT: PEPINSKY, R. B.  
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,257  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/235,403  
; FILING DATE: 28-APR-1994  
; APPLICATION NUMBER: US 07/934,375  
; FILING DATE: 21-AUG-1992  
; APPLICATION NUMBER: US 07/098,766  
; FILING DATE: 28-JUL-1993  
; APPLICATION NUMBER: PCT/US93/07833  
; FILING DATE: 19-AUG-1993  
; APPLICATION NUMBER: US 07/454,450  
; FILING DATE: 21-DEC-1989  
; APPLICATION NUMBER: US 07/636,662  
; FILING DATE: 02-JAN-1991  
; APPLICATION NUMBER: US 08/158,015  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B170 CIP 2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000

; TELEFAX: (212) 596-9090  
; TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 86 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: human immunodeficiency virus  
; STRAIN: type 1  
; US-08-450-257-1

Query Match 21.5%; Score 486; DB 1; Length 86;  
Best Local Similarity 100.0%; Pred. No. 8.9e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 320 EPVDPRLPEWKHPGSOPTACTNCYCKKCCFCQVCFITKALGISYGRKKRRRRPPQG 379  
DB 2 EPVDPRLPEWKHPGSOPTACTNCYCKKCCFCQVCFITKALGISYGRKKRRRRPPQG 61  
QY 380 SOTHQVSLSKQPTSQSRGDPGTGPK 404  
DB 62 SOTHQVSLSKQPTSQSRGDPGTGPK 86

RESULT 16

US-08-450-246-1  
; Sequence 1, Application US/08450246  
; Patent No. 5670617  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: PABO, Carl  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: FAWELL, Stephen E.  
; APPLICANT: PEPINSKY, R. B.  
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,246  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/235,403  
; FILING DATE: 28-APR-1994  
; APPLICATION NUMBER: US 07/934,375  
; FILING DATE: 21-AUG-1992  
; APPLICATION NUMBER: US 07/098,766  
; FILING DATE: 28-JUL-1993  
; APPLICATION NUMBER: PCT/US93/07833  
; FILING DATE: 19-AUG-1993  
; APPLICATION NUMBER: US 07/454,450  
; FILING DATE: 21-DEC-1989  
; APPLICATION NUMBER: US 07/636,662  
; FILING DATE: 02-JAN-1991  
; APPLICATION NUMBER: US 08/158,015  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794

```
;
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: human immunodeficiency virus
; STRAIN: type 1
; US-08-450-246-1

Query Match 21.5% Score 486; DB 1; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-42;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 320 EPVDPRLPEWHPGSPQPTACTNCYKCKCFHCQVCFITKALGISYGRKKRRRRPPQG 379
Db 2 EPVDPRLPEWHPGSPQPTACTNCYKCKCFHCQVCFITKALGISYGRKKRRRRPPQG 61

Qy 380 SOTHQVSLSKQPTQSOGDPTGPKE 404
Db 62 SOTHQVSLSKQPTQSOGDPTGPKE 86

RESULT 17
US-08-450-098-1
; Sequence 1, Application US/08450098
; Patent No. 5674980
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,098
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: human immunodeficiency virus
; STRAIN: type 1
; US-08-450-098-1

Query Match 21.5% Score 486; DB 1; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-42;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 320 EPVDPRLPEWHPGSPQPTACTNCYKCKCFHCQVCFITKALGISYGRKKRRRRPPQG 379
Db 2 EPVDPRLPEWHPGSPQPTACTNCYKCKCFHCQVCFITKALGISYGRKKRRRRPPQG 61

Qy 380 SOTHQVSLSKQPTQSOGDPTGPKE 404
Db 62 SOTHQVSLSKQPTQSOGDPTGPKE 86

RESULT 18
US-08-451-233-1
; Sequence 1, Application US/08451233
; Patent No. 5747641
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,233
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
```

;; FILING DATE: 02-JAN-1991  
;; APPLICATION NUMBER: US 08/158,015  
;; FILING DATE: 24-NOV-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Haley Jr., James F.  
;; REGISTRATION NUMBER: 27,794  
;; REFERENCE/DOCKET NUMBER: B170 CIP 2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 596-9000  
;; TELEFAX: (212) 596-9090  
;; TELEX: 14-8367  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 86 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; ORIGINAL SOURCE:  
;; ORGANISM: human immunodeficiency virus  
;; STRAIN: type 1  
US-08-451-233-1

Query Match 21.5%; Score 486; DB 1; Length 86;  
Best Local Similarity 100.0%; Pred. No. 8.9e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 EPVDRLEPWHKPGSQPTACTNCYCKCCFHCQVCFITKALGISYGRKKRRRRPPOG 379  
DB 2 EPVDRLEPWHKPGSQPTACTNCYCKCCFHCQVCFITKALGISYGRKKRRRRPPOG 61  
QY 380 SOTHQVSLSKOPTSQSRGDPGPK 404  
DB 62 SOTHQVSLSKOPTSQSRGDPGPK 86

RESULT 19  
US-08-450-236-1  
; Sequence 1, Application US/08450236  
; Patent No. 5804604  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: PABO, Carl  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: FAWELL, Stephen E.  
; APPLICANT: PEPINSKY, R. B.  
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/450,236  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/235,403  
; FILING DATE: 28-APR-1994  
; APPLICATION NUMBER: US 07/934,375  
; FILING DATE: 21-AUG-1992  
; APPLICATION NUMBER: US 07/098,766  
; FILING DATE: 28-JUL-1993  
; APPLICATION NUMBER: PCT/US93/07833  
; FILING DATE: 19-AUG-1993

;; APPLICATION NUMBER: US 07/454,450  
;; FILING DATE: 21-DEC-1989  
;; APPLICATION NUMBER: US 07/636,662  
;; FILING DATE: 02-JAN-1991  
;; APPLICATION NUMBER: US 08/158,015  
;; FILING DATE: 24-NOV-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Haley Jr., James F.  
;; REGISTRATION NUMBER: 27,794  
;; REFERENCE/DOCKET NUMBER: B170 CIP 2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 596-9000  
;; TELEFAX: (212) 596-9090  
;; TELEX: 14-8367  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 86 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; ORIGINAL SOURCE:  
;; ORGANISM: human immunodeficiency virus  
;; STRAIN: type 1  
US-08-450-236-1

Query Match 21.5%; Score 486; DB 1; Length 86;  
Best Local Similarity 100.0%; Pred. No. 8.9e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 EPVDRLEPWHKPGSQPTACTNCYCKCCFHCQVCFITKALGISYGRKKRRRRPPOG 379  
DB 2 EPVDRLEPWHKPGSQPTACTNCYCKCCFHCQVCFITKALGISYGRKKRRRRPPOG 61  
QY 380 SOTHQVSLSKOPTSQSRGDPGPK 404  
DB 62 SOTHQVSLSKOPTSQSRGDPGPK 86

RESULT 20  
US-07-808-452-1  
; Sequence 1, Application US/07808452  
; Patent No. 6063612  
; GENERAL INFORMATION:  
; APPLICANT: Jayasena, Sumedha D.  
; APPLICANT: Johnston, Brian H.  
; TITLE OF INVENTION: Antiviral Reagents Based on  
; TITLE OF INVENTION: RNA-Binding Proteins  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Peter Dehlinger  
; STREET: 350 Cambridge Avenue, Suite 300  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/808,452  
; FILING DATE: 19911213  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fabian, Gary R.  
; REGISTRATION NUMBER: 33,875  
; REFERENCE/DOCKET NUMBER: 8255-008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880  
; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 1:

```
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 86 amino acids
;   TYPE: AMINO ACID
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;     INDIVIDUAL ISOLATE: the sequence of the TAT protein of
;     INDIVIDUAL ISOLATE: HIV-1
; US-07-808-452-1

Query Match      21.5%; Score 486; DB 3; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-42;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 EPVDPRLPWPWKGSPKTKACTNCTCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 379
Db 2 EPVDPRLPWPWKGSPKTKACTNCTCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61

QY 380 STHQVSLSKOPTSQSRGDPGPK 404
Db 62 STHQVSLSKOPTSQSRGDPGPK 86

RESULT 22
US-09-124-900-6
; Sequence 6, Application US/09124900
; Patent No. 6268484
; GENERAL INFORMATION:
; APPLICANT: KATINGER, Hermann
; APPLICANT: BUCHACHER, Andrea
; APPLICANT: ERNST, Wolfgang
; APPLICANT: BALLAUN, Claudia
; APPLICANT: PURTSCHER, Martin
; APPLICANT: TRKOLA, Alexandra
; APPLICANT: PREDL, Renate
; APPLICANT: SCHMATZ, Christine
; APPLICANT: KLIMA, Annelies
; APPLICANT: STEINDL, Franz
; APPLICANT: MUSTER, Thomas
; TITLE OF INVENTION: HIV-Vaccines
; FILE REFERENCE: 1939-112P
; CURRENT APPLICATION NUMBER: US/09/124,900
; CURRENT FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: PCT/EP95/01481
; PRIOR FILING DATE: 1995-04-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; US-09-124-900-6

Query Match      21.5%; Score 486; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-42;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 EPVDPRLPWPWKGSPKTKACTNCTCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 379
Db 2 EPVDPRLPWPWKGSPKTKACTNCTCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61

QY 380 STHQVSLSKOPTSQSRGDPGPK 404
Db 62 STHQVSLSKOPTSQSRGDPGPK 86

RESULT 23
US-09-451-905-19
; Sequence 19, Application US/09451905
; Patent No. 6305613
; GENERAL INFORMATION:
; APPLICANT: Robert Z. Florkiewicz
; APPLICANT: Andrew Baird
; APPLICANT: Dale E. Warnock
; TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT
; FILE REFERENCE: 200124.402C4
; CURRENT APPLICATION NUMBER: US/09/451.905
; CURRENT FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-451-905-19

SEQUENCE CHARACTERISTICS:
;   LENGTH: 86 amino acids
;   TYPE: AMINO ACID
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;     INDIVIDUAL ISOLATE: the sequence of the TAT protein of
;     INDIVIDUAL ISOLATE: HIV-1
; US-07-808-452-1

Query Match      21.5%; Score 486; DB 3; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-42;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 EPVDPRLPWPWKGSPKTKACTNCTCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 379
Db 2 EPVDPRLPWPWKGSPKTKACTNCTCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61

QY 380 STHQVSLSKOPTSQSRGDPGPK 404
Db 62 STHQVSLSKOPTSQSRGDPGPK 86

RESULT 21
US-09-030-613-19
; Sequence 19, Application US/09030613
; Patent No. 6083706
; GENERAL INFORMATION:
; APPLICANT: Florkiewicz, Robert Z.
; APPLICANT: Baird, J. Andrew
; TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030.613
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083706tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.418C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 86 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
; US-09-030-613-19

Query Match      21.5%; Score 486; DB 3; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-42;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 EPVDPRLPWPWKGSPKTKACTNCTCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 379
Db 2 EPVDPRLPWPWKGSPKTKACTNCTCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61
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Query Match 21.5%; Score 486; DB 4; Length 86;  
Best Local Similarity 100.0%; Pred. No. 8.9e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 EPVDRLEPFWKHPGQPKTACTNCYKCCFHCQVCFITKALGISYGRKKRRRRPQG 379  
|||||  
Db 2 EPVDRLEPFWKHPGQPKTACTNCYKCCFHCQVCFITKALGISYGRKKRRRRPQG 61  
|||||

QY 380 SOTHVSLSKOPTSOSRGDPTGPK 404  
|||||  
Db 62 SOTHVSLSKOPTSOSRGDPTGPK 86  
|||||

## RESULT 24

US-08-235-403-1  
Sequence 1, Application US/08235403  
Patent No. 6316003  
GENERAL INFORMATION:  
APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOUM, James G.  
APPLICANT: FAWELL, Stephen E.  
APPLICANT: PEPINSKY, R. B.  
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/235,403  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: human immunodeficiency virus  
STRAIN: type 1  
US-08-235-403-1

Query Match 21.5%; Score 486; DB 4; Length 86;  
Best Local Similarity 100.0%; Pred. No. 8.9e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 EPVDRLEPFWKHPGQPKTACTNCYKCCFHCQVCFITKALGISYGRKKRRRRPQG 379  
|||||  
Db 2 EPVDRLEPFWKHPGQPKTACTNCYKCCFHCQVCFITKALGISYGRKKRRRRPQG 61  
|||||

QY 380 SOTHVSLSKOPTSOSRGDPTGPK 404  
|||||  
Db 62 SOTHVSLSKOPTSOSRGDPTGPK 86  
|||||

## RESULT 25

PCT-US92-10770-1  
Sequence 1, Application PC/TUS9210770  
GENERAL INFORMATION:  
APPLICANT: Jayasena, Sumedha D.  
APPLICANT: Johnston, Brian H.  
TITLE OF INVENTION: Antiviral Reagents Based on  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SRI International  
STREET: 333 Ravenswood Avenue  
CITY: Menlo Park  
STATE: CA  
COUNTRY: USA  
ZIP: 94025

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10770  
FILING DATE: 19921211  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,452  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: P-2962  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 859-4550  
TELEFAX: (415) 859-3880  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: the sequence of the TAT protein of  
INDIVIDUAL ISOLATE: HIV-1  
PCT-US92-10770-1

Query Match 21.5%; Score 486; DB 5; Length 86;  
Best Local Similarity 100.0%; Pred. No. 8.9e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 EPVDRLEPFWKHPGQPKTACTNCYKCCFHCQVCFITKALGISYGRKKRRRRPQG 379  
|||||  
Db 2 EPVDRLEPFWKHPGQPKTACTNCYKCCFHCQVCFITKALGISYGRKKRRRRPQG 61  
|||||

QY 380 SOTHVSLSKOPTSOSRGDPTGPK 404  
|||||

Db 62 SOTHQVLSKQPTSQSRGDPGPK 86

## RESULT 26

PCT-US95-06077-2

; Sequence 2, Application PC/TUS9506077

; GENERAL INFORMATION:

; APPLICANT: Immunobiology Research, Institute Inc.

; TITLE OF INVENTION: Vaccine Interdiction of Extracellular

; TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus

; TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar

; TITLE OF INVENTION: Intercellular Transactivating Strategies

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Howson and Howson

; STREET: Spring House Corporate Cntr, PO Box 457

; CITY: Spring House

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19477

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION NUMBER: PCT/US95/06077

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/247,991

; FILING DATE: 23-MAY-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Bak, Mary E.

; REGISTRATION NUMBER: 31,215

; REFERENCE/DOCKET NUMBER: IRI44PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-540-9200

; TELEFAX: 215-540-5818

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 86 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US95-06077-2

Query Match 21.5%; Score 486; DB 5; Length 86;

Best Local Similarity 100.0%; Pred. No. 8.9e-42;

Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 320 EPVDPRLPWHKPSQPTACTNCYKCCFHCQVCFITKALGISYGRKKRRRRRPPQG 379

Db 2 EPVDPRLPWHKPSQPTACTNCYKCCFHCQVCFITKALGISYGRKKRRRRRPPQG 61

Qy 380 SOTHQVLSKQPTSQSRGDPGPK 404

Db 62 SOTHQVLSKQPTSQSRGDPGPK 86

## RESULT 27

US-08-815-809-5

; Sequence 5, Application US/08815809

; Patent No. 6004777

; GENERAL INFORMATION:

; APPLICANT: TARTAGLIA, James

; APPLICANT: GOEBEL, Scott J.

; APPLICANT: COX, William I.

; APPLICANT: GETTIG, Russell R.

; APPLICANT: PINCUS, Steven E.

; APPLICANT: PAOLETTI, Enzo

; APPLICANT: JACOBS, Bertram L.

; TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND METHODS OF

; FILE REFERENCE: 454310-3010

; CURRENT APPLICATION NUMBER: US/08/815,809

; CURRENT FILING DATE: 1997-03-12

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 5

; LENGTH: 266

; TYPE: PRT

; ORGANISM: Vaccinia virus

US-08-815-809-5

Query Match 21.1%; Score 478.5; DB 3; Length 266;

Best Local Similarity 77.3%; Pred. No. 2.7e-40;

Matches 92; Conservative 4; Mismatches 6; Indels 17; Gaps 4;

Qy 177 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLIHSQRQDILDLDLWIYHTQGYFPDQW 236

Db 136 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLIHSQRQDILDLDLWIYHTQGYFPDQW 195

Qy 237 NYTPGPGVRYPLTFGWCYKLVPEPDKEVEANKGENTSLLPVSLH-GMDDPPEVLEW 294

Db 196 NYTPGPGVRYPLTFGWCYKLVPM-----IETV-----PVKLPQMDGP---KVKQW 238

## RESULT 28

US-08-816-155B-43

; Sequence 43, Application US/08816155B

; Patent No. 5990091

; GENERAL INFORMATION:

; APPLICANT: TARTAGLIA, JAMES

; APPLICANT: COX, WILLIAM I.

; APPLICANT: GETTIG, RUSSELL R.

; APPLICANT: MARTINEZ, HECTOR

; APPLICANT: PAOLETTI, ENZO

; APPLICANT: PINCUS, STEVEN E.

; TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND

; TITLE OF INVENTION: METHODS OF MAKING AND USES THEREOF

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FROMMER LAWRENCE & HAUG LLP

; STREET: 745 FIFTH AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10151

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/816,155B

; FILING DATE: 12-MAR-1997

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: KOWALSKI, THOMAS J.

; REGISTRATION NUMBER: 32,147

; REFERENCE/DOCKET NUMBER: 454310-2990

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-588-0800

; TELEFAX: 212-588-0500

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 280 amino acids

; TYPE: amino acid

; STRANDEDNESS: n/a

; TOPOLOGY: linear

; MOLECULE TYPE: amino acid

US-08-816-155B-43

Query Match 21.1%; Score 478.5; DB 2; Length 280;  
 Best Local Similarity 77.3%; Pred. No. 2.9e-40;  
 Matches 92; Conservative 4; Mismatches 6; Indels 17; Gaps 4;

QY 177 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGGLHSRRQDILDLIWIYHTQGYFPDQW 236  
 DB 150 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGGLHSRRQDILDLIWIYHTQGYFPDQW 209

QY 237 NYTPGPGVRYPLTFGWCYKLVPEPDKVEANKGENTSLHLPVSLH-GMDDPEREVLW 294  
 DB 210 NYTPGPGVRYPLTFGWCYKLVPM---IETV-----PVKLPGMDGP--KVKQW 252

RESULT 29  
 US-09-079-587-43  
 ; Sequence 43, Application US/09079587  
 ; Patent No. 6130066  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TARTAGLIA, JAMES  
 ; APPLICANT: COX, WILLIAM I.  
 ; APPLICANT: GETTIG, RUSSELL R.  
 ; APPLICANT: MARTINEZ, HECTOR  
 ; APPLICANT: PAOLETTI, ENZO  
 ; APPLICANT: PINCUS, STEVEN E.  
 ; TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND  
 ; METHODS OF MAKING AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 48  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FROMMER LAWRENCE & HAUG LLP  
 ; STREET: 745 FIFTH AVENUE  
 ; CITY: NEW YORK  
 ; STATE: NEW YORK  
 ; COUNTRY: USA  
 ; ZIP: 10151  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09079587  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/916,155  
 ; FILING DATE: 12-MAR-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KOWALSKI, THOMAS J.  
 ; REGISTRATION NUMBER: 32,147  
 ; REFERENCE/DOCKET NUMBER: 454310-2990  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-588-0800  
 ; TELEFAX: 212-588-0500  
 ; INFORMATION FOR SEQ ID NO: 43:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 280 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: n/a  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: amino acid  
 US-09-079-587-43

Query Match 21.1%; Score 478.5; DB 4; Length 280;  
 Best Local Similarity 77.3%; Pred. No. 2.9e-40;  
 Matches 92; Conservative 4; Mismatches 6; Indels 17; Gaps 4;

QY 177 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGGLHSRRQDILDLIWIYHTQGYFPDQW 236  
 DB 150 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGGLHSRRQDILDLIWIYHTQGYFPDQW 209

QY 237 NYTPGPGVRYPLTFGWCYKLVPEPDKVEANKGENTSLHLPVSLH-GMDDPEREVLW 294

DB 210 NYTPGPGVRYPLTFGWCYKLVPM---IETV-----PVKLPGMDGP--KVKQW 252

RESULT 30  
 US-08-505-210-1  
 ; Sequence 1, Application US/080505210  
 ; Patent No. 5981258  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MEHTALI, Majid  
 ; APPLICANT: GUSS, Tania  
 ; TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS  
 ; TITLE OF INVENTION: OF VIRAL PROTEINS FOR OBTAINING AN ANTIVIRAL EFFECT  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
 ; STREET: 1737 King Street, Suite 500  
 ; CITY: Alexandria  
 ; STATE: Virginia  
 ; COUNTRY: United States  
 ; ZIP: 22314-2756  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/505,210  
 ; FILING DATE: 14-AUG-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/215,248  
 ; FILING DATE: 21-MAR-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: WO PCT/FR94/01457  
 ; FILING DATE: 13-DEC-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dadio, Susan M.  
 ; REGISTRATION NUMBER: 40,373  
 ; REFERENCE/DOCKET NUMBER: 017753-066  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 836-6620  
 ; TELEFAX: (703) 836-2021  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 86 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Human immunodeficiency virus type 1  
 ; STRAIN: Lai  
 ; INDIVIDUAL ISOLATE: sequence of the TAT protein of HIV-1  
 US-08-505-210-1

Query Match 20.8%; Score 470; DB 2; Length 86;  
 Best Local Similarity 96.5%; Pred. No. 3.7e-40;  
 Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 320 EPVDPRLPEWKHPGSPKTAQCTACTNYCKKCCPHQVCFITTKALGISYGRKKRRRRPPQG 379  
 DB 2 EPVDPRLPEWKHPGSPKTAQCTACTNYCKKCCPHQVCFITTKALGISYGRKKRRRRPPQG 61

QY 380 SOTHQVSLSKOPTSOSRGDPTGPKE 404  
 DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86

us-09-509-239-21.ra1

Mon Aug 26 09:05:54 2002

Search completed: August 26, 2002, 08:10:41  
Job time: 130 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 08:15:42 ; Search time 40.39 Seconds  
(without alignments)  
395.919 Million cell updates/sec

Title: US-09-509-239-21

Perfect score: 2264

Sequence: 1 MDPSSSHSNWANTQMSDKI.....QSRGDPGPKETSGHHHHH 413

Scoring table: BLOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1130	49.9	206	1	NEF_HV1BR
2	1114	49.2	206	1	NEF_HV1PV
3	1111	49.1	206	1	NEF_HV1LW
4	1108	48.9	206	1	NEF_HV1I2
5	1088.5	48.1	205	1	NEF_HV1B6
6	1019	45.0	218	1	NEF_HV1B8
7	1005.5	44.4	205	1	NEF_HV1S3
8	997.5	44.1	211	1	NEF_HV1OY
9	997	44.0	210	1	NEF_HV1A2
10	994	43.9	208	1	NEF_HV1RH
11	991.5	43.8	214	1	NEF_HV1Y2
12	981	43.3	216	1	NEF_HV1J1
13	974	43.0	208	1	NEF_HV1S1
14	927.5	41.0	206	1	NEF_HV1E1
15	911	40.2	212	1	NEF_HV1Z6
16	903.5	39.9	207	1	NEF_HV1ND
17	872	38.5	205	1	NEF_HV1U4
18	842	37.2	182	1	NEF_HV1M4
19	837	37.0	205	1	NEF_HV1Z8
20	834.5	36.9	209	1	NEF_HV1M4
21	832	36.7	205	1	NEF_HV1C2
22	819	36.2	239	1	NEF_HV1SC
23	645	28.5	123	1	NEF_HV1H2
24	638	28.2	123	1	NEF_HV1B1
25	553.5	24.4	364	1	GLPQ_HAEIN
26	486	21.5	86	1	TAT_HV1B1
27	481	21.2	86	1	TAT_HV1PV
28	478	21.1	86	1	TAT_HV1I2
29	470	20.8	86	1	TAT_HV1BR
30	461	20.4	102	1	TAT_HV1RH
31	454	20.1	86	1	TAT_HV1H2
32	446	19.7	101	1	TAT_HV1JR
33	439.5	19.4	97	1	NEF_HV1Z2

34 439 19.4 253 1 NEF\_HV2KR Q74127 human immun  
35 437 19.3 101 1 TAT\_HV1SC P05906 human immun  
36 435 19.2 101 1 TAT\_HV1C4 P05907 human immun  
37 435 19.2 101 1 TAT\_HV1S1 P19553 human immun  
38 434 19.2 101 1 TAT\_HV1Y2 P35965 human immun  
39 431 19.0 101 1 TAT\_HV1MN P05905 human immun  
40 431 19.0 101 1 TAT\_HV1S3 P19552 human immun  
41 429.5 19.0 309 1 NEF\_SIVS4 P12482 simian immun  
42 426.5 18.8 261 1 NEF\_SIVSP P19501 simian immun  
43 421 18.6 257 1 NEF\_HV2D1 P17753 human immun  
44 419 18.5 101 1 TAT\_HV1A2 P04614 human immun  
45 419 18.5 101 1 TAT\_HV1OY P20893 human immun

## ALIGNMENTS

RESULT 1

NEF\_HV1BR  
ID NEF\_HV1BR STANDARD; PRT; 206 AA.  
AC P03406;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
GN NEF.  
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1), and  
OS Human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11686, 11698;  
RN [1]  
RP SEQUENCE FROM N.A. (CLONE PNL4-3).  
RC STRAIN=ISOLATE BRU;  
RX MEDLINE=8509333; PubMed=2981635;  
RA Wain-Hobson S., Sonigo P., Danos O., Cole S., Alison M.;  
RT "Nucleotide sequence of the AIDS virus, LAV.";  
RL Cell 40:9-17(1985).  
RN [2]  
RP SEQUENCE FROM N.A. (CLONE PNL4-3).  
RC STRAIN=ISOLATE NEW YORK-5;  
RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;  
RL Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.  
RX MEDLINE=88039140; PubMed=3118220;  
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,  
RA Montagnier L., Lecocq J.-P.;  
RT "HIV F3' orf encodes a phosphorylated GTP-binding protein resembling  
RT an oncogene product.";  
RL Nature 330:286-289(1987).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 54-205 IN COMPLEX WITH NEF.  
RX MEDLINE=96279837; PubMed=8681387;  
RA Lee C.H., Sakseila K., Mirza U.A., Chait B.T., Kuriyan J.;  
RT "Crystal structure of the conserved core of HIV-1 Nef complexed with  
RT a Src family SH3 domain.";  
RL Cell 85:931-942(1996).  
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; K02013; AAB59752.1; -  
DR EMBL; M19921; AAA44993.1; -  
DR EMBL; A04321; CAA00353.1; -  
DR PIR; A04008; ASLJFV  
DR PDB; 1EFN; 11-JAN-97.

```
DR HIV; K02013; NEFSBRU.
DR HIV; M19921; NEFSNL43.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; Myristate; GTP-binding; Phosphorylation; 3D-structure.
FT LIPID 2 MYRISTATE.
FT MOD_RES 15 15 PHOSPHORYLATION (BY PKC).
FT VARIANT 11 11 V -> I (IN CLONE PNL4-3).
FT VARIANT 15 15 T -> A (IN CLONE PNL4-3).
FT VARIANT 33 33 A -> V (IN CLONE PNL4-3).
FT VARIANT 51 51 T -> N (IN CLONE PNL4-3).
SQ SEQUENCE 206 AA; 23342 MW; 77453FC80B6004F2 CRC64;

Query Match 49.9%; Score 1130; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.4e-86;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVAASRDLEKKGAISSNTAATNAACAWLEA 171
DB 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 172 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRRQDILDWIYHTQY 231
DB 61 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRRQDILDWIYHTQY 120

QY 232 FPDWQNTYTPGCVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDPPEV 291
DB 121 FPDWQNTYTPGCVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDPPEV 180

QY 292 LEWRFDSRLAFHHVARELHPEYFKNC 317
DB 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 2
NEF_HV1PV
ID NEF_HV1PV STANDARD; PRT; 206 AA.
AC P03405.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11700;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85111157; PubMed=2982104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
RT AIDS/lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).
RN [2]
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
RX MEDLINE=88039140; PubMed=3118220;
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
RA Montagnier L., Lecocq J.-P.;
RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
RT an oncogene product.";
RL Nature 330:266-269(1987).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC
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CC
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CC
DR EMBL; K02083; AAB59874.1;
DR EMBL; X01762; -; NOT_ANNOTATED_CDS.
DR PIR; A04007; ASLJVL.
DR HSP; P03406; IEFN.
DR HIV; K02083; NEFSPV22.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; Myristate; GTP-binding.
FT LIPID 2 MYRISTATE.
SQ SEQUENCE 206 AA; 23352 MW; EDE64281A17C6735 CRC64;

Query Match 49.2%; Score 1114; DB 1; Length 206;
Best Local Similarity 97.6%; Pred. No. 3e-85;
Matches 201; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVAASRDLEKKGAISSNTAATNAACAWLEA 171
DB 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 172 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRRQDILDWIYHTQY 231
DB 61 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRRQDILDWIYHTQY 120

QY 232 FPDWQNTYTPGCVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDPPEV 291
DB 121 FPDWQNTYTPGCVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDPPEV 180

QY 292 LEWRFDSRLAFHHVARELHPEYFKNC 317
DB 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 3
NEF_HV1LW
ID NEF_HV1LW STANDARD; PRT; 206 AA.
AC Q70627.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (LW12.3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP STRUCTURE BY NMR OF 56-206.
RX MEDLINE=9737445; PubMed=9194185;
RA Grzesiek S., Bax A., Hu J.S., Kaufman J., Palmer I., Stahl S.J.,
RA Tjandra N., Wingfield P.F.;
RT "Refined solution structure and backbone dynamics of HIV-1 Nef.";
RL Protein Sci. 6:1248-1263(1997).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC
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CC
CC EMBL; U12055; AAA76691.1;
DR
```

PDB: 2NEF; 07-JUL-97.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; Myristate: GTP-binding; 3D-structure.  
FT LIPID 2 MYRISTATE.  
SQ SEQUENCE 206 AA; 23414 MW; ED81F68F6B61278E CRC64;

Query Match 49.18; Score 1111; DB 1; Length 206;  
Best Local Similarity 97.18; Pred. No. 5.4e-85;  
Matches 200; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 171  
Db 1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
Qy 172 QEEVEGPPVTPQVPLRPMYKAAVDLSHFLKKEGGLIHSQRQDILDWIYHTQY 231  
Db 61 QEEVEGPPVTPQVPLRPMYKAAVDLSHFLKKEGGLIHSQRQDILDWIYHTQY 120  
Qy 232 FPDWQNYTPGCVRYPLTFGCYKLVPEPKVEANKGENTSLHHPVSLHGMDPPERV 291  
Db 121 FPDWQNYTPGCVRYPLTFGCYKLVPEPKVEANKGENTSLHHPVSLHGMDPPERV 180  
Qy 292 LEWRFDLSLAFHHVARELHPEYKNC 317  
Db 181 LEWRFDLSLAFHHVARELHPEYKNC 206

RESULT 4  
NEF\_HV112  
ID NEF\_HV112 STANDARD; PRT; 206 AA.  
AC P04324;  
DT 20-MAR-1987 (Rel. 04, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
GN NEF.  
OS Human immunodeficiency virus type 1 (clone 12) (HIV-1).  
OC Viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11679;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86177573; PubMed=3008154;  
RA Arya S.K., Gallo R.C.;  
RT "Three novel genes of human T-lymphotropic virus type III: Immune reactivity of their products with sera from acquired immune deficiency syndrome patients."  
RT Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).  
RL (2)  
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.  
RX MEDLINE=88039140; PubMed=3118220;  
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,  
RA Montagnier L., Lecocq J.-P.;  
RT "HIV F3' orf encodes a phosphorylated GTP-binding protein resembling an oncogene product."  
RT Nature 330:266-269(1987).  
RL Nature 330:266-269(1987).  
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
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CC  
CC EMBL; M11840; AAA45001.1;  
DR PIR; A04006; ASLJ12.  
DR HSSP; P03406; 1EFN.  
DR HIV; M11840; NEFSPCV12.  
DR InterPro; IPR001558; F-protein.

Pfam: PF00469; F-protein; 1.  
KW AIDS; Myristate: GTP-binding.  
FT LIPID 2 MYRISTATE.  
SQ SEQUENCE 206 AA; 23366 MW; 218F5B2980F79A46 CRC64;

Query Match 48.98; Score 1108; DB 1; Length 206;  
Best Local Similarity 97.18; Pred. No. 9.5e-85;  
Matches 200; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 171  
Db 1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
Qy 172 QEEVEGPPVTPQVPLRPMYKAAVDLSHFLKKEGGLIHSQRQDILDWIYHTQY 231  
Db 61 QEEVEGPPVTPQVPLRPMYKAAVDLSHFLKKEGGLIHSQRQDILDWIYHTQY 120  
Qy 232 FPDWQNYTPGCVRYPLTFGCYKLVPEPKVEANKGENTSLHHPVSLHGMDPPERV 291  
Db 121 FPDWQNYTPGCVRYPLTFGCYKLVPEPKVEANKGENTSLHHPVSLHGMDPPERV 180  
Qy 292 LEWRFDLSLAFHHVARELHPEYKNC 317  
Db 181 LEWRFDLSLAFHHVARELHPEYKNC 206

RESULT 5  
NEF\_HV1B8  
ID NEF\_HV1B8 STANDARD; PRT; 205 AA.  
AC P05855;  
DT 01-NOV-1998 (Rel. 09, Created)  
DT 01-NOV-1998 (Rel. 09, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
GN NEF.  
OS Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).  
OC Viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11684;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85111123; PubMed=2578615;  
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,  
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,  
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,  
RA Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,  
RA Wong-Staal F.;  
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III."  
RT Nature 313:277-284(1985).  
RL (2)  
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.  
RX MEDLINE=88039140; PubMed=3118220;  
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,  
RA Montagnier L., Lecocq J.-P.;  
RT "HIV F3' orf encodes a phosphorylated GTP-binding protein resembling an oncogene product."  
RT Nature 330:266-269(1987).  
RL Nature 330:266-269(1987).  
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
CC  
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CC  
CC EMBL; K02011; -; NOT\_ANNOTATED\_CDS.  
DR HSSP; P03406; 1EFN.  
DR HIV; K02011; NEFSBH8.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.

```
KW AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 205 AA; 23305 MW; 8EC12F6650DD111 CRC64;

Query Match 48.1%; Score 1088.5; DB 1; Length 205;
Best Local Similarity 96.6%; Pred. No. 3.9e-83;
Matches 199; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 112 MGGKWSKSSVVGWPTVRMRRAEPAADGGAASRDLEKKGAISSNTAATNAACAWLEA 171
DB 1 MGGKWSKSSVVGWPAVRMRRAEPAADGGAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 172 QEEVEVGFPTVPQVPLRPMTYKAAVDLSHFLKKGGLGGLIHSORRQDILDWIHTQGY 231
DB 61 QEEVEVGFPTVPQVPLRPMTYKAAVDLSHFLKKGGLGGLIHSORRQDILDWIHTQGY 120

QY 232 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPREV 291
DB 121 FPDQNTYTPGCVRYPLTFGWCYKLVPEPEK-EEANKGENTSLHPVSLHGMDDPREV 179

QY 292 LEWFRDSRLAFHHVARELHPEYFKNC 317
DB 180 LEWFRDSRLAFHHMARELHPEYFKNC 205

RESULT 6
NEF_HV1BN ID NEF_HV1BN STANDARD; PRT; 218 AA.
AC P12479;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11693;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89085613; PubMed=2789516;
RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P.,
RA Dandekar S.;
RT "Biological and molecular characterization of human immunodeficiency
RT virus (HIV-1BR) from the brain of a patient with progressive
RT dementia.";
RL Virology 168:79-89(1989).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -!- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS
CC HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
CC -----
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CC -----
CC HSP; M21098; AAA4222.1;
CC DR PIR; D31687; ASLJB.
CC DR HSP; P03406; IEFN.
CC DR HIV; M21098; NEFSBRVA.
CC DR Pfam; PF00469; F-protein; 2.
CC KW AIDS; Myristate; GTP-binding.
CC FT LIPID 2
CC SQ SEQUENCE 218 AA; 25032 MW; FC4DABA1045C460E CRC64;

Query Match 45.0%; Score 1019; DB 1; Length 218;
Best Local Similarity 84.1%; Pred. No. 2.4e-77;

KW AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 205 AA; 23305 MW; 8EC12F6650DD111 CRC64;

Query Match 44.4%; Score 1005.5; DB 1; Length 205;
Best Local Similarity 86.4%; Pred. No. 2.9e-76;
Matches 178; Conservative 19; Mismatches 8; Indels 1; Gaps 1;

QY 112 MGGKWSKSSVVGWPTVRMRRAEPAADGGAASRDLEKKGAISSNTAATNAACAWLEA 171
DB 1 MGGKWSKSK-MGWPAVRMRRAEPAADGGAASRDLEKKGAISSNTAATNAACAWLEA 59

QY 172 QEEVEVGFPTVPQVPLRPMTYKAAVDLSHFLKKGGLGGLIHSORRQDILDWIHTQGY 231
DB 60 QEEVEVGFPTVPQVPLRPMTYKAAVDLSHFLKKGGLGGLVYSQRQDILDWIHTQGY 119

QY 232 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPREV 291
```

Db 120 PDQWNYTPGCVRPPLTFGWCFLKVPVEPEKVEANEGENNSLLHPMSLHGMDPEKEV 179

Qy 292 LEWRFDSRLAFHHVARELHPEYKNC 317

Db 180 LKWKFDKSLAFRRHARELHPEYKDC 205

## RESULT 8

NEF\_HV10Y ID NEF\_HV10Y STANDARD; PRT; 211 AA.

AC P20886; 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Negative factor (F-protein) (27 kDa protein) (3'ORF).

GN NEF.

OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).

OC Viruses; Retrovirdae; Lentivirus.

OX NCBI\_TaxID-11699;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-90148544; PubMed-2559749;

RA Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.,

RT "A highly defective HIV-1 strain isolated from a healthy Gabonese

RT individual presenting an atypical western blot.";

RL AIDS 3:707-715(1989).

CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING

CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

CC -!- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A

CC HEALTHY GABONESE INDIVIDUAL.

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CC

DR EMBL; M26727; AAA83398.1; -

DR HSSP; P03406; IEFN.

DR HIV; M26727; NEFSOYI.

DR InterPro: IPR001558; F-protein.

DR Pfam; PF00469; F-protein; 1.

KW AIDS; Myristate; GTP-binding.

FT LIPID 2 2 MYRISTATE.

SQ SEQUENCE 211 AA; 24067 MW; 64D846EEC55DAB8C CRC64;

Query Match 44.1%; Score 997.5; DB 1; Length 211;

Best Local Similarity 82.9%; Pred. No. 1.4e-75;

Matches 175; Conservative 22; Mismatches 9; Indels 5; Gaps 1;

Qy 112 MGKWSKSSVGVWPTVRERMRRA----EPAADGVGAASRDLEKKGAISSNTAATNAAC 166

Db 1 MGKWSKSKMGKWPTRERKRAELQPPPEAAGVGAASRDLEKKGAISSNTAATNADC 60

Qy 167 AWLEAQEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLTHSQRQDILDWY 226

Db 61 AWLEAQEEVEGFPVTPQVPLRPMTYKGAALDLSHFLKEKGLGLTHSQRQDILDWY 120

Qy 227 HQGVPDQWNTPGGVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMD 286

Db 121 HQGVPDQWNTPGGVRYPLTFGCYKLVPEPKVEANKGENTSLHPVSLHGMD 180

Qy 287 PEREVLWRFDSRLAFHHVARELHPEYKNC 317

Db 181 PEKVLWRFDSRLAFHHVARELHPEYKDC 211

## RESULT 9

NEF\_HV1A2 ID NEF\_HV1A2 STANDARD; PRT; 208 AA.

NEF\_HV1A2 ID NEF\_HV1A2 STANDARD; PRT; 210 AA.

AC P03407; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Negative factor (F-protein) (27 kDa protein) (3'ORF).

GN NEF.

OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).

OC Viruses; Retrovirdae; Lentivirus.

OX NCBI\_TaxID-11685;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-85090453; PubMed-2578227;

RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,

RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,

RA Levy J.A., Dina D., Luciw P.A.;

RT "Nucleotide sequence and expression of an AIDS-associated retrovirus

RT (ARV-2).";

RL Science 227:484-492(1985).

CC [2]

RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.

RX MEDLINE-88039140; PubMed-3118220;

RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,

RA Montagnier L., Lecocq J.-P.;

RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling

RT an oncogene product.";

RL Nature 330:286-289(1987).

CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING

CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

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CC

DR EMBL; K02007; AAB59883.1; -

DR PIR; A04009; ASLJO2.

DR HSSP; P03406; IEFN.

DR HIV; K02007; NEFSF2.

DR InterPro: IPR001558; F-protein.

DR Pfam; PF00469; F-protein; 1.

KW AIDS; Myristate; GTP-binding.

FT LIPID 2 2 MYRISTATE.

SQ SEQUENCE 210 AA; 24042 MW; ED255233F8A17DAB CRC64;

```

AC P05858;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (RE/HAT isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11701;
RN [1]
RP SEQUENCE FROM N.A.
RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S.,
RA Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
RA Wong-Staal F.;
RL Submitted (XXX-1987) to the HIV data bank.
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -----
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CC -----
DR EMBL; M17451; AAA45058.1;
DR HSP; P03406; IEFN.
DR HIV; M17451; NEFSRF.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 208 AA; 23532 MW; 8F836FE8980F084C CRC64;

Query Match 43.9%; Score 994; DB 1; Length 208;
Best Local Similarity 84.6%; Pred. No. 2.7e-75;
Matches 176; Conservative 16; Mismatches 14; Indels 2; Gaps 1;

QY 112 MGGKWSKSSVVGWPTVR-----ERMRRAPADGVGAASRDLEKKGAISSNTAA 171
DB 1 MGGKWSKSKMGWPAVRERMQAEPADGVGAASRDLEKKGAISSNTAA 171
QY 172 Q--EEEEVGFPVTPQVPLRPMYTKAAVDLSHFLKKGGLGLHSORRODIL 229
DB 61 QEDDEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKKGGLGLHSORRODIL 229
QY 230 GYFPDQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSL 289
DB 121 GYFPDQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSL 289
QY 290 EVLEWRPDSRLAFHVAHRELHPEYKNC 317
DB 181 EYLVNKFDSRLAFHVAHRELHPEYKNC 317

RESULT 11
NEF_HV1Y2
ID NEF_HV1Y2 STANDARD; PRT; 214 AA.
AC P35959;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=36377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93021387; PubMed=1404605;
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,

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RA Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological
RT properties of human immunodeficiency virus type 1 in vivo: evidence
RT for limited defectiveness and complementation.";
RL J. Virol. 66:6587-6600(1992).
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -----
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CC -----
DR EMBL; M93258; -; NOT_ANNOTATED_CDS.
DR PIR; I44001; I44001.
DR HSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 214 AA; 24532 MW; E188D43D7B084D04 CRC64;

Query Match 43.8%; Score 991.5; DB 1; Length 214;
Best Local Similarity 84.2%; Pred. No. 4.5e-75;
Matches 181; Conservative 12; Mismatches 11; Indels 11; Gaps 2;

QY 112 MGGKWSKSSVVGWPTVR-----ERMRRAPADGVGAASRDLEKKGAISSNTAA 161
DB 1 MGGKWSKSKMGWPTVRERMRRAEPADGVGAASRDLEKKGAISSNTAA 161
QY 162 TNAACAMLEAQEEEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKKGGLGLHSORRODIL 221
DB 61 TNAACAMLEAQEEEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKKGGLGLHSORRODIL 221
QY 222 DLWYHTQGYFPDQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSL 281
DB 121 DLWYHTQGYFPDQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSL 281
QY 282 HGMDPPELEWRPDSRLAFHVAHRELHPEYKNC 316
DB 180 HGMDPPELEWRPDSRLAFHVAHRELHPEYKNC 316

RESULT 12
NEF_HV1JR
ID NEF_HV1JR STANDARD; PRT; 216 AA.
AC P20867;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (JRCFS isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen I.S.Y.;
RL Submitted (DEC-1988) to the HIV data bank.
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -----
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CC -----
DR EMBL: M38429; AAB03750.1; -.
DR HSP; P03406; IEFN.
DR HIV; M38429; NEFSJRCFSF.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; Myristate; GTP-binding.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
SQ SEQUENCE 216 AA; 24567 MW; D163FFA8C71529DC CRC64;

Query Match 43.3%; Score 981; DB 1; Length 216;
Best Local Similarity 81.9%; Pred. No. 3.4e-74;
Matches 177; Conservative 15; Mismatches 14; Indels 10; Gaps 1;

QY 112 MGGKWSKSSVGVPTVRMRRAEPAAD-----GVGAASRDLEKHGAITSNTAA 161
DB 1 MGGKWSKSSVGVPTVRMRRAEPAADRVQTEPAAGVAVGAVSRDLEKHGAITSNTAA 60
QY 162 TNAACAWLEAQEEVGPVTPQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSQRQDIL 221
DB 61 TNADCAWLEAYEDEVGPVTPQVPLRPMTYKAAVDLSHFLKEKGLEGLIYSQRQDIL 120
QY 222 DLWIYHTQGYFDPQNYTPGCVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSL 281
DB 121 DLWIYHTQGYFDPQNYTAGCVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSL 180
QY 282 HGMDDPERVLEWRDLSLAFHVAHRELHPEYFKNC 317
DB 181 HGMDDPERVLEWRDLSLAFHVAHRELHPEYFKNC 216

RESULT 13
NEF_HV1S1
ID NEF_HV1S1 STANDARD; PRT; 208 AA.
AC P19546;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL J. Virol. 64:4390-4398(1990).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -----
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CC -----
DR EMBL; M65024; AAA45073.1; -.
DR HSP; P03406; IEFN.
DR HIV; M38428; NEFSF162.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; Myristate; GTP-binding.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
SQ SEQUENCE 208 AA; 23684 MW; A0B1007D14E46E32 CRC64;

Query Match 43.0%; Score 974; DB 1; Length 208;
Best Local Similarity 79.1%; Pred. No. 8.5e-70;
Matches 163; Conservative 24; Mismatches 18; Indels 1; Gaps 1;
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Best Local Similarity 84.2%; Pred. No. 1.2e-73;
Matches 176; Conservative 16; Mismatches 13; Indels 4; Gaps 2;

QY 112 MGGKWSKSSVGVPTVRMR---AEPADGVGAASRDLEKHGAITSNTAATNAACAW 168
DB 1 MGGKWSK-RMSGWSAVRERMKRAEPAEPAADGVGAASRDLEKHGAITSNTAANNADCAW 59
QY 169 LEAQEEVEGPPVTPQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSQRQDILDWIYHT 228
DB 60 LEAQEEDEVGPVTPQVPLRPMTYKAAVDLSHFLKEKGLEGLIYSQRQDILDWIYHT 119
QY 229 QGYFDPQNYTPGCVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPE 288
DB 120 QGYFDPQNYTPGCVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPE 179
QY 289 REVLEWRDLSLAFHVAHRELHPEYFKNC 317
DB 180 KEVLVWRDLSLAFHVAHRELHPEYFKNC 208

RESULT 14
NEF_HV1E1
ID NEF_HV1E1 STANDARD; PRT; 206 AA.
AC P04604;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86245056; PubMed=2424612;
RA Allison M., Wain-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
RT of two isolates from African patients.";
RL Cell 46:63-74(1986).
RN [2]
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
RX MEDLINE=88039140; PubMed=3118220;
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
RA Montagnier L., Lecocq J.-P.;
RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
RT an oncogene product.";
RL Nature 330:266-269(1987).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -----
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CC -----
DR EMBL; K03454; AAA44330.1; -.
DR EMBL; A07108; CAA00617.1; -.
DR HSP; P03406; IEFN.
DR HIV; K03454; NEFSCLI.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; Myristate; GTP-binding.
FT LIPID 2 2 MYRISTATE.
SQ SEQUENCE 206 AA; 23612 MW; 4CFF9F18AEB503C CRC64;

Query Match 41.0%; Score 927.5; DB 1; Length 206;
Best Local Similarity 79.1%; Pred. No. 8.5e-70;
Matches 163; Conservative 24; Mismatches 18; Indels 1; Gaps 1;
```





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QY 231 YPDQNYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPERE 290
Db 121 IFPDQNYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPERQ 180

QY 291 VLEWRDSDRLAFHVAHELHPEYFKNC 317
Db 161 VLMWRNSRLALEKHARELHPEYFKDC 207

RESULT 17
NEF_HV104
ID NEF_HV104 STANDARD; PRT; 205 AA.
AC P24741;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (strain Ugandan / isolate U455)
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11703;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9109081; PubMed=2265025;
RA Oram J.D., Downing R.G., Roff M., Clegg J.C.S., Serwadda D.,
RA Carswell J.W.;
RT "Nucleotide sequence of a Ugandan HIV-1 provirus reveals genetic
RT diversity from other HIV-1 isolates.";
RL AIDS Res. Hum. Retroviruses 6:1073-1078 (1990).
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -----
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CC -----
DR EMBL; M62320; AAA75023.1; -
DR HSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 205 AA; 23253 MW; 869AB03E6E7893C4 CRC64;

Query Match 38.5%; Score 872; DB 1; Length 205;
Best Local Similarity 75.18; Pred. No. 3.4e-65;
Matches 154; Conservative 24; Mismatches 27; Indels 0; Gaps 0;

QY 112 MGGKWSKSVVGVPTVRMRRAEPAADGVAASRDLEKHGALTSSNTAATNAACAWLEA 171
Db 1 MGGKWSKSRVPEVRKMRMTPTAAAGVAVSODLDKYGAVTSSNTASCAWLEA 60

QY 172 QEEVEVGFPVTPQVPLRPMYKAAVDLSHFLKEGGLIHSQRQDILDLYIHTQGY 231
Db 61 QEEGVGFPVTPQVPLRPMYKAAVDLSHFLKEGGLIHSQRQDILDLYIHTQGF 120

QY 232 FPDQNYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPEREV 291
Db 121 FPDQNYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPEREV 180

QY 292 LEWRDSDRLAFHVAHELHPEYFKN 316
Db 161 LMKFDSTLALKHARELHPEYFKD 205

RESULT 18
NEF_HV104

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ID NEF_HV104 STANDARD; PRT; 182 AA.
AC P05856;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11696;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536 (1988).
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
CC PATIENT IN 1984.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M17449; AAA44858.1; -
DR HSP; P03406; IEFN.
DR HIV; M17449; NEFSMN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; Myristate; GTP-binding.
FT LIPID 2
SQ SEQUENCE 182 AA; 20632 MW; 2C5B5A6E3EF13B26 CRC64;

Query Match 37.2%; Score 842; DB 1; Length 182;
Best Local Similarity 87.4%; Pred. No. 8.8e-63;
Matches 153; Conservative 11; Mismatches 7; Indels 4; Gaps 2;

QY 112 MGGKWSKSVVGVPTVRMRRAEPAADGVAASRDLEKHGALTSSNTAATNAACAW 168
Db 1 MGGKWSK-RVTGWPVTRMRRAEPAADGVAASRDLEKHGALTSSNTAATNAACAW 59

QY 169 LEAQEEVEVGFPVTPQVPLRPMYKAAVDLSHFLKEGGLIHSQRQDILDLYIHT 228
Db 60 LEAQEEVEVGFPVTPQVPLRPMYKAAVDLSHFLKEGGLIHSQRQDILDLYIHT 119

QY 229 QGYFPDQNYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHG 283
Db 120 QGYFPDQNYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHG 174

RESULT 19
NEF_HV12H
ID NEF_HV12H STANDARD; PRT; 205 AA.
AC P05859;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (Zaire H2321 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11692;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8922766; PubMed=2713163;
RA Srinivasan A., York D., Butler D. Jr., Jannoun-Nasr R., Getchell J.,

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RA McCormick J., Ou C.Y., Myers G., Smith T., Chen E.;  
 RT "Molecular characterization of HIV-1 isolated from a serum collected  
 in 1976: nucleotide sequence comparison to recent isolates and  
 generation of hybrid HIV-1";  
 RL AIDS Res. Hum. Retroviruses 5:121-129(1989).  
 CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 CC -----  
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 CC -----  
 DR EMBL; M15896; AAB53951.1; -;  
 DR PIR; B44963; B44963.  
 DR HSP; P03406; IEFN.  
 DR HIV; M15896; NEFS2321.  
 DR InterPro; IPR001558; F-protein.  
 DR Pfam; PF00469; F-protein; 1.  
 DR AIDS; Myristate; GTP-binding.  
 KW AIDS; Myristate; GTP-binding.  
 FT LIPID 2 MYRISTATE.  
 SQ SEQUENCE 205 AA; 23306 MW; EA55B18AF412A9D0 CRC64;

Query Match 37.08; Score 837; DB 1; Length 205;  
 Best Local Similarity 73.29; Pred. No. 2,7e-62;  
 Matches 153; Conservative 23; Mismatches 25; Indels 8; Gaps 3;

QY 112 MGGKWSKSSVVGWPTVRERMR---AEPADGVGAASRDLEKHAITSNTAATNAACAW 168  
 DB 1 MGNKWSK----GWPAVRERIRHTPPAPPAEGVGAASQDLAKHGAISSNTATNPDCAW 56  
 QY 169 LEAQEEVEGVFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGEGLIHSORRODILDLWIYH 227  
 DB 57 LEAQEESEVGVFPVTPQVPLRPMTYKGAFLDLSFLKEKGLDGLIYSKKREILDWLVIYH 116  
 QY 228 TQGFPPDMQNTPGGVRYPTTFGCYKLVPEVDKVEEANKGENTSLHLVPSVLHGMDP 287  
 DB 117 TQGFPPDMQNTPGGVRYPTTFGCYKLVPEVDKVEEANKGENTSLHLVPSVLHGMDP 176  
 QY 288 EREVLEWRFSRLAFHFAHRELHPEYKNC 316  
 DB 177 EREVLMWAFDSSLARKHLAREHPEYKNC 205

RESULT 20  
 NEF\_HV1MA  
 ID NEF\_HV1MA STANDARD; PRT; 209 AA.  
 AC P04603;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
 GN NEF.  
 OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11697;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86245056; PubMed=2424612;  
 RA Allison M., Wain-Hobson S., Montagnier L., Sonigo P.;  
 RT "Genetic variability of the AIDS virus: nucleotide sequence analysis  
 of two isolates from African patients";  
 RL Cell 46:63-74(1986).  
 RN [2]  
 RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.  
 RX MEDLINE=88039140; PubMed=3118220;  
 RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,  
 RA Montagnier L., Lecocq J.-P.;  
 RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling

an oncogene product.";  
 RT Nature 330:266-269(1987).  
 CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 CC -----  
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 CC -----  
 DR EMBL; X04415; CAA28017.1; -;  
 DR EMBL; A07116; CAA00624.1; -;  
 DR HSP; P03406; IEFN.  
 DR HIV; K03456; NEFSMAL.  
 DR InterPro; IPR001558; F-protein.  
 DR Pfam; PF00469; F-protein; 1.  
 DR AIDS; Myristate; GTP-binding.  
 KW AIDS; Myristate; GTP-binding.  
 FT LIPID 2 MYRISTATE.  
 SQ SEQUENCE 209 AA; 23644 MW; DOB30A2442C8CC44 CRC64;

Query Match 36.98; Score 834.5; DB 1; Length 209;  
 Best Local Similarity 70.18; Pred. No. 4.4e-62;  
 Matches 148; Conservative 26; Mismatches 30; Indels 7; Gaps 2;

QY 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVG-----AASRDLEKHAITSNTAATNAAC 166  
 DB 1 MGGKWSKSSVVGWPTVRERIRIRPTTGTGCGAVSQDVSQDLKCGAASSPPANNASC 60  
 QY 167 AWLEAQEEVEGVFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGEGLIHSORRODILDLWIY 226  
 DB 61 E-PPEEEVEGVFPVTPQVPLRPMTYKGAFLDLSFLKEKGLDGLVWSPKREILDWLVIY 118  
 QY 227 HTQGYFDMQNTPGGVRYPTTFGCYKLVPEVDKVEEANKGENTSLHLVPSVLHGMD 286  
 DB 119 HTQGYFDMQNTPGGVRYPTTFGCYKLVPEVDKVEEANKGENTSLHLVPSVLHGMD 178  
 QY 287 PEREVLEWRFSRLAFHFAHRELHPEYKNC 317  
 DB 179 AEREVLWKFDSLSALRHAREHPEYKNC 209

RESULT 21  
 NEF\_SIVCZ  
 ID NEF\_SIVCZ STANDARD; PRT; 205 AA.  
 AC P17664;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
 GN NEF.  
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11723;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90259077; PubMed=2188136;  
 RA Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;  
 RT "Genetic variability of a chimpanzee lentivirus related to HIV-1";  
 RL Nature 345:356-359(1990).  
 CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 CC -----  
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 CC -----

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CC ----- X52154; CAA36408.1; -
DR PIR: S09991; ASLJIK.
DR HSP: P03406; IEFN.
DR HIV: X52154; NEFSCP.
DR InterPro: IPR001558; F-protein.
DR Pfam: PF00469; F-protein; 1.
DR KW AIDS: Myristate; GTP-binding.
DR LIPID 2
SQ SEQUENCE 205 AA; 23850 MW; 21E0A3EC99F1811F CRC64;

Query Match 36.7%; Score 832; DB 1; Length 205;
Best Local Similarity 70.2%; Pred. No. 6.9e-62;
Matches 144; Conservative 27; Mismatches 34; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRERMRRAEPAADVGGAASRDLEKKGAISSNTAATNAACAWLEA 171
Db 1 MGTWKSLSLVGPEVRRIRREAPTAAGVGEVSKDLERHGAITSRNPETNOTLAWLEE 60
Qy 172 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDLYIHTQGY 231
Db 61 MDNEEVGFPVRQVPTVRPMYKAAFDLSHFLKEKGLGSLVSRQRDILDLYIHTQGF 120
Qy 232 FPDQNYTGPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDLYIHTQGY 291
Db 121 FPDQNYTGTGCTPLCGFCWCKLVPTEQVEQANEGDNNCLLHPICQHGMEDEKVEV 180
Qy 292 LEWREDSRLAFHHVARELHPEYFKN 316
Db 181 LWREDSRLALRHIAREQHPEYKD 205

RESULT 22
NEF_HV1SC STANDARD; PRT; 239 AA.
ID NEF_HV1SC
AC P03657;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgu C., Guo H.-G., Franchini G., Aldovini G., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
FT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -!- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
CC 1984 IN SOUTHERN CALIFORNIA.
CC -----
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CC -----
DR EMBL: M17450; AAA45064.1; -
DR HSP: P03406; IEFN.
DR HIV: M17450; NEFSSC.
DR InterPro: IPR001558; F-protein.
DR Pfam: PF00469; F-protein; 1.
DR KW AIDS: Myristate; GTP-binding.
DR LIPID 2
SQ SEQUENCE 239 AA; 26799 MW; 70AA17E54763A99B CRC64;

-----
Query Match 36.2%; Score 819; DB 1; Length 239;
Best Local Similarity 75.5%; Pred. No. 1e-60;
Matches 157; Conservative 16; Mismatches 31; Indels 4; Gaps 2;

Qy 112 MGGKWSKSSVVGWPTVRERMRRAEPAADVGGAASRDLEKKGAISSNTAATNAACAWLEA 171
Db 1 MGGKWSKSSVVGWPTVRERMRRAEPAADVGGAASRDLEKKGAISSNTAATNAACAWLEA 60
Qy 172 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDLYIHTQGY 231
Db 61 QEEVEVGFPVRQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDLYIHTQGY 118
Qy 232 FPDQNYT--PDQVGYPLTGTGWCYKLVPEPDKVEBANKGENTSLHLPVSLHGMDDPER 289
Db 119 ATSLIGRTTHGQSGDIPLCFCWCKLVPKPEKTEENEGENNSLLHPSLHGMDDPER 178
Qy 290 EVLEWRFDLSRLAFHHVARELHPEYFKN 317
Db 179 EVLEWRFDLSRLAFHHVARELHPEYKDC 206

RESULT 23
NEF_HV1H2 STANDARD; PRT; 123 AA.
ID NEF_HV1H2
AC P04601; O09780;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
FT "Complete nucleotide sequences of functional clones of the AIDS
RT virus.";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]
RP REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
RX MEDLINE=88039140; PubMed=3118220;
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
RA Montagnier L., Lecocq J.-P.;
FT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
RT an oncogene product.";
RL Nature 330:266-269(1987).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -!- MISCELLANEOUS: IN THIS ISOLATE A MUTATION IN POSITION 124 ADDS A
CC STOP CODON AND THE PROTEIN IS MUCH SHORTER THAN IN OTHER ISOLATES
CC (210 AA).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: K03455; AAB50263.1; -
DR EMBL: AF033819; AAC82597.1; -
DR HSP: Q70627; 2NEF.
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```
CC ----- X52154; CAA36408.1; -
DR PIR: S09991; ASLJIK.
DR HSP: P03406; IEFN.
DR HIV: X52154; NEFSCP.
DR InterPro: IPR001558; F-protein.
DR Pfam: PF00469; F-protein; 1.
DR KW AIDS: Myristate; Gtp-binding.
DR LIPID 2
SQ SEQUENCE 205 AA; 23850 MW; 21E0A3EC99F1811F CRC64;

Query Match 36.7%; Score 832; DB 1; Length 205;
Best Local Similarity 70.2%; Pred. No. 6.9e-62;
Matches 144; Conservative 27; Mismatches 34; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRERMRRAEPAADVGGAASRDLEKKGAISSNTAATNAACAWLEA 171
Db 1 MGTWKSLSLVGPEVRRIRREAPTAAGVGEVSKDLERHGAITSRNPETNOTLAWLEE 60
Qy 172 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDLYIHTQGY 231
Db 61 MDNEEVGFPVRQVPTVRPMYKAAFDLSHFLKEKGLGSLVSRQRDILDLYIHTQGF 120
Qy 232 FPDQNYTGPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDLYIHTQGY 291
Db 121 FPDQNYTGTGCTPLCGFCWCKLVPTEQVEQANEGDNNCLLHPICQHGMEDEKVEV 180
Qy 292 LEWREDSRLAFHHVARELHPEYFKN 316
Db 181 LWREDSRLALRHIAREQHPEYKD 205

RESULT 22
NEF_HV1SC STANDARD; PRT; 239 AA.
ID NEF_HV1SC
AC P03657;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgu C., Guo H.-G., Franchini G., Aldovini G., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
FT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -!- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
CC 1984 IN SOUTHERN CALIFORNIA.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M17450; AAA45064.1; -
DR HSP: P03406; IEFN.
DR HIV: M17450; NEFSSC.
DR InterPro: IPR001558; F-protein.
DR Pfam: PF00469; F-protein; 1.
DR KW AIDS: Myristate; GTP-binding.
DR LIPID 2
SQ SEQUENCE 239 AA; 26799 MW; 70AA17E54763A99B CRC64;

-----
Query Match 36.2%; Score 819; DB 1; Length 239;
Best Local Similarity 75.5%; Pred. No. 1e-60;
Matches 157; Conservative 16; Mismatches 31; Indels 4; Gaps 2;

Qy 112 MGGKWSKSSVVGWPTVRERMRRAEPAADVGGAASRDLEKKGAISSNTAATNAACAWLEA 171
Db 1 MGGKWSKSSVVGWPTVRERMRRAEPAADVGGAASRDLEKKGAISSNTAATNAACAWLEA 60
Qy 172 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDLYIHTQGY 231
Db 61 QEEVEVGFPVRQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDLYIHTQGY 118
Qy 232 FPDQNYT--PDQVGYPLTGTGWCYKLVPEPDKVEBANKGENTSLHLPVSLHGMDDPER 289
Db 119 ATSLIGRTTHGQSGDIPLCFCWCKLVPKPEKTEENEGENNSLLHPSLHGMDDPER 178
Qy 290 EVLEWRFDLSRLAFHHVARELHPEYFKN 317
Db 179 EVLEWRFDLSRLAFHHVARELHPEYKDC 206

RESULT 23
NEF_HV1H2 STANDARD; PRT; 123 AA.
ID NEF_HV1H2
AC P04601; O09780;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
FT "Complete nucleotide sequences of functional clones of the AIDS
RT virus.";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]
RP REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
RX MEDLINE=88039140; PubMed=3118220;
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
RA Montagnier L., Lecocq J.-P.;
FT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
RT an oncogene product.";
RL Nature 330:266-269(1987).
CC -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
CC -!- MISCELLANEOUS: IN THIS ISOLATE A MUTATION IN POSITION 124 ADDS A
CC STOP CODON AND THE PROTEIN IS MUCH SHORTER THAN IN OTHER ISOLATES
CC (210 AA).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: K03455; AAB50263.1; -
DR EMBL: AF033819; AAC82597.1; -
DR HSP: Q70627; 2NEF.
```

DR HIV: K03455; NEFSXB2.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; Myristate; GTP-binding; Phosphorylation.  
FT LIPID 2 MYRISTATE.  
FT MOD\_RES 15 15 PHOSPHORYLATION (BY PKC).  
SQ SEQUENCE 123 AA; 13692 MW; B5007753CCD244CF CRC64;

Query Match 28.5%; Score 645; DB 1; Length 123;  
Best Local Similarity 98.4%; Pred. No. 1.1e-46;  
Matches 121; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 112 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGALTSNTAATNACAWLEA 171  
Db 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGALTSNTAATNACAWLEA 60  
QY 172 QEEVEVGFVPTQVPLRPMTYKAAVDLSHFLKKGGLGSLHSORRODILDLYIHTQGY 231  
Db 61 QEEVEVGFVPTQVPLRPMTYKAAVDLSHFLKKGGLGSLHSORRODILDLYIHTQGY 120  
QY 232 FPD 234  
Db 121 FPD 123

RESULT 24  
NEF\_HV1B1  
ID NEF\_HV1B1 STANDARD; PRT; 123 AA.  
AC P03404;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).  
GN NEF.  
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11678;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8511123; PubMed=2578615;  
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,  
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,  
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,  
RA Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,  
RA Wong-Staal F.;  
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";  
RL Nature 313:277-284(1985).  
RN [2]  
RP POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.  
RX MEDLINE=88039140; PubMed=3118220;  
RA Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,  
RA Montagnier L., Lecocq J.-P.;  
RT "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling  
RT an oncogene product.";  
RL Nature 330:266-269(1987).  
CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
CC -1- MISCELLANEOUS: IN THIS ISOLATE A MUTATION IN POSITION 124 ADDS A  
CC STOP CODON AND THE PROTEIN IS MUCH SHORTER THAN IN OTHER ISOLATES  
CC (210 AA).  
CC -----  
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CC -----  
CC EMBL: M15654; AAA44206.1; -.  
CC PIR: A04005; ASLJH3.  
CC HSSP: Q70627; 2NEF.  
DR

DR HIV: M15654; NEFSBH102.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; Myristate; GTP-binding.  
FT LIPID 2 MYRISTATE.  
SQ SEQUENCE 123 AA; 13606 MW; 0811735345F0EB8B CRC64;

Query Match 28.2%; Score 638; DB 1; Length 123;  
Best Local Similarity 97.8%; Pred. No. 4.2e-46;  
Matches 120; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 112 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGALTSNTAATNACAWLEA 171  
Db 1 MGGKWSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKKGALTSNTAATNACAWLEA 60  
QY 172 QEEVEVGFVPTQVPLRPMTYKAAVDLSHFLKKGGLGSLHSORRODILDLYIHTQGY 231  
Db 61 QEEVEVGFVPTQVPLRPMTYKAAVDLSHFLKKGGLGSLHSORRODILDLYIHTQGY 120  
QY 232 FPD 234  
Db 121 FPD 123

RESULT 25  
GLPQ\_HAEIN  
ID GLPQ\_HAEIN STANDARD; PRT; 364 AA.  
AC Q06282;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Glycophosphoryl diester phosphodiesterase precursor (EC 3.1.4.46)  
DE (Glycophosphodiester phosphodiesterase) (Surface-exposed lipoprotein  
DE D) (Protein D) (Immunoglobulin D-binding protein) (IGD-binding  
DE protein).  
GN GLPQ OR HPD OR HI0689.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=RD / KW20 / ATCC 51907;  
RX MEDLINE=95350630; PubMed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kierlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
RA Uterback T.R., Hanna M.C., Spriggs T., Saudek D.M., Brandon R.C.,  
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus  
RT influenzae Rd.";  
RL Science 269:496-512(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=NTHI 772;  
RX MEDLINE=91099948; PubMed=1987023;  
RA Janson H., Heden L.-O., Grubb A., Ruan M., Forsgren A.;  
RT "Protein D, an immunoglobulin D-binding protein of haemophilus  
RT influenzae: cloning, nucleotide sequence, and expression in  
RT Escherichia coli.";  
RL Infect. Immun. 59:119-125(1991).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX STRAIN=MINNA / SEROTYPE B;  
RX MEDLINE=94011360; PubMed=8104899;  
RA Janson H., Ruan M., Forsgren A.;  
RT "Limited diversity of the protein D gene (hpd) among encapsulated and  
RT nonencapsulated Haemophilus influenzae strains.";

RL Infect. Immun. 61:4546-4552(1993).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-EAGAN, 3639, 3640, NCTC 8468, 6-7626, AND HK695;  
 RX MEDLINE=95122210; PubMed=7822043;  
 RA Song X.-M., Forsgren A., Janson H.;  
 RT "The gene encoding protein D (hpd) is highly conserved among  
 Haemophilus influenzae type b and nontypeable strains.";  
 RL Infect. Immun. 63:696-699(1995).  
 RN [5]  
 RP CHARACTERIZATION.  
 RC STRAIN-NTHI 772;  
 RX MEDLINE=92192801; PubMed=1548059;  
 RA Janson H., Heden L.-O., Forsgren A.;  
 RT "Protein D, the immunoglobulin D-binding protein of Haemophilus  
 influenzae, is a lipoprotein.";  
 RL Infect. Immun. 60:1336-1342(1992).  
 CC -1- FUNCTION: GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE HYDROLYZES  
 DEACETYLATED PHOSPHOLIPIDS TO G3P AND THE CORRESPONDING ALCOHOLS.  
 CC HAS A SPECIFIC AFFINITY FOR HUMAN IMMUNOGLOBULIN D MYELOMA  
 CC PROTEIN.  
 CC -1- CATALYTIC ACTIVITY: A glycerophosphodiester + H(2)O -> an alcohol +  
 sn-glycerol 3-phosphate.  
 CC -1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid  
 anchor.  
 CC -1- PTM: CONTAINS BOTH ESTER- AND AMIDE-LINKED FATTY ACIDS.  
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAINS NTHI 772 AND  
 RD / KW20.  
 CC -1- SIMILARITY: TO E.COLI AND B.SUBTILIS GLPQ.  
 CC -----  
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 CC -----  
 DR EMBL; U32751; AAC22348.1; -  
 DR EMBL; M37487; AAA24998.1; -  
 DR EMBL; L12445; AAA24999.1; -  
 DR EMBL; Z35656; CAA84715.1; -  
 DR EMBL; Z35657; CAA84716.1; -  
 DR EMBL; Z35658; CAA84717.1; -  
 DR EMBL; Z35659; CAA84718.1; -  
 DR EMBL; Z35660; CAA84719.1; -  
 DR EMBL; Z35661; CAA84720.1; -  
 DR TIGR; H10689; -  
 DR InterPro; IPR004129; GDDP.  
 DR Pfam; PF03009; GDDP; 1.  
 DR PROSITE; PS00013; PROKARYOTIC LIPOPROTEIN; 1.  
 KW Glycerol metabolism; Hydrolase; Signal; Lipoprotein; Outer membrane;  
 KW Complete proteome.  
 FT SIGNAL 1 18  
 FT CHAIN 19 364  
 FT  
 FT GLYCEROPHOSPHORYL DIESTER  
 FT PHOSPHODIESTERASE.  
 FT N-ACYL DIGLYCERIDE.  
 FT A -> T (IN STRAIN NCTC 8468).  
 FT L -> V (IN STRAIN NCTC 8468).  
 FT N -> S (IN STRAIN NCTC 8468).  
 FT N -> K (IN STRAIN 6-7626).  
 FT D -> H (IN STRAIN NCTC 8468).  
 FT H -> Q (IN STRAINS EAGAN; 3639; 3640;  
 6-7626; HK695; MINNA).  
 FT S -> A (IN STRAINS EAGAN; 3639; 3640;  
 NCTC 8468; 6-7626; HK695; MINNA).  
 FT Y -> H (IN STRAINS EAGAN; 3639; 3640;  
 NCTC 8468; 6-7626; HK695; MINNA).  
 FT R -> H (IN STRAIN NCTC 8468).  
 FT K -> Q (IN STRAIN 6-7626).  
 FT T -> R (IN STRAIN 6-7626).  
 FT K -> A (IN STRAINS EAGAN; 3639; 3640;  
 NCTC 8468; 6-7626; HK695; MINNA).  
 FT

FT VARIANT 253 253 P -> S (IN STRAIN 6-7625).  
 FT VARIANT 310 310 Q -> K (IN STRAINS EAGAN; 3639; NCTC  
 FT VARIANT 327 327 E -> A (IN STRAINS EAGAN; 3639; NCTC  
 FT VARIANT 338 338 8468; 6-7626; HK695; MINNA).  
 FT VARIANT 364 364 A -> V (IN STRAINS EAGAN; 3640; HK695;  
 FT VARIANT 364 364 MINNA).  
 FT VARIANT 364 364 K -> E (IN STRAIN 6-7626).  
 SQ SEQUENCE 364 AA; 41902 MW; A6079B3ABF70E820 CRC64;  
 Query Match 24.4%; Score 553.5; DB 1; Length 364;  
 Best Local Similarity 45.9%; Pred. No. 1.7e-38;  
 Matches 141; Conservative 21; Mismatches 72; Indels 73; Gaps 11;  
 QY 4 SSSHSNANTOMKSDKIIIIHRAHGASGYLPHTLESKALAFQAQADYLEQDLAMTKDGRLV 63  
 DB 20 SSSHSNANTOMKSDKIIIIHRAHGASGYLPHTLESKALAFQAQADYLEQDLAMTKDGRLV 79  
 QY 64 VIHDFLDGLTDVAKKPHRHRKDGRIYVDFTLKEIQSLEMTENFETMGK----- 115  
 DB 80 VIHDFLDGLTDVAKKPHRHRKDGRIYVDFTLKEIQSLEMTENFETMGKQQAQVYVNR 139  
 QY 116 ---W-----SKSVVG-WPTVRMRRAEPAADGVGAASRDLEK 150  
 DB 140 FPLKSHFRIHTEFEDETEFIQGLEKSTGKVGIVPEIKAPWFHQNGKDIAETLKVLLK 199  
 QY 151 HGATSSNTAATNACAWLEAQEEVEGFPVTPQVPLRPPTYKAANDLSHFLKEKGGLEG 210  
 DB 200 GYDKKTD-----WVYLTDFNELKRIKTELQPMQMDLK-LVQLIATYDMK----- 246  
 QY 211 LIHSORQDILDLYHTQGYFPDQW-----NVTGPGVRYPLTFGWCYKLVPE 260  
 DB 247 ---ETQEKDPKGYWV---NINYDMFKPGMAEVVYADGVGP-----GW-YALVYK 292  
 QY 261 ---PDV 264  
 DB 293 ESKPDNI 299  
 RESULT 26  
 TAT\_HVIB1  
 ID TAT\_HVIB1 STANDARD; PRT; 86 AA.  
 AC P04606;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE TAT protein (Transactivating regulatory protein).  
 GN TAT.  
 OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1), and  
 OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OC NCBI\_TaxID=11678, 11707;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ISOLATE BH10;  
 RX MEDLINE=85111123; PubMed=2578615;  
 RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,  
 RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,  
 RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,  
 RA Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C.,  
 RA Wong-Staal F.;  
 RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";  
 RL Nature 313:277-284(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ISOLATE HXB3;  
 RX MEDLINE=85228248; PubMed=2988795;  
 RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,  
 RA Shaw G.M., Wong-Staal F., Reddy E.P.;  
 RT "HTLV-III env gene products synthesized in E. coli are recognized by  
 antibodies present in the sera of AIDS patients.";  
 RL Cell 41:979-986(1985).  
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE

```
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -!- MISCELLANEOUS: THE TWO ISOLATES TAT SEQUENCE ARE IDENTICAL.
CC -----
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CC -----
CC EMBL; M14100; AAA44676.1; -
CC EMBL; M15654; TAT$BH102.
CC HIV; M14100; TAT$HBX3.
CC InterPro: IPR001831; HIV_Tat.
CC Pfam; PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC SEQUENCE 86 AA; 9784 MW; 4DD609415FAF9015 CRC64;
CC -----
CC Query Match 21.5%; Score 486; DB 1; Length 86;
CC Best Local Similarity 100.0%; Pred. No. 1e-33;
CC Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
QY 320 EPVDPRLPEPKHGPSQPKTACTNCYKCCFHCQVCFTKALGISYGRKKRRRPPQG 379
DB 2 EPVDPRLPEPKHGPSQPKTACTNCYKCCFHCQVCFTKALGISYGRKKRRRPPQG 61
QY 380 SOTHQVLSKQPTSQSRGDPGPK 404
DB 62 SOTHQVLSKQPTSQSRGDPGPK 86
CC -----
RESULT 27
TAT_HV1P
ID TAT_HV1P STANDARD; PRT; 86 AA.
AC P04607;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11700;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511157; PubMed=2982104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
RT AIDS/lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
QY 320 EPVDPRLPEPKHGPSQPKTACTNCYKCCFHCQVCFTKALGISYGRKKRRRPPQG 379
DB 2 EPVDPRLPEPKHGPSQPKTACTNCYKCCFHCQVCFTKALGISYGRKKRRRPPQG 61
QY 380 SOTHQVLSKQPTSQSRGDPGPK 404
DB 62 SOTHQVLSKQPTSQSRGDPGPK 86
CC -----
RESULT 28
TAT_HV112
ID TAT_HV112 STANDARD; PRT; 86 AA.
AC P04326;
DT 20-MAR-1987 (Rel. 04, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (clone 12) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11679;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177573; PubMed=3008154;
RA Arya S.K., Gallo R.C.;
RT "Three novel genes of human T-lymphotropic virus type III: immune
RT reactivity of their products with sera from acquired immune
RT deficiency syndrome patients.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M11840; AAA44999.1; -
CC PIR; A04017; TNLJ12.
CC HIV; M11840; TAT$PCV12.
CC InterPro: IPR001831; HIV_Tat.
CC Pfam; PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC SEQUENCE 86 AA; 9758 MW; 4DD609414FBE9115 CRC64;
CC -----
CC Query Match 21.1%; Score 478; DB 1; Length 86;
```

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K02083; AAB59870.1; -
CC EMBL; X01762; -; NOT_ANNOTATED_CDS.
CC HIV; K02083; TAT$SPV2.
CC InterPro: IPR001831; HIV_Tat.
CC Pfam; PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC SEQUENCE 86 AA; 9794 MW; 4DD5C6415FAF9015 CRC64;
CC -----
CC Query Match 21.2%; Score 481; DB 1; Length 86;
CC Best Local Similarity 98.8%; Pred. No. 2.7e-33;
CC Matches 84; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC -----
QY 320 EPVDPRLPEPKHGPSQPKTACTNCYKCCFHCQVCFTKALGISYGRKKRRRPPQG 379
DB 2 EPVDPRLPEPKHGPSQPKTACTNCYKCCFHCQVCFTKALGISYGRKKRRRPPQG 61
QY 380 SOTHQVLSKQPTSQSRGDPGPK 404
DB 62 SOTHQVLSKQPTSQSRGDPGPK 86
CC -----
RESULT 28
TAT_HV112
ID TAT_HV112 STANDARD; PRT; 86 AA.
AC P04326;
DT 20-MAR-1987 (Rel. 04, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (clone 12) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11679;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177573; PubMed=3008154;
RA Arya S.K., Gallo R.C.;
RT "Three novel genes of human T-lymphotropic virus type III: immune
RT reactivity of their products with sera from acquired immune
RT deficiency syndrome patients.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M11840; AAA44999.1; -
CC PIR; A04017; TNLJ12.
CC HIV; M11840; TAT$PCV12.
CC InterPro: IPR001831; HIV_Tat.
CC Pfam; PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC SEQUENCE 86 AA; 9758 MW; 4DD609414FBE9115 CRC64;
CC -----
CC Query Match 21.1%; Score 478; DB 1; Length 86;
```



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 08:14:56 ; Search time 86.53 Seconds  
(without alignments)  
825.689 Million cell updates/sec

Title: US-09-509-239-21

Perfect score: 2264

Sequence: 1 MDPSSSHSNMANTQMSDKI.....QSRGDTGPKETSGHHHHH 413

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1129	49.9	206	15 Q9WM24	Q9wm24 human immun
2	1124	49.6	206	15 Q9WLM4	Q9wlm4 human immun
3	1119	49.4	206	15 O40177	O40177 human immun
4	1115	49.2	206	15 Q90VU7	Q90vu7 human immun
5	1108	48.9	206	15 Q9PW9	Q9pxw9 human immun
6	1105	48.8	206	15 Q9WM16	Q9wm16 human immun
7	1104	48.8	206	15 Q9WM30	Q9wm30 human immun
8	1101	48.6	206	15 Q9PW8	Q9pxw8 human immun
9	1096	48.4	206	15 Q90179	Q90179 human immun
10	1096	48.4	206	15 Q85588	Q85588 aids-associ
11	1096	48.4	206	15 Q78244	Q78244 human immun
12	1092	48.2	206	15 Q9WLM7	Q9wlm7 human immun
13	1090	48.1	206	15 Q74905	Q74905 human immun
14	1087	48.0	206	15 Q89561	Q89561 human immun
15	1085	47.9	206	15 Q74913	Q74913 human immun
16	1080	47.7	206	15 Q74917	Q74917 human immun

17	1079	47.7	206	15 Q74914	Q74914 human immun
18	1079	47.7	206	15 Q74915	Q74915 human immun
19	1077	47.6	206	15 Q74909	Q74909 human immun
20	1076	47.5	202	15 Q9QPN3	Q9qpn3 human immun
21	1072	47.3	206	15 Q9Q596	Q9q596 human immun
22	1072	47.3	206	15 Q9Q595	Q9q595 human immun
23	1071	47.3	208	15 Q9YU9	Q9yvu9 human immun
24	1068	47.2	206	15 Q9W7X3	Q9w7x3 human immun
25	1065	47.0	206	15 Q9DQ01	Q9dqu1 human immun
26	1064	47.0	206	15 Q9W7U0	Q9w7u0 human immun
27	1062	46.9	206	15 Q93010	Q93010 human immun
28	1061	46.9	206	15 Q93012	Q93012 human immun
29	1060	46.8	206	15 Q9Q597	Q9q597 human immun
30	1057	46.7	206	15 Q9W7X2	Q9w7x2 human immun
31	1054	46.6	206	15 Q9Q594	Q9q594 human immun
32	1053	46.5	206	15 Q9Q5A3	Q9q5a3 human immun
33	1053	46.5	206	15 Q9DQ09	Q9dqt9 human immun
34	1052	46.5	205	15 Q74823	Q74823 human immun
35	1051	46.4	206	15 Q74824	Q74824 human immun
36	1050	46.4	206	15 Q9QRD5	Q9qrd5 human immun
37	1050	46.4	206	15 Q9Q599	Q9q599 human immun
38	1049	46.3	206	15 Q89630	Q89630 human immun
39	1049	46.3	206	15 Q71956	Q71956 human immun
40	1048	46.3	206	15 Q9Q5A8	Q9q5a8 human immun
41	1048	46.3	206	15 Q72421	Q72421 human immun
42	1047	46.2	206	15 Q89537	Q89537 human immun
43	1047	46.2	206	15 Q9Q5D3	Q9q5d3 human immun
44	1047	46.2	206	15 Q72985	Q72985 human immun
45	1047	46.2	210	15 P90275	P90275 human immun

#### ALIGNMENTS

RESULT 1

Q9WM24  
ID Q9WM24 PRELIMINARY; PRT; 206 AA.  
AC Q9WM24;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=12-IT;  
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,  
RA Johansson B., Vahine A., Sonnerborg A.;  
RT "Hiv-1 nef mutations and clinical long-term non progression: a  
RT molecular epidemiology study";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL; AF011480; AAD01458.1;  
DR HSSP; P03406; 1EFN.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23328 MW; FCC69458158F1A03 CRC64;

Query Match 49.9%; Score 1129; DB 15; Length 206;  
Best Local Similarity 99.5%; Pred. No. 3,6e-83;  
Matches 205; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 112 MGGKWSKSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 171  
|||||  
Db 1 MGGKWSKSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60

QY 172 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLAEKGLGLELIHSQRQDILDLIWIHTQCY 231



|||||  
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSHSRRQDILDLWIYHTGY 120  
Qy 232 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 291  
Db 121 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 180  
Qy 292 LEWRDLSRLAFHHVARELHPEYFNC 317  
Db 181 LEWRDLSRLAFHHVARELHPEYFNC 206

RESULT 2  
Q9WLM4  
ID Q9WLM4 PRELIMINARY; PRT; 206 AA.  
AC Q9WLM4  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=21-SW;  
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,  
RA Johansson B., Wahine A., Sonnerborg A.;  
RT "HIV-1 nef mutations and clinical long-term non progression: a  
RT molecular epidemiology study";  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4 (T4) ANTIGEN.  
DR EMBL; AF047087; AAD02461.1; -;  
DR HSP; P03406; IEFN.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
DR AIDS; GTP-binding; Myristate.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23341 MW; FCD22B1CEB655BB9 CRC64;

Query Match 49.6%; Score 1124; DB 15; Length 206;  
Best Local Similarity 99.0%; Pred. No. 9.2e-83;  
Matches 204; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVAASRDLEKKGAISSNTAANAACAWLEA 171  
Db 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVAASRDLEKKGAISSNTAANAACAWLEA 60  
Qy 172 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSHSRRQDILDLWIYHTGY 231  
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSHSRRQDILDLWIYHTGY 120  
Qy 232 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 291  
Db 121 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 180  
Qy 292 LEWRDLSRLAFHHVARELHPEYFNC 317  
Db 181 LEWRDLSRLAFHHVARELHPEYFNC 206

RESULT 3  
O40177  
ID O40177 PRELIMINARY; PRT; 206 AA.  
AC O40177  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PNL4-3;  
RA Fang G., Weiser B., Visosky A., Burger H.;  
RT "Constructing full-length chimeric HIV-1 molecular clones by PCR-  
RT mediated recombination";  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4 (T4) ANTIGEN.  
DR EMBL; AF003887; AAB64279.1; -;  
DR HSP; P03406; IEFN.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
DR AIDS; GTP-binding; Myristate.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23428 MW; 9F94AEB9CAFC6F6 CRC64;

Query Match 49.4%; Score 1119; DB 15; Length 206;  
Best Local Similarity 98.5%; Pred. No. 2.3e-82;  
Matches 203; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVAASRDLEKKGAISSNTAANAACAWLEA 171  
Db 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVAASRDLEKKGAISSNTAANAACAWLEA 60  
Qy 172 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSHSRRQDILDLWIYHTGY 231  
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGSHSRRQDILDLWIYHTGY 120  
Qy 232 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 291  
Db 121 FPDQNTYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDPPEV 180  
Qy 292 LEWRDLSRLAFHHVARELHPEYFNC 317  
Db 181 LEWRDLSRLAFHHVARELHPEYFNC 206

RESULT 4  
Q90VU7  
ID Q90VU7 PRELIMINARY; PRT; 206 AA.  
AC Q90VU7  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NEF PROTEIN.  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NL4-3;  
RC MEDLINE=96036482; PubMed=7483282;  
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,  
RA Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;  
RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes  
RT from primary virus cultures using the polymerase chain reaction.";  
RL Virology 213:80-86(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NL4-3;  
RC MEDLINE=86281827; PubMed=3016298;  
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
RA Martin M.A.;  
RT "Production of acquired immunodeficiency syndrome-associated  
RT retrovirus in human and nonhuman cells transfected with an infectious  
RT molecular clone";  
RL J. Virol. 59:284-291(1986).  
DR EMBL; U26942; AAB60579.1; -;  
SQ SEQUENCE 206 AA; 23367 MW; 65AF3B6184DC2FE7 CRC64;

Query Match 49.28; Score 1115; DB 15; Length 206;  
Best Local Similarity 98.18; Pred. No. 4.9e-82;  
Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGGLHSGRQDILDLWIYHTQY 171  
Db 1 MGGKWSKSSVIGWPAVRERMRRAEPAADGVGAASRDLEKKGGLHSGRQDILDLWIYHTQY 60

Qy 172 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLHSGRQDILDLWIYHTQY 231  
Db 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLHSGRQDILDLWIYHTQY 120

Qy 232 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 291  
Db 121 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180

Qy 292 LEWRFDSRLAFHHVARELHPEYFKNC 317  
Db 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 5  
Q9PXX9 PRELIMINARY; PRT; 206 AA.  
AC Q9PXX9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=93152025; PubMed=1301062;  
RA Kohleisen B., Neumann M., Herrmann R., Brack-Werner R., Krohn K.J.,  
RA Ovod V., Rankl A., Erfle V.;  
RT "Cellular localization of Nef expressed in persistently HIV-1-infected  
RT low-producer astrocytes.";  
RL AIDS 6:1427-1436(1992).  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR HSP; P03406; IEFN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23454 MW; 65D5DDE4FB748072 CRC64;

Query Match 48.98; Score 1108; DB 15; Length 206;  
Best Local Similarity 97.18; Pred. No. 1.8e-81;  
Matches 200; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGGLHSGRQDILDLWIYHTQY 171  
Db 1 MGGKWSKSSVIGWPAVRERMRRAEPAADGVGAASRDLEKKGGLHSGRQDILDLWIYHTQY 60

Qy 172 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLHSGRQDILDLWIYHTQY 231  
Db 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLHSGRQDILDLWIYHTQY 120

Qy 232 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 291  
Db 121 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180

Qy 292 LEWRFDSRLAFHHVARELHPEYFKNC 317  
Db 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

Query Match 48.88; Score 1105; DB 15; Length 206;  
Best Local Similarity 97.18; Pred. No. 3.1e-81;  
Matches 200; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGGLHSGRQDILDLWIYHTQY 171  
Db 1 MGGKWSKSSVIGWPAVRERMRRAEPAADGVGAASRDLEKKGGLHSGRQDILDLWIYHTQY 60

Qy 172 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLHSGRQDILDLWIYHTQY 231  
Db 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLHSGRQDILDLWIYHTQY 120

Qy 232 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 291  
Db 121 FPDQNYTPGCVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180

Qy 292 LEWRFDSRLAFHHVARELHPEYFKNC 317  
Db 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 7  
Q9WM30 PRELIMINARY; PRT; 206 AA.  
AC Q9WM30;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=8-IT;  
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,  
RA Johansson B., Vahlne A., Sonnerborg A.;  
RT "HIV-1 nef mutations and clinical long-term non progression: a  
RT molecular epidemiology study.";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

RESULT 6  
Q9WM16 PRELIMINARY; PRT; 206 AA.  
AC Q9WM16;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=7-IT;  
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,  
RA Johansson B., Vahlne A., Sonnerborg A.;  
RT "HIV-1 nef mutations and clinical long-term non progression: a  
RT molecular epidemiology study.";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL; AF011494; AAD01472.1;  
DR HSP; P03406; IEFN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23333 MW; 2EBF2A6A3ECAF5EA CRC64;

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DR EMBL; AF011469; AAD01447.1; -.
DR HSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23345 MW; 0ED69927C2E03BB6 CRC64;

Query Match 48.8%; Score 1104; DB 15; Length 206;
Best Local Similarity 97.1%; Pred. No. 3.7e-81;
Matches 200; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHAITSNTAATNAACAWLEA 171
Db 1 MGGKWSKSSVIGWPAVRMRRAEPAADGVGAASRDLEKHAITSNTAANNAACAWLEA 60

Qy 172 QEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKEKGGLEGLHSQRRODILDWIYHTQGY 231
Db 61 QEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKEKGGLEGLHSQRRODILDWIYHTQGY 120

Qy 232 FPDQNTYTPGCGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 291
Db 121 FPDQNTYTPGCGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 180

Qy 292 LEWRFDLSRLAFHHVARELHPEYFKNC 317
Db 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206

RESULT 8
Q9PXW8 PRELIMINARY; PRT; 206 AA.
AC Q9PXW8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93152025; PubMed=1301062;
RA Kohleisen B., Neumann M., Herrmann R., Brack-Werner R., Krohn K.J.,
RA Ovod V., Ranki A., Erfle V.;
RT "Cellular localization of Nef expressed in persistently HIV-1-infected
RT low-producer astrocytes.";
RL AIDS 6:1427-1436(1992).
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC AIDS 6:1427-1436(1992).
CC -1- ACTIVITIES: IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR HSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; GTP-binding; Myristate.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23439 MW; 8478CF194D39D5B9 CRC64;

Query Match 48.6%; Score 1101; DB 15; Length 206;
Best Local Similarity 96.1%; Pred. No. 6.5e-81;
Matches 198; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHAITSNTAATNAACAWLEA 171
Db 1 MGGKWSKSSVIGWPAVRMRRAEPAADGVGAASRDLEKHAITSNTAANNAACAWLEA 60

Qy 172 QEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKEKGGLEGLHSQRRODILDWIYHTQGY 231
Db 61 QEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKEKGGLEGLHSQRRODILDWIYHTQGY 120

Qy 232 FPDQNTYTPGCGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 291
Db 121 FPDQNTYTPGCGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 180
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Qy 292 LEWRFDLSRLAFHHVARELHPEYFKNC 317
Db 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206

RESULT 9
Q90179 PRELIMINARY; PRT; 206 AA.
AC Q90179
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95074930; PubMed=7983770;
RA Fang H., Pincus S.H.;
RT "Unique insertion sequence and pattern of CD4 expression in variants
RT selected with immunotoxins from human immunodeficiency virus type 1-
RT infected T cells.";
RL J. Virol. 69:75-81(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Fang H., Pincus S.H.;
RT "Spontaneous activation of human immunodeficiency virus type 1 in an
RT immunotoxin-resistant variant T cell line.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES: IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF070521; AAC28453.1; -.
DR HSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; GTP-binding; Myristate.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23334 MW; 3E2B9C4017FDC68 CRC64;

Query Match 48.4%; Score 1096; DB 15; Length 206;
Best Local Similarity 95.6%; Pred. No. 1.6e-80;
Matches 197; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHAITSNTAATNAACAWLEA 171
Db 1 MGGKWSKSSVIGWPAVRMRRAEPAADGVGAASRDLEKHAITSNTAANNAACAWLEA 60

Qy 172 QEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKEKGGLEGLHSQRRODILDWIYHTQGY 231
Db 61 QEEVEGFPVTPQVPLRPMYTKAAVDLSHFLKEKGGLEGLHSQRRODILDWIYHTQGY 120

Qy 232 FPDQNTYTPGCGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 291
Db 121 FPDQNTYTPGCGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDDPEREV 180

Qy 292 LEWRFDLSRLAFHHVARELHPEYFKNC 317
Db 181 LEWRFDLSRLAFHHVARELHPEYFKNC 206

RESULT 10
Q85588 PRELIMINARY; PRT; 206 AA.
AC Q85588
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Aids-associated retrovirus.
```

Viruses; Retroviral viruses; Retroviridae.  
[1]  
NCBI\_TaxID=11966;  
SEQUENCE FROM N.A.  
MEDLINE-86067228; PubMed-2999715;  
RA Ratner L., Starcich B., Josephs S.F., Hahn B.H., Reddy E.P., Arya S.K.,  
RA Livak K.J., Pettaway S.R.Jr., Pearson M.L., Haseltine W.A., Arya S.K.,  
RA Wong-staal F.,  
RA "Polymorphism of the 3' open reading frame of the virus associated  
RT with the acquired immune deficiency syndrome, human T-lymphotropic  
RT virus type III";  
RL Nucleic Acids Res. 13:8219-8229(1985).  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL; X03188; CAA26947.1; -  
DR HSP; P03406; 1EFN.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23419 MW; 3B25EB332A479A46 CRC64;  
  
Query Match 48.4%; Score 1096; DB 15; Length 206;  
Best Local Similarity 96.6%; Pred. No. 1.6e-80;  
Matches 199; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
QY 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 171  
Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
  
QY 172 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLIHSORRODILDWIYHTQY 231  
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLIHSORRODILDWIYHTQY 120  
  
QY 232 FPDQNTPTGPGVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDPDERV 291  
Db 121 FPDQNTPTGPGVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDPDERV 180  
  
QY 292 LEWRDLSLAFHHVARELHPEYFKNK 317  
Db 181 LEWRDLSLAFHHVARELHPEYFKNK 206  
  
RESULT 11  
Q78244  
ID Q78244 PRELIMINARY; PRT; 206 AA.  
AC Q78244;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
[1]  
PP SEQUENCE FROM N.A.  
RA Carlini F., Federico M., Equestre M., Ricci S., Ratti G., Zibai Q.,  
RA Verani P., Rossi G.B.;  
RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
RT chronically infected HUT-78 cellular clone.";  
RL J. Viral Diseases 1:40-55(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-89352106; PubMed-2765297;  
RA Federico M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
RA Macchi B., Mangione N., Verani P., Rossi G.;  
RT "Biological and molecular characterization of producer and non  
RT producer clones from HUT-78 infected with a patient HIV isolate.";  
RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Titti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,

Borsetti A., Saggio I., Verani P., Rossi G.;  
RT "Variability of HIV-1 virus: characteristics of an infected but not  
RT productive clone";  
RL Int. J. Immunopharmacol. 3:17-23(1990).  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL; Z11530; CAA77629.1; -  
DR HSP; P03406; 1EFN.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23398 MW; A31CC7244BBB2B43 CRC64;  
  
Query Match 48.4%; Score 1096; DB 15; Length 206;  
Best Local Similarity 96.6%; Pred. No. 1.6e-80;  
Matches 199; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 171  
Db 1 MGGKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60  
  
QY 172 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLIHSORRODILDWIYHTQY 231  
Db 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKEGGLIHSORRODILDWIYHTQY 120  
  
QY 232 FPDQNTPTGPGVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDPDERV 291  
Db 121 FPDQNTPTGPGVRYPLTFGWCYKLVPEPKVEANKGENTSLHPVSLHGMDPDERV 180  
  
QY 292 LEWRDLSLAFHHVARELHPEYFKNK 317  
Db 181 LEWRDLSLAFHHVARELHPEYFKNK 206  
  
RESULT 12  
Q9WLM7  
ID Q9WLM7 PRELIMINARY; PRT; 206 AA.  
AC Q9WLM7;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
[1]  
PP SEQUENCE FROM N.A.  
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,  
RA Johansson B., Vahine A., Sonnerborg A.;  
RT "HIV-1 nef mutations and clinical long-term non progression: a  
RT molecular epidemiology study";  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES. IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL; AF047084; AAD02458.1; -  
DR HSP; P03406; 1EFN.  
DR InterPro; IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23512 MW; E09E3BEF828A83C0 CRC64;

Query Match 48.2%; Score 1092; DB 15; Length 206;  
Best Local Similarity 95.6%; Pred. No. 3.5e-80;  
Matches 197; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
  
QY 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 171  
Db 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 172 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGLHSQRQDILDLDWIYHTQY 231  
 DB 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGLHSQRQDILDLDWIYHTQY 120  
 QY 232 FPDWQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHLPVSLHGMDDPEREV 291  
 DB 121 FPDWQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHLPVSLHGMDDPEREV 180  
 QY 292 LEWRFDSRLAFHHVARELHPEYFKNC 317  
 DB 181 LEWRFDSRLAFHHVARELHPEYFKNC 206  
 RESULT 13  
 ID Q74905 PRELIMINARY; PRT: 206 AA.  
 AC Q74905;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
 GN NEF.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Arens M.O., Ratner L., Joseph T., Bandres J.,  
 Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RL -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 DR EMBL; U44448; AAB38200.1; -  
 DR EMBL; U44447; AAB38199.1; -  
 DR HSP: Q70627; 2NEF.  
 DR InterPro: IPR001558; F-protein.  
 DR Pfam: PF00469; F-protein; 1.  
 DR AIDS; GTP-binding; Myristate.  
 KW AIDS; GTP-binding; Myristate.  
 SQ SEQUENCE 206 AA; 23617 MW; 5CAAB09C4730C38A CRC64;

Query Match 48.1%; Score 1090; DB 15; Length 206;  
 Best Local Similarity 95.1%; Pred. No. 5e-80; Indels 0; Gaps 0;  
 Matches 196; Conservative 6; Mismatches 4;  
 QY 112 MGGKWSKSVVGVPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 171  
 DB 1 MGGKWSKSVVGVPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 QY 172 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGLHSQRQDILDLDWIYHTQY 231  
 DB 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGLHSQRQDILDLDWIYHTQY 120  
 QY 232 FPDWQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHLPVSLHGMDDPEREV 291  
 DB 121 FPDWQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHLPVSLHGMDDPEREV 180  
 QY 292 LEWRFDSRLAFHHVARELHPEYFKNC 317  
 DB 181 LEWRFDSRLAFHHVARELHPEYFKNC 206  
 RESULT 14  
 ID Q89561 PRELIMINARY; PRT: 206 AA.  
 AC Q89561;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
 GN NEF.

OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Arens M.O., Ratner L., Joseph T., Bandres J.,  
 Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RL -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 DR EMBL; U44448; AAB38200.1; -  
 DR EMBL; U44447; AAB38199.1; -  
 DR HSP: Q70627; 2NEF.  
 DR InterPro: IPR001558; F-protein.  
 DR Pfam: PF00469; F-protein; 1.  
 DR AIDS; GTP-binding; Myristate.  
 KW AIDS; GTP-binding; Myristate.  
 SQ SEQUENCE 206 AA; 23629 MW; BF467FB1B7147CDE CRC64;

Query Match 48.0%; Score 1087; DB 15; Length 206;  
 Best Local Similarity 94.7%; Pred. No. 8.7e-80; Indels 0; Gaps 0;  
 Matches 195; Conservative 7; Mismatches 4;  
 QY 112 MGGKWSKSVVGVPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 171  
 DB 1 MGGKWSKSVVGVPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
 QY 172 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGLHSQRQDILDLDWIYHTQY 231  
 DB 61 QEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGLHSQRQDILDLDWIYHTQY 120  
 QY 232 FPDWQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHLPVSLHGMDDPEREV 291  
 DB 121 FPDWQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHLPVSLHGMDDPEREV 180  
 QY 292 LEWRFDSRLAFHHVARELHPEYFKNC 317  
 DB 181 LEWRFDSRLAFHHVARELHPEYFKNC 206  
 RESULT 15  
 ID Q74913 PRELIMINARY; PRT: 206 AA.  
 AC Q74913;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
 GN NEF.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ratner L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,  
 Hahn B., Powderly W., Arens M.,  
 Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RL -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
 CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
 DR EMBL; U44453; AAB38205.1; -  
 DR HSP: P03406; IEFN.  
 DR InterPro: IPR001558; F-protein.  
 DR Pfam: PF00469; F-protein; 1.  
 DR AIDS; GTP-binding; Myristate.  
 KW AIDS; GTP-binding; Myristate.  
 SQ SEQUENCE 206 AA; 23649 MW; E5B997FA0B70FC175 CRC64;

Query Match 47.9%; Score 1085; DB 15; Length 206;  
 Best Local Similarity 95.6%; Pred. No. 1.3e-79; Indels 0; Gaps 0;  
 Matches 196; Conservative 5; Mismatches 4;



SQ SEQUENCE 206 AA; 23648 MW; E5BD6FA0B70FC175 CRC64;

Query Match 47.7%; Score 1079; DB 15; Length 206;  
Best Local Similarity 95.6%; Pred. No. 3.8e-79;  
Matches 195; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 112 MGGKSKSSVGVWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 171  
|||||  
DB 1 MGGKSKSSVGVWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
QY 172 QEEVEGVFPTQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSQRQDILDWIYHTQY 231  
|||||  
DB 61 QEEVEGVFPTQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSQRQDILDWIYHTQY 120  
QY 232 FPDWQNTPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 291  
|||||  
DB 121 FPDWQNTPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180  
QY 292 LEWRDLSRLAFHHVARELHPEYFK 315  
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DB 181 LEWRDLSRLAFHHVARELHPEYFK 204

RESULT 19  
Q74909 PRELIMINARY; PRT: 206 AA.  
AC Q74909;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RX MEDLINE=96400183; PubMed=8806559;  
RA Rather L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,  
Hahn B., Powderly W., Arens M.;  
RT "Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects  
at different stages of disease";  
RL Virology 223:245-250(1996).  
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL: U44449; AAB38201.1; -;  
DR HSSP: Q70627; 2NEF.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23488 MW; F0596D6FAAA81A05 CRC64;

Query Match 47.6%; Score 1077; DB 15; Length 206;  
Best Local Similarity 94.2%; Pred. No. 5.6e-79;  
Matches 194; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 112 MGGKSKSSVGVWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 171  
|||||  
DB 1 MGGKSKSSVGVWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
QY 172 QEEVEGVFPTQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSQRQDILDWIYHTQY 231  
|||||  
DB 61 QEEVEGVFPTQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSQRQDILDWIYHTQY 120  
QY 232 FPDWQNTPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 291  
|||||  
DB 121 FPDWQNTPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180  
QY 292 LEWRDLSRLAFHHVARELHPEYFKNC 317  
|||||  
DB 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

RESULT 20  
Q9QPN3 PRELIMINARY; PRT: 202 AA.  
AC Q9QPN3;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN) (FRAGMENT).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HIV-1LAI;  
RA Piedade J., Esteves A., Parreira R., Venenno T., Barros M.F.,  
Canas-Ferreira W.F.;  
RT "Cloning and expression of HIV-1 nef gene in the carrier-adjutant  
pVUB3 expression system based on the major lipoprotein (Opr1) from the  
outer membrane of Pseudomonas aeruginosa";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL: AF166101; AAD47831.1; -;  
DR HSSP: P03406; 1EFN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
FT NON\_TER 202  
SQ SEQUENCE 202 AA; 23033 MW; CD61DFA6F386CC89 CRC64;

Query Match 47.5%; Score 1076; DB 15; Length 202;  
Best Local Similarity 97.5%; Pred. No. 6.5e-79;  
Matches 197; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 112 MGGKSKSSVGVWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 171  
|||||  
DB 1 MGGKSKSSVGVWPTVRMRRAEPAADGVGAASRDLEKHGAITSNTAATNAACAWLEA 60  
QY 172 QEEVEGVFPTQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSQRQDILDWIYHTQY 231  
|||||  
DB 61 QEEVEGVFPTQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSQRQDILDWIYHTQY 120  
QY 232 FPDWQNTPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 291  
|||||  
DB 121 FPDWQNTPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180  
QY 292 LEWRDLSRLAFHHVARELHPEY 313  
|||||  
DB 181 LEWRDLSRLAFHHVARELHPEY 202

RESULT 21  
Q9Q596 PRELIMINARY; PRT: 206 AA.  
AC Q9Q596;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wang B., Sakana N.K.;  
RT "HIV-1 Strains from a cohort of American subjects reveal the presence  
of a V2 region extension unique to slow progressors and non-  
progressors";

RL AIDS 0.0-0(2000).  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL: AF203197; AAF25320.1; -  
DR HSP: P03406; IEFN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS: Gtp-binding; Myristate.  
SQ SEQUENCE 206 AA; 23510 MW; 081DF3A12ESA7576 CRC64;

Query Match 47.3%; Score 1072; DB 15; Length 206;  
Best Local Similarity 94.7%; Pred. No. 1.4e-78;  
Matches 195; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 112 MGGKWSKSSVVGWPTVRRMRRAEPAADGGAASRDLEKKGAISSNTAATNAACAWLEA 171  
DB 1 MGGKWSKRIKGGWPAVRERMRRAEPAADGGAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRODILDWLYHTQGY 231  
DB 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRODILDWLYHTQGY 120

QY 232 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDPPER 291  
DB 121 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDPPER 180

QY 292 LEWRFDSRLAFHHVARELHPEYFKN 317  
DB 181 LEWRFDSRLAFHHVARELHPEYFKN 206

RESULT 22  
Q90595  
ID Q90595 PRELIMINARY; PRT; 206 AA.  
AC Q90595  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wang B., Saksena N.K.;  
RT "Hiv-1 strains from a cohort of American subjects reveal the presence of a v2 region extension unique to slow progressors and non-progressors."  
RL AIDS 0.0-0(2000).  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL: AF203198; AAF25320.1; -  
DR HSP: P03406; IEFN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS: Gtp-binding; Myristate.  
SQ SEQUENCE 206 AA; 23420 MW; A66FC8B78FECFD2 CRC64;

Query Match 47.3%; Score 1072; DB 15; Length 206;  
Best Local Similarity 93.7%; Pred. No. 1.4e-78;  
Matches 193; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 112 MGGKWSKSSVVGWPTVRRMRRAEPAADGGAASRDLEKKGAISSNTAATNAACAWLEA 171  
DB 1 MGGKWSKRSKGGWPAVRERMRRAEPAADGGAASRDLEKKGAISSNTAATNAACAWLEA 60

QY 172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRODILDWLYHTQGY 231  
DB 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRODILDWLYHTQGY 120

QY 232 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDPPER 291  
DB 121 FPDQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDPPER 180

QY 292 LEWRFDSRLAFHHVARELHPEYFKN 317  
DB 181 LEWRFDSRLAFHHVARELHPEYFKN 206

RESULT 23  
Q9YYU9  
ID Q9YYU9 PRELIMINARY; PRT; 208 AA.  
AC Q9YYU9  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=8-IT;  
RA Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,  
RA Johansson B., Vahine A., Sonnerborg A.;  
RT "Hiv-1 nef mutations and clinical long-term non progression: a molecular epidemiology study."  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL: AF011470; AAD01448.1; -  
DR HSP: P03406; IEFN.  
DR InterPro: IPR001538; F-protein.  
DR Pfam: PF00469; F-protein; 1.  
KW AIDS: Gtp-binding; Myristate.  
SQ SEQUENCE 208 AA; 23681 MW; 1C891C3AD230C6A8 CRC64;

Query Match 47.3%; Score 1071; DB 15; Length 208;  
Best Local Similarity 94.2%; Pred. No. 1.7e-78;  
Matches 196; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 112 MGGKWSKSSVVGWPTVRRMRRAEPA--ADGGAASRDLEKKGAISSNTAATNAACAWL 169  
DB 1 MGGKWSKRSKRSKGGWPAVRERMRRAEPAAXGAVSRDLEKKGAISSNTAATNAACAWL 60

QY 170 EAQEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRODILDWLYHTQ 229  
DB 61 EAQEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRODILDWLYHTQ 120

QY 230 GYFPDMQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDPPER 289  
DB 121 GYFPDMQNTYTPGQVRYPLTFGWCYKLVPEPKVEEANKGENTSLHHPVSLHGMDPPER 180

QY 290 EVLEWRFDSRLAFHHVARELHPEYFKN 317  
DB 181 KYLEWRFDSRLAFHHVARELHPEYFKN 208

RESULT 24  
Q9W7X3  
ID Q9W7X3 PRELIMINARY; PRT; 206 AA.  
AC Q9W7X3  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]



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RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 27;
RA McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,
RA Pemberton L., Brew B.J.;
RT "Anomalies in Nef expression within the central nervous system of HIV-
RT 1 positive individuals/AIDS patients with or without AIDS dementia
RT complex."
RL J. Neurovirol. 4:0-0(1998).
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF064676; AAC18376.1; -.
DR HSSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23499 MW; DEE21CAF05891D6B CRC64;

Query Match 47.2%; Score 1068; DB 15; Length 206;
Best Local Similarity 91.7%; Pred. No. 3e-78; 3; Indels 0; Gaps 0;
Matches 189; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

QY 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 171
D 1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60
QY 172 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTOGY 231
D 61 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTOGY 120
QY 232 FPDQNYTPGCVRYPLTFGWCYKLVPPVEPKVEEANKGENTSLHHPVSLHGMDDPEREV 291
D 121 FPDQNYTPGCVRYPLTFGWCYKLVPPVEPKVEEANKGENTSLHHPVSLHGMDDPEREV 180
QY 292 LEWRFDSRLAFHHVARELHPEYFKNC 317
D 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 25
Q9DQ01 ID Q9DQ01 PRELIMINARY; PRT; 206 AA.
AC Q9DQ01;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 27;
RA McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,
RA Pemberton L., Brew B.J.;
RT "Anomalies in Nef expression within the central nervous system of HIV-
RT 1 positive individuals/AIDS patients with or without AIDS dementia
RT complex."
RL J. Neurovirol. 4:0-0(1998).
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF064676; AAC18376.1; -.
DR HSSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23499 MW; DEE21CAF05891D6B CRC64;

Query Match 47.0%; Score 1065; DB 15; Length 206;
Best Local Similarity 93.2%; Pred. No. 5.2e-78;
Matches 192; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

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QY 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 171
D 1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60
QY 172 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTOGY 231
D 61 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTOGY 120
QY 232 FPDQNYTPGCVRYPLTFGWCYKLVPPVEPKVEEANKGENTSLHHPVSLHGMDDPEREV 291
D 121 FPDQNYTPGCVRYPLTFGWCYKLVPPVEPKVEEANKGENTSLHHPVSLHGMDDPEREV 180
QY 292 LEWRFDSRLAFHHVARELHPEYFKNC 317
D 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 26
Q9W7U0 ID Q9W7U0 PRELIMINARY; PRT; 206 AA.
AC Q9W7U0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 27;
RA McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,
RA Pemberton L., Brew B.J.;
RT "Anomalies in Nef expression within the central nervous system of HIV-
RT 1 positive individuals/AIDS patients with or without AIDS dementia
RT complex."
RL J. Neurovirol. 4:0-0(1998).
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF064676; AAC18376.1; -.
DR HSSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23514 MW; DC681CAF05891D6B CRC64;

Query Match 47.0%; Score 1064; DB 15; Length 206;
Best Local Similarity 91.7%; Pred. No. 6.2e-78;
Matches 189; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

QY 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 171
D 1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60
QY 172 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTOGY 231
D 61 QEEVEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDWIYHTOGY 120
QY 232 FPDQNYTPGCVRYPLTFGWCYKLVPPVEPKVEEANKGENTSLHHPVSLHGMDDPEREV 291
D 121 FPDQNYTPGCVRYPLTFGWCYKLVPPVEPKVEEANKGENTSLHHPVSLHGMDDPEREV 180
QY 292 LEWRFDSRLAFHHVARELHPEYFKNC 317
D 181 LEWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 27
Q93010 ID Q93010 PRELIMINARY; PRT; 206 AA.
AC Q93010;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 27;
RA McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,
RA Pemberton L., Brew B.J.;
RT "Anomalies in Nef expression within the central nervous system of HIV-
RT 1 positive individuals/AIDS patients with or without AIDS dementia
RT complex."
RL J. Neurovirol. 4:0-0(1998).
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF064676; AAC18376.1; -.
DR HSSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23464 MW; B72E0AA736374B64 CRC64;

Query Match 47.0%; Score 1065; DB 15; Length 206;
Best Local Similarity 93.2%; Pred. No. 5.2e-78;
Matches 192; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

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ID O93010 PRELIMINARY; PRT; 206 AA.
AC O93010;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrodroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 9;
RX MEDLINE=98097260; PubMed=9436760;
RA Kang M.R., Cho Y.K., Chun J., Kim Y.B., Lee I., Lee H.J., Kim S.H.,
RA Kim Y.K., Yoon K., Yang J.M., Kim J.M., Shin Y.O., Kang C., Lee J.S.,
RA Choi K.W., Kim D.G., Fitch W.M., Kim S.;
RT "Phylogenetic analysis of the nef gene reveals a distinctive
RT monophyletic clade in Korean HIV-1 cases.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 17:58-68(1998).
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF063922; AAC17893.1; -
DR HSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
DR AIDS; GTP-binding; Myristate.
KW SEQUENCE 206 AA; 23348 MW; 4D5AEDF55FAE93E3 CRC64;
SQ

Query Match 46.9%; Score 1062; DB 15; Length 206;
Best Local Similarity 94.58; Pred. No. 9e-78; Indels 0; Gaps 0;
Matches 194; Conservative 3; Mismatches 8;

Qy 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVAASRDLEKKGAISSNTAATNAACAWLEA 171
Db 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVAASRDLEKKGAISSNTAATNAACAWLEA 60
Qy 172 QEEVEVGPVTPQVPLRPMTYKAAVDLSHFLKKGEGLEIHSORRQDILDWIYHTQGY 231
Db 61 QEEVEVGPVTPQVPLRPMTYKAAVDLSHFLKKGEGLEIHSORRQDILDWIYHTQGY 120
Qy 232 FPDQNTPTGPGVRYPLTFGCYKLVPEPKVEANKGENTSLHVPVSLHGMDPPEV 291
Db 121 FPDQNTPTGPGVRYPLTFGCYKLVPEPKVEANKGENTSLHVPVSLHGMDPPEV 180
Qy 292 LEWRFSRLAFHHVARELHPEYFKN 316
Db 181 LEWRFSRLAFHHVARELHPEYKDC 206

RESULT 28
O93012
ID O93012 PRELIMINARY; PRT; 206 AA.
AC O93012;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrodroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 27;
RA McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,
RA Pemberton L., Brew B.J.;
RT "Anomalies in Nef expression within the central nervous system of HIV-
RT 1 positive individuals/AIDS patients with or without AIDS dementia
RT complex.";
RL J. Neurovirol. 4:0-0(1998).
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
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CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF064673; AAC18374.1; -
DR HSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23472 MW; 2255A447ECE85456 CRC64;

Query Match 46.9%; Score 1061; DB 15; Length 206;
Best Local Similarity 91.7%; Pred. No. 1.1e-77;
Matches 189; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVAASRDLEKKGAISSNTAATNAACAWLEA 171
Db 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVAASRDLEKKGAISSNTAATNAACAWLEA 60
Qy 172 QEEVEVGPVTPQVPLRPMTYKAAVDLSHFLKKGEGLEIHSORRQDILDWIYHTQGY 231
Db 61 QEEVEVGPVTPQVPLRPMTYKAAVDLSHFLKKGEGLEIHSORRQDILDWIYHTQGY 120
Qy 232 FPDQNTPTGPGVRYPLTFGCYKLVPEPKVEANKGENTSLHVPVSLHGMDPPEV 291
Db 121 FPDQNTPTGPGVRYPLTFGCYKLVPEPKVEANKGENTSLHVPVSLHGMDPPEV 180
Qy 292 LEWRFSRLAFHHVARELHPEYFKN 317
Db 181 LEWRFSRLAFHHVAREKHPYKDC 206

RESULT 29
O90597
ID O90597 PRELIMINARY; PRT; 206 AA.
AC O90597;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
GN NEF.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrodroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang B., Sakana N.K.;
RT "HIV-1 Strains from a cohort of American subjects reveal the presence
RT of a V2 region extension unique to slow progressors and non-
RT progressors.";
RL AIDS 0:0-0(2000).
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
DR EMBL; AF203196; AAF25318.1; -
DR HSP; P03406; IEFN.
DR InterPro; IPR001558; F-protein.
DR Pfam; PF00469; F-protein; 1.
KW AIDS; GTP-binding; Myristate.
SQ SEQUENCE 206 AA; 23599 MW; 9C887A58541A9905 CRC64;

Query Match 46.8%; Score 1060; DB 15; Length 206;
Best Local Similarity 92.7%; Pred. No. 1.3e-77;
Matches 191; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 112 MGGKWSKSSVVGWPTVRMRRAEPAADGVAASRDLEKKGAISSNTAATNAACAWLEA 171
Db 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVAASRDLEKKGAISSNTAATNAACAWLEA 60
Qy 172 QEEVEVGPVTPQVPLRPMTYKAAVDLSHFLKKGEGLEIHSORRQDILDWIYHTQGY 231
Db 61 QEEVEVGPVTPQVPLRPMTYKAAVDLSHFLKKGEGLEIHSORRQDILDWIYHTQGY 120
Qy 232 FPDQNTPTGPGVRYPLTFGCYKLVPEPKVEANKGENTSLHVPVSLHGMDPPEV 291
Db 181 LEWRFSRLAFHHVAREKHPYKDC 206
```

Db 121 FPDQNYTPGPIRVPLTFCWCYKLVPEQKVKANEKNTSLHHPMSLHGMDDEPERV 180  
QY 292 LEWRDLSRLAFHHVARELHPEYFKNC 317  
Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

## RESULT 30

Q9W7X2  
ID Q9W7X2 PRELIMINARY: PRT: 206 AA.  
AC Q9W7X2;  
DT 01-NOV-1999 (TREMELrel. 12, Created)  
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)  
DE 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).  
GN NEF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN-PATIENT 27;  
RA McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,  
RA Pemberton L., Brew B.J.;  
RT "Anomalies in Nef expression within the central nervous system of HIV-  
RT 1 positive individuals/AIDS patients with or without AIDS dementia  
RT complex."  
RL J. Neurovirol. 4:0-0(1998).  
CC -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING  
CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.  
DR EMBL; AF064677; AAC18378.1; -  
DR HSP; P03406; 1EEN.  
DR InterPro: IPR001558; F-protein.  
DR Pfam; PF00469; F-protein; 1.  
KW AIDS; GTP-binding; Myristate.  
SQ SEQUENCE 206 AA; 23442 MW; DCGA96AF05891D6B CRC64;

Query Match 46.7%; Score 1057; DB 15; Length 206;  
Best Local Similarity 91.3%; Pred. No. 2.3e-77;  
Matches 188; Conservative 13; Mismatches 5; Indels 0; Gaps 0;  
QY 112 MCGKSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 171  
Db 1 MCGKSKSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60  
QY 172 QEEVEGVFPVTPQVPLRPMTYKAADVLSHFLKEKGLGIIHSQRQDILDLYHTQGY 231  
Db 61 QKEEEVGFPPVPPQVPLRPMTYKAALDISHFLKEKGLGIIHSQRQDILDLYHTQGY 120  
QY 232 FPDQNYTPGPIRVPLTFCWCYKLVPEQKVKANEKNTSLHHPMSLHGMDDEPERV 291  
Db 121 FPDQNYTPGPIRVPLTFCWCYKLVPEQKVKANEKNTSLHHPMSLHGMDDEPERV 180  
QY 292 LEWRDLSRLAFHHVARELHPEYFKNC 317  
Db 181 LEWRDLSRLAFHHVARELHPEYFKNC 206

Search completed: August 26, 2002, 08:14:57  
Job time: 385 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 08:12:30 ; Search time 99.16 Seconds  
(without alignments)  
106.414 Million cell updates/sec

Title: US-09-509-239-23  
Perfect score: 552  
Sequence: 1 MPVDRLEPKWPGSQPKT.....QSKGPTGPKETSGHHHHH 95

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	552	100.0	95	20	AA02356 A representative H
2	552	100.0	95	22	AAG63238 Amino acid sequenc
3	547	99.1	302	20	AA02357 A representative H
4	547	99.1	302	22	AAG63239 Amino acid sequenc
5	541	98.0	95	20	AA02350 A representative H
6	541	98.0	95	22	AAG63232 Amino acid sequenc
7	536	97.1	302	20	AA02351 A representative H
8	536	97.1	302	22	AAG63233 Amino acid sequenc
9	536	97.1	411	20	AA02353 A representative L
10	536	97.1	411	22	AAG63235 Amino acid sequenc
11	536	97.1	413	20	AA02355 A representative L

12	536	97.1	413	22	AAG63237	Amino acid sequenc
13	479	86.8	86	20	AA02356	Lys41 mutant tat a
14	478	86.6	86	8	AA070598	HIV virus recombin
15	478	86.6	86	10	AA091903	Tat protein derive
16	478	86.6	86	10	AA091905	CDNA for tat prote
17	478	86.6	86	10	AA093140	Synthetic Tat prot
18	478	86.6	86	14	AA038618	Sequence of the HI
19	478	86.6	86	17	AA086625	HIV Tat. Human im
20	478	86.6	86	18	AA031202	Human Immunodefici
21	478	86.6	86	18	AA026443	HIV tat protein.
22	478	86.6	86	19	AA071385	Amino acid sequenc
23	478	86.6	86	19	AA076148	HIV Type I Tat pro
24	478	86.6	86	21	AA096881	Human immunodefici
25	478	86.6	86	22	AA085996	Amino acid sequenc
26	478	86.6	87	12	AA013379	TAT protein. Synt
27	466	84.4	86	20	AA022959	Cys22 mutant tat a
28	462	83.7	86	11	AA020227	Sequence of the tr
29	462	83.7	86	16	AA078742	Wild type Tat HIV
30	457.5	82.9	83	20	AA022962	Lys41-RGD-delta mu
31	456.5	82.7	83	20	AA022961	RGD-delta mutant t
32	452	81.9	83	20	AA022958	Wild type Tat amin
33	451	81.7	86	15	AA048966	Diversified HIV-1
34	451	81.7	86	15	AA057346	Peptide fragment o
35	448	81.2	86	21	AA010050	HIV-1 tat protein.
36	446	80.8	86	15	AA048964	Full length Tat.
37	446	80.8	86	22	AA064257	Human protein: SEQ
38	442	80.1	86	22	AA046679	HIV-1 Tat peptide
39	442	80.1	86	22	AA046685	HIV-1 Tat peptide
40	433	78.4	86	16	AA077542	Trans-dominant var
41	430	77.9	101	21	AA014224	HIV Tat-SF162. Hu
42	418	75.7	102	21	AA014225	HIV Tat-Cys822-SF16
43	411	74.5	101	12	AA012259	HIV-1 strain ORF 1
44	411	74.5	101	21	AA030514	Sequence of the ta
45	408	73.9	72	7	AA060699	Trans-acting trans

## ALIGNMENTS

RESULT 1  
AA02356  
ID AA02356 standard; Protein; 95 AA.  
XX  
AC AA02356;  
XX  
DT 09-JUL-1999 (first entry)  
XX  
DE A representative HIV-1 mutant Nef-His protein.  
XX  
DE HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
KW vaccine; HIV infection; protein D.  
XX  
OS Synthetic.  
OS Human immunodeficiency virus type 1.  
XX  
PN WO9916884-A1.  
XX  
PD 08-APR-1999.  
XX  
PF 17-SEP-1998; 98WO-EP06040.  
XX  
PR 26-SEP-1997; 97GB-0020585.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Bruck C, Godart SAG, Marchand M;  
XX  
DR WPT; 1999-302282/25.  
DR N-PSDB; AAX35692.  
XX  
PT HIV Tat or Nef protein linked to a fusion partner  
PS Disclosure; Fig 2; 66pp; English.

XX CC The present sequence represents a representative HIV-1 mutant Nef-His  
 CC protein. The protein is used in the creation of the fusion proteins of  
 CC the invention, in conjunction with a fusion partner (e.g. protein D).  
 CC The specification also describes fusion proteins comprising HIV-1 Tat  
 CC protein. The fusion protein can be used in a vaccine to prevent HIV  
 CC infection.

XX SQ Sequence 95 AA;

Query Match 100.0%; Score 552; DB 20; Length 95;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-50;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPVDPRLPEPKHPSQKPTACTNCYCKKCCFHCQVCFTTAALGISYGRKKRRRPPQ 60  
 Db 1 mepvdprlepkhpsqkptactncycckccfchcqvcfitaalgisyrkrrrrppq 60  
 QY 61 GSOTHOVSLSKQPTSQSKGPTGPKETSGHHHHH 95  
 Db 61 gsqthqvsksqptsqskgptgpketsgghhhhh 95

RESULT 2

ID AAG63238 standard; Protein; 95 AA.

XX AAG63238;

DT 01-OCT-2001 (first entry)

XX Amino acid sequence of a His-tagged mutant Tat protein of HIV.

DE HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.

KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.

XX Synthetic.

OS Human immunodeficiency virus.

XX WO200154719-A2.

XX 02-AUG-2001.

XX 29-JAN-2001; 2001WO-EP00944.

XX 31-JAN-2000; 2000GB-0002200.

PR 14-APR-2000; 2000GB-0009336.

PR 06-JUN-2000; 2000GB-0013806.

PR 28-JUN-2000; 2000WO-EP05998.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX Voss G;

XX WPI; 2001-476172/51.

DR N-PSDB; AAH42882.

XX New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
 PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
 PT protein or polynucleotide for the manufacture of a vaccine .

XX Disclosure; Fig 1; 90pp; English.

XX The present sequence represents a His-tagged mutant Tat protein of HIV.  
 CC The protein is expressed in the yeast Pichia pastoris, and is used to  
 CC produce the vaccine of the invention. The specification describes  
 CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the  
 CC manufacture of a vaccine. The vaccine is used for the prophylactic or  
 CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
 CC in synergy with gp120 in the treatment and prevention of HIV. The  
 CC vaccine reduces the HIV viral load in HIV infected humans and results  
 CC in a maintenance of CD4+ levels over those levels found in the absence  
 CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.

XX SQ Sequence 95 AA;

Query Match 100.0%; Score 552; DB 22; Length 95;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-50;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPVDPRLPEPKHPSQKPTACTNCYCKKCCFHCQVCFTTAALGISYGRKKRRRPPQ 60  
 Db 1 mepvdprlepkhpsqkptactncycckccfchcqvcfitaalgisyrkrrrrppq 60  
 QY 61 GSOTHOVSLSKQPTSQSKGPTGPKETSGHHHHH 95  
 Db 61 gsqthqvsksqptsqskgptgpketsgghhhhh 95

RESULT 3

AAV02357

ID AAV02357 standard; Protein; 302 AA.

XX AAV02357;

DT 09-JUL-1999 (first entry)

XX A representative HIV-1 mutant Tat-His protein.

DE HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
 KW vaccine; HIV infection; protein D.

XX Synthetic.

OS Human immunodeficiency virus type 1.

XX WO9916884-A1.

PN 08-APR-1999.

XX 17-SEP-1998; 98WO-EP06040.

XX 26-SEP-1997; 97GB-0020585.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

PI Bruck C, Godart SAG, Marchand M;

XX WPI; 1999-302282/25.

DR N-PSDB; AAX35693.

XX HIV Tat or Nef protein linked to a fusion partner

XX Disclosure; Fig 2; 66pp; English.

XX The present sequence represents a representative HIV-1 mutant Tat-His  
 CC protein. The protein is used in the creation of the fusion proteins of  
 CC the invention, in conjunction with a fusion partner (e.g. protein D).  
 CC The specification also describes fusion proteins comprising HIV-1 Nef  
 CC protein. The fusion protein can be used in a vaccine to prevent HIV  
 CC infection.

XX SQ Sequence 302 AA;

Query Match 99.1%; Score 547; DB 20; Length 302;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-49;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EPVDPRLPEPKHPSQKPTACTNCYCKKCCFHCQVCFTTAALGISYGRKKRRRPPQ 61  
 Db 209 epvdprrlepkhpsqkptactncycckccfchcqvcfitaalgisyrkrrrrppq 268  
 QY 62 SOTHOVSLSKQPTSQSKGPTGPKETSGHHHHH 95  
 Db 269 sqthqvsksqptsqskgptgpketsgghhhhh 302

RESULT 4  
AAG63239  
ID AAG63239 standard; Protein; 302 AA.

XX AC AAG63239;  
XX DT 01-OCT-2001 (first entry)  
XX DE Amino acid sequence of a His-tagged mutant His protein of HIV.  
XX DE HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.

XX OS Synthetic.  
XX OS Human immunodeficiency virus.

XX PN WO200154719-A2.

XX PD 02-AUG-2001.

XX PF 29-JAN-2001; 2001WO-EP00944.

XX PR 31-JAN-2000; 2000GB-0002200.

XX PR 14-APR-2000; 2000GB-0009336.

XX PR 06-JUN-2000; 2000GB-0013806.

XX PR 28-JUN-2000; 2000WO-EP05998.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Voss G;

XX DR WPI; 2001-476172/51.

XX DR N-PSDB; AAH42883.

XX PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
XX PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
XX PT protein or polynucleotide for the manufacture of a vaccine -

XX PS Disclosure; Fig 1; 90pp; English.

XX CC The present sequence represents a His-tagged mutant His protein of HIV.  
XX CC The protein is expressed in the yeast Pichia pastoris, and is used to  
XX CC produce the vaccine of the invention. The specification describes  
XX CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the  
XX CC manufacture of a vaccine. The vaccine is used for the prophylactic or  
XX CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
XX CC in synergy with gp120 in the treatment and prevention of HIV. The  
XX CC vaccine reduces the HIV viral load in HIV infected humans and results  
XX CC in a maintenance of CD4+ levels over those levels found in the absence  
XX CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.

XX SQ Sequence 302 AA;

Query Match 99.18; Score 547; DB 22; Length 302;  
Best Local Similarity 100.0%; Pred. No. 3.8e-49;  
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EPVDPRLPEWKHPGSGPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQG 61  
Db 209 epvdpriepwkhpqsgpkactncycckkccfhcqvcfitaalgisyrkrrrrppqg 268  
|||||

Qy 62 SQTHQVSLSKQPTSQSKGEPGPKETSGHHHHH 95  
Db 269 sqthqvslskqptsqskgeptgpketsghhhhh 302  
|||||

RESULT 5  
AAY02350  
ID AAY02350 standard; Protein; 95 AA.  
XX AC AAY02350;

XX 09-JUL-1999 (first entry)  
XX DT A representative HIV-1 Tat-His protein.  
XX DE HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
XX KW vaccine; HIV infection; protein D.  
XX OS Synthetic.  
XX OS Human immunodeficiency virus type 1.

XX PN WO9916884-A1.

XX PD 08-APR-1999.

XX PF 17-SEP-1998; 98WO-EP06040.

XX PR 26-SEP-1997; 97GB-0020585.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Bruck C, Godart SAG, Marchand M;

XX DR WPI; 1999-302282/25.

XX DR N-PSDB; AAX35686.

XX PT HIV Tat or Nef protein linked to a fusion partner

XX PS Disclosure; Fig 2; 66pp; English.

XX CC The present sequence represents a representative HIV-1 Tat-His protein.  
XX CC The protein is used in the creation of the fusion proteins of  
XX CC the invention, in conjunction with a fusion partner (e.g. protein D).  
XX CC The specification also describes fusion proteins comprising HIV-1 Nef  
XX CC protein. The fusion protein can be used in a vaccine to prevent HIV  
XX CC infection.

XX SQ Sequence 95 AA;

Query Match 98.0%; Score 541; DB 20; Length 95;  
Best Local Similarity 96.8%; Pred. No. 4.8e-49;  
Matches 92; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPWKHPGSGPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
Db 1 mepvdprlepwkhpqsgpkactncycckkccfhcqvcfitaalgisyrkrrrrppq 60  
|||||

Qy 61 GSQTHQVSLSKQPTSQSKGEPGPKETSGHHHHH 95  
Db 61 gsqthqvslskqptsqskrgdptgpketsghhhhh 95  
|||||

RESULT 6

AAG63232  
ID AAG63232 standard; Protein; 95 AA.

XX AC AAG63232;

XX DT 01-OCT-2001 (first entry)

XX DE Amino acid sequence of a His-tagged Tat protein of HIV.

XX KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.

XX OS Synthetic.

XX OS Human immunodeficiency virus.

XX PN WO200154719-A2.

XX PD 02-AUG-2001.

XX PF 29-JAN-2001; 2001WO-EP00944.

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XX PR 31-JAN-2000; 2000GB-0002200.
XX PR 14-APR-2000; 2000GB-0009336.
XX PR 06-JUN-2000; 2000GB-0013806.
XX PR 28-JUN-2000; 2000WO-EP05998.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Voss G;
XX CC The present sequence represents a His-tagged Tat protein of HIV. The
XX CC protein is expressed in the yeast Pichia pastoris, and is used to
XX CC produce the vaccine of the invention. The specification describes
XX CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the
XX CC manufacture of a vaccine. The vaccine is used for the prophylactic or
XX CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act
XX CC in synergy with gp120 in the treatment and prevention of HIV. The
XX CC vaccine reduces the HIV viral load in HIV infected humans and results
XX CC in a maintenance of CD4+ levels over those levels found in the absence
XX CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.
XX SQ Sequence 95 AA;

Query Match 98.0%; Score 541; DB 22; Length 95;
Best Local Similarity 96.8%; Pred. No. 4.8e-49;
Matches 92; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEVDPRLEPKHPSQPKTACTNCKYKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
DB 1 mepvdprlepwhpsqpkactnckycckccfchcqvctkalgisygrkkrrrrppq 60
QY 61 GSQTHOVSLSKOPTSOSKGEPTGPKETSGHHHHH 95
DB 61 gsqthqvskskptsqsgrgdtpgktsghhhhh 95

RESULT 7
AAY02351
ID AAY02351 standard; Protein: 302 AA.
XX AC AAY02351;
XX CC AAY02351;
XX DT 09-JUL-1999 (first entry)
XX DE A representative HIV-1 Nef-Tat-His protein.
XX KW HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;
XX KW vaccine; HIV infection; protein D.
XX OS Synthetic.
XX OS Human immunodeficiency virus type 1.
XX PN WO9916884-A1.
XX PD 08-APR-1999.
XX PF 17-SEP-1998; 98WO-EP06040.
XX PR 26-SEP-1997; 97GB-0020585.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Bruck C, Godart SAG, Marchand M;

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XX DR WPI; 1999-302282/25.
XX DR N-PSDB; AAX35687.
XX PT HIV Tat or Nef protein linked to a fusion partner
XX PS Disclosure; Fig 2; 66pp; English.
XX CC The present sequence represents a representative HIV-1 Nef-Tat-His
XX CC protein. The protein is used in the creation of the fusion proteins of
XX CC the invention, in conjunction with a fusion partner (e.g. protein D).
XX CC The fusion protein can be used in a vaccine to prevent HIV infection.
XX SQ Sequence 302 AA;

Query Match 97.1%; Score 536; DB 20; Length 302;
Best Local Similarity 96.8%; Pred. No. 5.3e-48;
Matches 91; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EPVDPRLEPKHPSQPKTACTNCKYKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 61
DB 209 epvdprlepwhpsqpkactnckycckccfchcqvctkalgisygrkkrrrrppqg 268
QY 62 SOTHQVSLSKOPTSOSKGEPTGPKETSGHHHHH 95
DB 269 sqthqvskskptsqsgrgdtpgktsghhhhh 302

RESULT 8
AAG63233
ID AAG63233 standard; Protein: 302 AA.
XX AC AAG63233;
XX CC AAG63233;
XX DT 01-OCT-2001 (first entry)
XX DE Amino acid sequence of a His-tagged Nef-Tat linked protein of HIV.
XX KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.
XX OS Synthetic.
XX OS Human immunodeficiency virus.
XX PN WO200154719-A2.
XX PD 02-AUG-2001.
XX PF 29-JAN-2001; 2001WO-EP00944.
XX PR 31-JAN-2000; 2000GB-0002200.
XX PR 14-APR-2000; 2000GB-0009336.
XX PR 06-JUN-2000; 2000GB-0013806.
XX PR 28-JUN-2000; 2000WO-EP05998.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Voss G;
XX CC WPI; 2001-476172/51.
XX CC N-PSDB; AAH42877.
XX PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef
XX PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120
XX PT protein or polynucleotide for the manufacture of a vaccine -
XX PS Disclosure; Fig 1; 90pp; English.
XX CC The present sequence represents a His-tagged Nef-Tat linked protein of
XX CC HIV. The protein is expressed in the yeast Pichia pastoris, and is used
XX CC to produce the vaccine of the invention. The specification describes
XX CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the
XX CC manufacture of a vaccine. The vaccine is used for the prophylactic or

```

CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
CC in synergy with gp120 in the treatment and prevention of HIV. The  
CC vaccine reduces the HIV viral load in HIV infected humans and results  
CC in a maintenance of CD4+ levels over those levels found in the absence  
CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.  
XX  
SQ Sequence 302 AA;

Query Match 97.1%; Score 536; DB 22; Length 302;  
Best Local Similarity 96.8%; Pred. No. 5.3e-48;  
Matches 91; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EPVDPRLPEWKHPGSGPKTACTNCYCKCCFHCQVCFTTAALGISYGRKKRRQRRPPQG 61  
DB 209 epvdpriepwkhpqsgpqtactncycckccfhcqvcftkalgisygrkkrrirppqg 268  
QY 62 SOTHQVLSKQPTSQSGKEPTGPKETSGHHHHH 95  
DB 269 sqthqvsksqptsqsgrdptgpketsghhhhhh 302

RESULT 9  
AAY02353  
ID AAY02353 standard; Protein; 411 AA.

AC. AAY02353;

DT 09-JUL-1999 (first entry)

DE A representative Lipod-Tat-His fusion protein.

XX HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
KW vaccine; HIV infection; protein D.

XX Synthetic.

OS Human immunodeficiency virus type 1.

XX WO9916884-A1.

PD 08-APR-1999.

PF 17-SEP-1998; 98WO-EP06040.

PR 26-SEP-1997; 97GB-0020585.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

PI Bruck C, Godart SAG, Marchand M;

XX WPI; 1999-302282/25.

DR N-PSDB; AAX35689.

XX HIV Tat or Nef protein linked to a fusion partner

PS Disclosure; Fig 2; 66pp; English.

XX The present sequence represents a fusion protein comprising Lipod-HIV-1  
CC Tat-His. The protein is exemplified the fusion proteins of  
CC the invention. The specification also describes fusion proteins  
CC comprising HIV-1 Nef protein. The fusion protein can be used in a  
CC vaccine to prevent HIV infection.

XX Sequence 411 AA;

Query Match 97.1%; Score 536; DB 20; Length 411;  
Best Local Similarity 96.8%; Pred. No. 7.3e-48;  
Matches 91; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EPVDPRLPEWKHPGSGPKTACTNCYCKCCFHCQVCFTTAALGISYGRKKRRQRRPPQG 61  
DB 318 epvdpriepwkhpqsgpqtactncycckccfhcqvcftkalgisygrkkrrirppqg 377

QY 62 SOTHQVLSKQPTSQSGKEPTGPKETSGHHHHH 95  
DB 378 sqthqvsksqptsqsgrdptgpketsghhhhhh 411

RESULT 10

AAG63235  
ID AAG63235 standard; Protein; 411 AA.

AC AAG63235;

DT 01-OCT-2001 (first entry)

XX Amino acid sequence of a His tagged LipD-Nef-Tat linked protein.  
DE HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.

XX Synthetic.

OS Human immunodeficiency virus.

XX Key Location/Qualifiers  
FT Peptide 1..109  
/note= "ProtD fusion partner"

PN WO200154719-A2.

XX 02-AUG-2001.

PF 29-JAN-2001; 2001WO-EP00944.

XX 31-JAN-2000; 2000GB-0002200.

PR 14-APR-2000; 2000GB-0009336.

PR 06-JUN-2000; 2000GB-0013806.

XX 28-JUN-2000; 2000WO-EP05998.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

PI Voss G;

XX WPI; 2001-476172/51.

DR N-PSDB; AAX42879.

XX New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
PT protein or polynucleotide for the manufacture of a vaccine -

PS Disclosure; Fig 1; 90pp; English.

XX The present sequence represents a His-tagged Nef-Tat linked protein of  
CC HIV, with a lipidation signal sequence (Lipod) which is removed after  
CC processing and a protD fusion partner. The protein is expressed in  
CC Escherichia coli, and is used to produce the vaccine of the invention.  
CC The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat;  
CC and HIV gp120 in the manufacture of a vaccine. The vaccine is used for  
CC the prophylactic or therapeutic immunization of humans against HIV.  
CC Tat, Nef or Nef-Tat act in synergy with gp120 in the treatment and  
CC prevention of HIV. The vaccine reduces the HIV viral load in HIV  
CC infected humans and results in a maintenance of CD4+ levels over those  
CC levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat  
CC and HIV gp120.

XX Sequence 411 AA;

Query Match 97.1%; Score 536; DB 22; Length 411;  
Best Local Similarity 96.8%; Pred. No. 7.3e-48;  
Matches 91; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EPVDPRLPEWKHPGSGPKTACTNCYCKCCFHCQVCFTTAALGISYGRKKRRQRRPPQG 61  
DB 318 epvdpriepwkhpqsgpqtactncycckccfhcqvcftkalgisygrkkrrirppqg 377



```

QY 62 SOTHQVSLSKQPTSQSKGPTGPKETSGHHHHH 95
Db 378 sqthqvslskqptsqsgrdptgpketsgghhhhh 411

RESULT 11
AAY02355 standard; Protein; 413 AA.
XX AC AAY02355;
XX DT 09-JUL-1999 (first entry)
XX DE A representative Lipod-Tat fusion protein.
XX KW HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;
XX KW vaccine; HIV infection; protein D.
XX OS Synthetic.
XX OS Human immunodeficiency virus type 1.
XX PN WO9916884-A1.
XX PD 08-APR-1999.
XX PF 17-SEP-1998; 98WO-EP06040.
XX PR 26-SEP-1997; 97GB-0020585.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Bruck C, Godart SAG, Marchand M;
XX DR WPI; 1999-302282/25.
XX DR N-PSDB; AAX35691.
XX PT HIV Tat or Nef protein linked to a fusion partner
XX PS Disclosure; Fig 2; 66pp; English.
XX CC The present sequence represents a fusion protein comprising Lipod-HIV-1
CC Tat. The protein is exemplifies the fusion proteins of
CC the invention. The specification also describes fusion proteins
CC comprising HIV-1 Nef protein. The fusion protein can be used in a
CC vaccine to prevent HIV infection.
XX SQ Sequence 413 AA;

Query Match 97.1%; Score 536; DB 20; Length 413;
Best Local Similarity 96.8%; Pred. No. 7.3e-48;
Matches 91; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EPVDPRLEPKHPSQPKTACTNCYKCKCFHCQVCFTALGSGYGRKKRRRRPPQG 61
Db 320 epvdprlepkhpsqpkactactncycckcfhcqvcftkalgisygrkkrrrrppqg 379

QY 62 SOTHQVSLSKQPTSQSKGPTGPKETSGHHHHH 95
Db 380 sqthqvslskqptsqsgrdptgpketsgghhhhh 413

RESULT 12
AAG63237
ID AAG63237 standard; Protein; 413 AA.
XX AC AAG63237;
XX DT 01-OCT-2001 (first entry)
XX DE Amino acid sequence of a His tagged ProtD-Nef-Tat fusion protein.
XX KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.

```

```

XX OS Synthetic.
XX OS Human immunodeficiency virus.
XX FT Key Location/Qualifiers
XX FT Peptide 1...111
XX PN /note= "ProtD fusion partner"
XX PN WO200154719-A2.
XX PD 02-AUG-2001.
XX PF 29-JAN-2001; 2001WO-EP00944.
XX PR 31-JAN-2000; 2000GB-0002200.
XX PR 14-APR-2000; 2000GB-0009336.
XX PR 06-JUN-2000; 2000GB-0013806.
XX PR 28-JUN-2000; 2000WO-EP05998.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Voss G;
XX DR WPI; 2001-476172/51.
XX DR N-PSDB; AAH42881.
XX PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef
XX PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120
XX PT protein or polynucleotide for the manufacture of a vaccine.
XX PS Disclosure; Fig 1; 90pp; English.
XX CC The present sequence represents a His-tagged ProtD-Nef-Tat fusion
XX CC protein. The protein is expressed in Escherichia coli, and is used to
XX CC produce the vaccine of the invention. The specification describes
XX CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the
XX CC manufacture of a vaccine. The vaccine is used for the prophylactic or
XX CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act
XX CC in synergy with gp120 in the treatment and prevention of HIV. The
XX CC vaccine reduces the HIV viral load in HIV infected humans and results
XX CC in a maintenance of CD4+ levels over those levels found in the absence
XX CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.
XX SQ Sequence 413 AA;

Query Match 97.1%; Score 536; DB 22; Length 413;
Best Local Similarity 96.8%; Pred. No. 7.3e-48;
Matches 91; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EPVDPRLEPKHPSQPKTACTNCYKCKCFHCQVCFTALGSGYGRKKRRRRPPQG 61
Db 320 epvdprlepkhpsqpkactactncycckcfhcqvcftkalgisygrkkrrrrppqg 379

QY 62 SOTHQVSLSKQPTSQSKGPTGPKETSGHHHHH 95
Db 380 sqthqvslskqptsqsgrdptgpketsgghhhhh 413

RESULT 13
AAY22960
ID AAY22960 standard; Protein; 86 AA.
XX AC AAY22960;
XX DT 20-AUG-1999 (first entry)
XX DE Lys41 mutant tat amino acid sequence of HIV-1.
XX KW HIV Tat protein; AIDS; tumour; HIV infection; dendritic cell;
XX KW Kaposi's sarcoma cell; activated endothelial cell;
XX KW cytokine-activated endothelial cell; vaccine.

```



CC All or part of it can be produced by recombinant vaccinia virus by  
 CC integrating it into the genome region nonessential for vaccinia virus  
 CC proliferation and then infecting animal cells with the recombinant virus.  
 CC Tat protein can be used to diagnose HIV infection and for prophylaxis  
 CC for AIDS or ARC patients. It can also be used to develop a live vaccine  
 CC using temperature-sensitive Lister strain of vaccinia virus.  
 XX  
 SQ Sequence 86 AA;

Query Match 86.6%; Score 478; DB 10; Length 86;  
 Best Local Similarity 96.5%; Pred. No. 1.6e-42;  
 Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPVDPRLEPWKHPGSPKACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
 DB 1 MEPVDPRLEPWKHPGSPKACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
 QY 61 GSQTHOVSLSKOPTSQSKGPTGPKE 86  
 DB 61 GSQTHOVSLSKOPTSQSKGPTGPKE 86

## RESULT 16

AAP91905  
 ID AAP91905 standard; protein; 86 AA.

AC AAP91905;

XX 12-MAY-1990 (first entry)

DE cDNA for tat protein of human immunodeficiency virus (HIV).

XX tat protein; HIV; recombinant vaccinia virus.

XX Human immunodeficiency virus.

FT Key Location/Qualifiers  
 FT CDS 46...306  
 FT /\*tag= a

XX JP01085092-A.

XX 30-MAR-1989.

XX 25-SEP-1987; 87JP-0240513.

XX 25-SEP-1987; 87JP-0240513.

XX (KOKU-) KOKURITSU YOBO EISE (JAPC).

XX WPI; 1989-140777/19.

XX N-PSDB; AAP91905.

XX Prodn. of protein(s)

PT - using recombinant vaccinia viruses contg. protein of

PT Human Immunodeficiency Virus

XX Fig 5; page 863; 9pp; Japanese.

CC It is inserted into the genome of vaccinia viruses in a  
 CC region which is not essential for their propagation to create recombinant  
 CC vaccinia viruses. These viruses are propagated in animal cells together  
 CC with recombinant vaccinia viruses which contain DNA coding for a useful  
 CC protein, for example, human growth hormone, insulin, interferons,  
 CC interleukin-2; haemagglutination factor, hepatitis-B surface antigen,  
 CC amylase, protease. The presence of tat protein assists the mass-  
 CC production of the useful protein.

XX Sequence 86 AA;

Query Match 86.6%; Score 478; DB 10; Length 86;

Best Local Similarity 96.5%; Pred. No. 1.6e-42;  
 Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MEPVDPRLEPWKHPGSPKACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
 DB 1 MEPVDPRLEPWKHPGSPKACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
 QY 61 GSQTHOVSLSKOPTSQSKGPTGPKE 86  
 DB 61 GSQTHOVSLSKOPTSQSKGPTGPKE 86

## RESULT 17

AAP93140  
 ID AAP93140 standard; protein; 86 AA.

XX AAP93140;

XX 21-MAR-1990 (first entry)

DE Synthetic TAT protein.

XX TAT protein; HIV-1; tat gene; trans-activator; anti-terminator;

XX WO8909824-A.

XX 19-OCT-1989.

XX 14-APR-1989; 89WO-GB00384.

XX 15-APR-1988; 88GB-0008892.

XX (BRBI-) BRITISH BIOTECHNOLOGY.

XX Edwards RM, Adams SE;

XX WPI; 1989-324229/44.

XX N-PSDB; AAN91837.

PT Synthesis of double stranded DNA, esp. TAT gene of HIV - by prepq. DNA

XX contg. a single and double stranded portion and in vivo gap repair.

XX Disclosure; fig.2; 23pp; English.

CC The synthetic tat DNA encoding this protein has useful restriction sites  
 CC to facilitate modification for structural and immunological studies. TAT  
 CC is a transactivator involved in the activation of HIV long terminal  
 CC repeat, acting as an anti-terminator.

XX Sequence 86 AA;

Query Match 86.6%; Score 478; DB 10; Length 86;

Best Local Similarity 96.5%; Pred. No. 1.6e-42;  
 Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPVDPRLEPWKHPGSPKACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
 DB 1 MEPVDPRLEPWKHPGSPKACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60

QY 61 GSQTHOVSLSKOPTSQSKGPTGPKE 86

DB 61 GSQTHOVSLSKOPTSQSKGPTGPKE 86

## RESULT 18

AAR38618  
 ID AAR38618 standard; protein; 86 AA.

XX AAR38618;

XX 13-DEC-1993 (first entry)

XX

DE Sequence of the HIV-1 TAT protein.  
 XX Human immunodeficiency virus 1; HIV-1; TAT protein; transactivator;  
 KW long terminal repeat; transactivation response element; TAR;  
 KW RNA binding; RNA cleavage.  
 XX  
 XX Human immunodeficiency virus 1.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 49..57  
 FT /label= nuclear targeting domain  
 FT Region 49..72  
 FT /note= "proteolytic product of wt TAT protein  
 FT which binds specifically to TAR-element-  
 FT contg. RNA"  
 XX  
 PN WO9312234-A.  
 XX  
 XX 24-JUN-1993.  
 PD  
 XX 11-DEC-1992; 92WO-US10770.  
 PF  
 XX 13-DEC-1991; 91US-0808452.  
 PR 21-JAN-1992; 92US-0826934.  
 XX  
 XX (STRI ) SRI INT.  
 PA  
 XX Jayasena SD, Johnston BH;  
 PI WPI; 1993-214176/26.  
 XX  
 XX Viral polypeptide(s) with site-specific RNA binding - contain  
 PT moiety to cleave RNA backbone and are used to inhibit HIV antigen  
 PT expression in infected cells  
 XX  
 XX Claim 2; Figure 2A; 94pp; English.  
 PS  
 XX TAT is a potent transactivator of long terminal repeat (LTR)-  
 CC directed viral gene expression. TAR-induced transactivation requires  
 CC the present of the TAR (transactivation response) element, located  
 CC at the 5'UTR of the viral mRNA element. The sequence of RNA target  
 CC molecules were chosen based on previous studies characterising the  
 CC binding properties of the HIV-encoded TAT protein and the TAR target  
 CC region from both HIV-1 and HIV-2. HIV-1 TAR is the 57-nt RNA stem-  
 CC loop structure found in HIV-1 mRNA (nt 1-57). The RNA substrate is  
 CC given in AAQ44139.  
 XX  
 SQ Sequence 86 AA;  
 Query Match 86.6%; Score 478; DB 14; Length 86;  
 Best Local Similarity 96.5%; Pred. No. 1.6e-42;  
 Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRPPQ 60  
 DB 1 mepvdprlepkhgpsqpkactncycckccfqcvcfctkalgisygrkkrrrrppq 60  
 QY 61 GSQTHQVSLSKQPTSQSGEPTGPK 86  
 DB 61 gsqthqvskskptsqsgtdgtgpk 86  
 RESULT 19  
 AAR86625  
 ID AAR86625 standard; Protein; 86 AA.  
 AC AAR86625;  
 XX 28-JUN-1996 (first entry)  
 DT  
 XX HIV TAT.  
 DE  
 XX

KW Immunogen; cellular uptake region; transactivating protein; TAT; HIV;  
 KW viraemia; antibody.  
 XX  
 OS Human immunodeficiency virus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 46..63  
 FT /note= "Cellular uptake region"  
 XX  
 XX WO9531999-A1.  
 PN  
 XX 30-NOV-1995.  
 PD  
 XX 16-MAY-1995; 95WO-US06077.  
 PF  
 XX 23-MAY-1994; 94US-0247991.  
 PR  
 XX (IMMU-) IMMUNOLOGY RES INST INC.  
 PA  
 XX Culler MD, Goldstein G, Shenbagamurthi P;  
 PI WPI; 1996-049298/05.  
 DR N-PSDB; AAT06634.  
 XX  
 XX Immunogen containing cellular uptake region of viral TAT protein -  
 PT induces high antibody titre against TAT, partic. for preventing or  
 PT treating HIV infection  
 XX  
 PS Disclosure; Figure 1; 54pp; English.  
 XX  
 CC This sequence represents the HIV transactivating protein, TAT. The  
 CC sequences given in AAR86601-19 are immunogens derived from the cellular  
 CC uptake region of this protein. These peptides are based on the region  
 CC comprising amino acids 46-63. The immunogenic peptides are used to  
 CC protect against infection by HIV. They may also be used to reduce  
 CC viraemia in already infected patients. These immunogens may be used  
 CC to identify, or generate, antibodies specific for TAT.  
 XX  
 SQ Sequence 86 AA;  
 Query Match 86.6%; Score 478; DB 17; Length 86;  
 Best Local Similarity 96.5%; Pred. No. 1.6e-42;  
 Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRPPQ 60  
 DB 1 mepvdprlepkhgpsqpkactncycckccfqcvcfctkalgisygrkkrrrrppq 60  
 QY 61 GSQTHQVSLSKQPTSQSGEPTGPK 86  
 DB 61 gsqthqvskskptsqsgtdgtgpk 86  
 RESULT 20  
 AAW31202  
 ID AAW31202 standard; protein; 86 AA.  
 XX  
 AC AAW31202;  
 XX 20-MAR-1998 (first entry)  
 DT  
 XX Human Immunodeficiency Virus Type 1 Tat protein.  
 DE  
 XX Human immunodeficiency virus; HIV Type 1; Tat protein;  
 KW cargo molecules; intracellular delivery; fusion protein;  
 KW therapeutic; prophylactic; diagnostic; transport polypeptide.  
 XX  
 XX Human immunodeficiency virus type 1.  
 OS  
 XX Key Location/Qualifiers  
 FT Region 22..36  
 FT /label= cysteine-rich

```

FT Region 49..57
FT /label= basic_region
FT Domain 73..86
FT /label= carboxy_terminal_domain
PN US5674980-A.
XX
XX PD 07-OCT-1997.
XX
XX PF 21-DEC-1989; 89US-0454450.
XX
XX PR 28-APR-1994; 94US-0235403.
XX PR 21-DEC-1989; 89US-0454450.
XX PR 02-JAN-1991; 91US-0636662.
XX PR 21-AUG-1992; 92US-0934375.
XX PR 19-AUG-1993; 93WO-US07833.
XX PR 24-NOV-1993; 93US-0158015.
XX PR 25-MAY-1995; 95US-0450098.
XX
XX PA (BARS/) BARSOU J G.
XX PA (FAWE/) FAWELL S E.
XX PA (FRAN/) FRANKEL A.
XX PA (PABO/) PABO.
XX PA (PEPI/) PEPINSKY R B.
XX
XX PI Barsoum JG, Fawell SE, Frankel A, Pabo C, Pepinsky RB;
XX
XX DR WPI; 1997-502388/46.
XX
XX PT Fusion proteins containing truncated HIV tat sequences - useful for
XX intracellular delivery of viral repressor proteins
XX
XX PS Example I; Fig 1; 77pp; English.
XX
XX CC This sequence represents the Tat protein from Human Immunodeficiency
XX virus, Type 1 which can be used in a novel method for the delivery of
XX biologically active cargo molecules into the cytoplasm and nuclei of
XX eukaryotic cells. The tat protein from immunodeficiency virus (e.g.
XX HIV-1, HIV-2, SIV) is readily taken up into cells when present
XX extracellularly. By modifying the HIV tat protein i.e. removing the
XX cysteine-rich region and the carboxy-terminal domain and covalently
XX linking the protein to a cargo molecule to form a fusion protein,
XX the problems of spurious trans-activation and disulphide aggregation are
XX eradicated. The reduced size of transport polypeptides also minimises
XX interference with the biological activity of the cargo molecule. This is
XX applicable for therapeutic, prophylactic or diagnostic intracellular
XX delivery of small molecules and macromolecules e.g. proteins, nucleic
XX acids and polysaccharides.
XX
XX SQ Sequence 86 AA;

Query Match 86.6%; Score 478; DB 18; Length 86;
Best Local Similarity 96.5%; Pred. No. 1.6e-42;
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPVDPRLPEPKHPSQPKTACTNCYCKCFHCQVCFTTALGTSYGRKKRRRRPPQ 60
Db 1 mepvdpriepkhpqsgqpkactncycckcfhcqvcfttkalgsygrkrrrrppq 60

QY 61 GSQTHQVSLSKOPTSQSKGEPTGPKE 86
Db 61 gsqthqvskskptsqsgrgdptgpke 86

RESULT 21
ID AAW26443
XX AAW26443 standard; Protein; 86 AA.
XX
XX AC AAW26443;
XX
XX DT 16-DEC-1997 (first entry)
XX

```

```

DE HIV tat protein.
XX
XX KW HIV; tat protein; transport protein; cargo delivery.
XX
XX OS Human immunodeficiency virus type 1.
XX
XX FH Key Location/Qualifiers
XX FT Region 23..36
XX FT /label= Cys-rich_region
XX FT Region 47..59
XX FT /label= Basic_region
XX FT Region 73..86
XX FT /label= C-terminal
XX
XX PN US5652122-A.
XX
XX PD 29-JUL-1997.
XX
XX PF 21-DEC-1989; 89US-0454450.
XX
XX PR 28-APR-1994; 94US-0235403.
XX PR 21-DEC-1989; 89US-0454450.
XX PR 02-JAN-1991; 91US-0636662.
XX PR 21-AUG-1992; 92US-0934375.
XX PR 19-AUG-1993; 93WO-US07833.
XX PR 24-NOV-1993; 93US-0158015.
XX PR 25-MAY-1995; 95US-0450257.
XX
XX PA (BARS/) BARSOU J G.
XX PA (FAWE/) FAWELL S E.
XX PA (FRAN/) FRANKEL A.
XX PA (PABO/) PABO C.
XX PA (PEPI/) PEPINSKY R B.
XX
XX PI Barsoum JG, Fawell SE, Frankel A, Pabo C, Pepinsky RB;
XX
XX DR WPI; 1997-392943/36.
XX
XX PT New DNA constructs for transporting molecules to cells - encode a
XX fusion protein comprising a modified HIV tat protein and a
XX carboxy-terminal cargo moiety
XX
XX PS Disclosure; Fig 1; 76pp; English.
XX
XX CC This polypeptide comprises the HIV tat protein. Novel transport
XX proteins comprise modified HIV tat covalently attached to a cargo
XX molecule (see AAW26436-42). The modified tat protein (see AAW26444-49)
XX is characterised by the presence of the tat basic region (thought
XX to be required for nuclear localisation), and the absence of the
XX Cys-rich region and the exon 2-encoded C-terminal region. These
XX modifications solve the potential problems of spurious
XX trans-activation and disulphide aggregation, while the reduced size
XX of the transport proteins minimises interference with the
XX biological activity of the cargo molecule. DNA molecules that
XX encode the modified tat fusion proteins are claimed and can be
XX used to deliver polypeptides or nucleic acids to the cytoplasm
XX of nuclei of cells in vivo or in vitro.
XX
XX SQ Sequence 86 AA;

Query Match 86.6%; Score 478; DB 18; Length 86;
Best Local Similarity 96.5%; Pred. No. 1.6e-42;
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPVDPRLPEPKHPSQPKTACTNCYCKCFHCQVCFTTALGTSYGRKKRRRRPPQ 60
Db 1 mepvdpriepkhpqsgqpkactncycckcfhcqvcfttkalgsygrkrrrrppq 60

QY 61 GSQTHQVSLSKOPTSQSKGEPTGPKE 86
Db 61 gsqthqvskskptsqsgrgdptgpke 86

```

## RESULT 22

AAW71385  
ID AAW71385 standard; Protein: 86 AA.

XX AC AAW71385;

XX DT 04-DEC-1998 (first entry)

XX DE Amino acid sequence of HIV Tat 85.

XX KW HIV Tat 85; leaderless protein; inhibition; export; angiogenesis;  
XX KW restenosis; treatment; tumour; inflammation; cell proliferation;  
XX KW diabetes; retinopathy; infection; polycystic kidney disease;  
XX KW atherosclerosis.

XX OS Human immunodeficiency virus.

XX PN WO9837880-A1.

XX PD 03-SEP-1998.

XX PF 25-FEB-1998; 98WO-US03689.

XX PR 26-FEB-1997; 97US-0807014.

XX PA (CIBL-) CIBLEX CORP.

XX PI Baird A, Florkiewicz RZ;

XX DR WPI: 1998-495377/42.

XX DR N-PSDB; AAV60345.

XX PT Inhibiting export of leaderless protein with agent that inhibits  
PT binding to transporter protein - especially for treating  
PT angiogenesis and restenosis by preventing export of fibroblast  
PT growth factor, also methods for identifying leaderless proteins and  
PT their transporters

XX PS Claim 2; Page 70; 116pp; English.

XX CC The present sequence represents Human immunodeficiency virus (HIV) Tat  
CC 85, a leaderless protein. A leaderless protein refers to a protein that  
CC is found in an extracellular environment, but lacks a canonical leader  
CC sequence. The specification describes a method for inhibiting export of  
CC a leaderless protein from a cell. The method comprises treating  
CC the cell with an agent that inhibits binding between the leaderless  
CC protein and a transport molecule. Treatment with the inhibiting agent  
CC is specifically used to treat angiogenesis and restenosis, i.e. where  
CC expression of FGF-2 is inhibited, and the agent is applied to endothelial  
CC or smooth muscle cells. Other applications are treatment of tumours  
CC (melanoma, teratocarcinoma, ovarian carcinoma, bladder cancer and  
CC neuroblastoma), inflammation, cell proliferation, complications of  
CC diabetes (e.g. retinopathy), viral, bacterial or fungal infections,  
CC polycystic kidney disease and atherosclerosis.

XX SQ Sequence 86 AA;

Query Match 86.6%; Score 478; DB 19; Length 86;  
Best Local Similarity 96.5%; Pred. No. 1.6e-42;  
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKWPGSQPKTACTNCYCKKCFHCQVCFITTAALGTSYGRKKRRRRPPQ 60

Db 1 mepvdprlepkwpgsqpkttactncycckkcfhcqvcfittalgsygrkkrrrrppq 60

Qy 61 GSQTHQVSLSKQPTSQSKGEGTGPKE 86

Db 61 gsqthqvskskptsqsrqgdptgpke 86

## RESULT 23

AAW76148

ID AAW76148 standard; protein: 86 AA.

XX AC AAW76148;

XX DT 24-NOV-1998 (first entry)

XX DE HIV Type I TAT protein.

XX KW TAT protein; cargo molecule; therapy; diagnosis; transport protein;  
XX KW fusion protein; human papillomavirus E2 repressor; target cell.

XX OS Human immunodeficiency virus type 1.

XX PN US5804604-A.

XX PD 08-SEP-1998.

XX PF 25-MAY-1995; 95US-0450236.

XX PR 28-APR-1994; 94US-0235403.

XX PR 21-DEC-1989; 89US-0454450.

XX PR 02-JAN-1991; 91US-0636662.

XX PR 19-AUG-1993; 93WO-US07833.

XX PR 24-NOV-1993; 93US-0158015.

XX PR 25-MAY-1995; 95US-0450236.

XX PA (BIOJ ) BIOGEN INC.

XX PI Barsoum JG, Fawell SE, Frankel A, Pabo C, Pepinsky RB;

XX DR WPI: 1998-505702/43.

XX PT HIV tat-derived transport fusion proteins - used to deliver  
PT biological active molecules e.g. peptide(s) or nucleic acids,  
PT specifically into cytoplasm or nuclei of cells

XX PS Disclosure: Fig 1; 83pp; English.

XX CC This sequence represents the human immunodeficiency virus (HIV) Type I  
CC TAT protein which is used in a method for the delivery of biologically  
CC active cargo molecules into the cytoplasm and nuclei of cells, for  
CC therapeutic, prophylactic or diagnostic purposes. This is accomplished  
CC by the presence of a small, basic section of tat transport protein of  
CC HIV. This is used as it is this protein which is observed to cause human  
CC cells in culture to take up HIV. The method involves the use of a cargo  
CC moiety in combination with a transport moiety usually in the form of a  
CC fusion protein. The cargo moiety is a human papillomavirus E2 repressor  
CC and where the transport moiety is one of following HIV tat protein  
CC fragments (a) aa 47-58, (b) aa 47-72, (c) 38-72, (d) aa 38-58, (e)  
CC aa 37-58, (f) aa 1-21 and 38-72, (g) aa 47-62 or aa 38-62. The proteins  
CC allow delivery of specific peptides into cells at high concentrations  
CC due to use of existing transporters. Previous methods of delivery  
CC include bombardment and transforming, which only allow a fraction of the  
CC cell population to be infected and can additionally damage cells as  
CC they cause physical opening of the cell walls/membranes to allow entry.

XX SQ Sequence 86 AA;

Query Match 86.6%; Score 478; DB 19; Length 86;  
Best Local Similarity 96.5%; Pred. No. 1.6e-42;  
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKWPGSQPKTACTNCYCKKCFHCQVCFITTAALGTSYGRKKRRRRPPQ 60

Db 1 mepvdprlepkwpgsqpkttactncycckkcfhcqvcfittalgsygrkkrrrrppq 60

Qy 61 GSQTHQVSLSKQPTSQSKGEGTGPKE 86

Db 61 gsqthqvskskptsqsrqgdptgpke 86

```
RESULT 24
ID AAY96881 standard; Protein: 86 AA.
AC AAY96881;
XX
XX
DT 31-OCT-2000 (first entry)
XX
DE Human immunodeficiency virus Tat 85.
XX
KW Human immunodeficiency virus; HIV; Tat 85; transport molecule; golgi;
XX leaderless; endoplasmic reticulum; protein export; detection; inhibitor.
XX
OS Human immunodeficiency virus type 1.
XX
XX Key Location/Qualifiers
FH Misc-difference 53
FT /note= "Encoded by AGAA"
FT Misc-difference 80
FT /note= "Encoded by GAA"
XX
XX USG083706-A.
XX
XX PD 04-JUL-2000.
XX
XX PF 25-FEB-1998; 98US-0030613.
XX
XX PR 26-FEB-1997; 97US-0807014.
XX
XX PA (CIBL-) CIBLEX CORP.
XX
XX PI Baird A, Florkiewicz RZ;
XX
XX WPI: 2000-464338/40.
XX N-PSDB; AAA53572.
XX
XX Detecting transport molecules, useful for identifying proteins that
XX mediate leaderless protein export across cell membranes, by contacting
XX cell extracts with a fusion protein of leaderless protein and a tag to
XX form a complex
XX
XX PS Disclosure; Column 55-56; 64pp; English.
XX
XX CC Detecting a transport molecule involved in non-endoplasmic reticulum
XX (ER)/Golgi leaderless protein export, comprises contacting test cell
XX extracts or membranes with a fusion protein of a leaderless protein and
XX a tag to form a complex of the fusion protein bound to the transport
XX molecule, and detecting the transport molecule in an isolated complex.
XX The leaderless protein is a protein found in the extracellular
XX environment that lacks a canonical leader sequence, interleukin (IL)
XX 1-alpha, or 1-beta, fibroblast growth factor (FGF) 1 or 2, human
XX immunodeficiency virus (HIV) tat, platelet-derived endothelial cell
XX growth factor (PD-ECGF), ciliary neurotrophic factor (CNTF), sciatic
XX nerve growth-promoting activity, vas deferens protein, transglutaminase,
XX L-14 lectin, factor XIIIa, thioredoxin-like protein (ADF), thymosin,
XX parathyromosin, mammary-derived growth inhibitor, galectin or rhodanase.
XX The method is used to detect proteins, complexes of proteins, or parts of
XX a larger complex, that bind to and mediate the transport of leaderless
XX proteins, e.g. Na+/K+ ATPase which is an integral membrane protein
XX responsible for transporting sodium and potassium ions across the cell
XX membrane using ATP as the driving force. Transport molecules detected by
XX the method are used in assays to identify inhibitors of the interaction
XX with a leaderless protein.
XX
XX SQ Sequence 86 AA;
XX
XX Query Match 86.6%; Score 478; DB 21; Length 86;
XX Best Local Similarity 96.5%; Pred. No. 1.6e-42;
XX Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 MEPVDPRLPEPWKHPGSPQKTACTNCYCKKCCFHCQVCFTALGTSYGRKKRRRPPQ 60
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|||||
Db 1 mepvdpriepwkhpgsqktactncycckccfchqvcftkalgisggrkkrrrrppq 60
QY 61 GSQTHQVSLSKOPTSQSKGPTGPK 86
|||||
Db 61 gsqthqvskskqptsqsgrgdptgpk 86
|||||

RESULT 25
AAB85996
ID AAB85996 standard; Protein: 86 AA.
XX
XX AC AAB85996;
XX
XX DT 30-NOV-2001 (first entry)
XX
DE Amino acid sequence of HIV-1 isolate BH10 tat protein.
XX
XX KW HIV-1; gpl20; BH10; vaccine; immunization; tat protein.
XX
XX OS Human immunodeficiency virus type 1.
XX
XX PN USG268484-B1.
XX
XX PD 31-JUL-2001.
XX
XX PF 30-JUL-1998; 98US-0124900.
XX
XX PR 07-JUN-1995; 95US-0478536.
XX
XX PR 19-APR-1995; 95WO-EP01481.
XX
XX PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX
XX PI Katinger H, Buchacher A, Ernst W, Ballaun C, Purtscher M;
XX Trkola A, Predl R, Schmatz C, Klima A, Steindl F, Muster T;
XX
XX WPI: 2001-556601/62.
XX N-PSDB; AAH76385.
XX
XX New anti-idiotypic antibodies consisting of one or both amino acid
XX sequences corresponding to amino acid positions 79-84 or 326-400 of the
XX processed gp120 of HIV-isolate BH10, useful as vaccine against HIV-1
XX infections
XX
XX PS Claim 1; Columns 31-32; 27pp; English.
XX
XX CC The invention relates to a peptide fragment comprising of amino acid
XX sequences corresponding to sequences within the processed gp120 of HIV-1
XX isolate BH10 (GenBank accession M15654). The peptides are useful in the
XX detection, prevention and treatment of HIV-1 infections, and in AIDS
XX therapy. The antibodies are especially useful as vaccines for active and
XX passive immunization, or for the detection and/or determination of HIV-1
XX infected cells and/or HIV-1 viruses. The present sequence represents the
XX amino acid sequence of a tat protein from HIV-1 isolate BH10
XX (GenBank accession M15654).
XX
XX SQ Sequence 86 AA;
XX
XX Query Match 86.6%; Score 478; DB 22; Length 86;
XX Best Local Similarity 96.5%; Pred. No. 1.6e-42;
XX Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 MEPVDPRLPEPWKHPGSPQKTACTNCYCKKCCFHCQVCFTALGTSYGRKKRRRPPQ 60
|||||
Db 1 mepvdpriepwkhpgsqktactncycckccfchqvcftkalgisggrkkrrrrppq 60
|||||
QY 61 GSQTHQVSLSKOPTSQSKGPTGPK 86
|||||
Db 61 gsqthqvskskqptsqsgrgdptgpk 86
|||||

RESULT 26
```

AARL13379
ID AARL13379 standard; Protein; 87 AA.
XX AC
XX AARL13379;
XX DT 23-OCT-1991 (first entry)
XX DE TAT protein.
XX KW HIV; AIDS.
XX OS Synthetic.
XX PN EP441582-A.
XX PD 14-AUG-1991.
XX PF 04-FEB-1991; 91EP-0300903.
XX PR 09-FEB-1990; 90GB-0003010.
XX PA (GLAX ) GLAXO GROUP LTD.
XX PI Dykes CW, Ernst JF, Hobden AN;
XX DR WPI; 1991-240122/33.
XX DR N-PSDB; AAQI3188.
XX PT Gene expression system for yeast cells - with TAT protein mediated expression under the control of a HIV regulatory control sequence.
XX PS Disclosure; Page 10; 26pp; English.
XX CC The TAT protein here is encoded by the synthetic tat gene but is identical to the Tat protein found in HIV. The expression of the Tat protein in transformed yeast enables Tat inhibitory agents to be screened to obtain potential anti-viral agents esp. anti-HIV therapeutic agents.
XX SQ Sequence 87 AA;
Query Match 86.6%; Score 478; DB 12; Length 87; Best Local Similarity 96.5%; Pred. No. 1.6e-42; Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MEPVDPRLEPWKPGSPKTACTNICYKKCCFHQCVCFTTAALGISYGRKKRRRPPQ 60       Db 1 mepvdprlepwkpgspktactnicykkccfhqcvcftkalgisyrgrrrrppq 60 
Qy 61 GSOTHQVSLSKQPTSQSKEPTGPKE 86       Db 61 gsqthqvslskqptsqsrgdptgpke 86
RESULT 27
RAY22959
ID RAY22959 standard; Protein; 86 AA.
XX AC
XX AC RAY22959;
XX DT 20-AUG-1999 (first entry)
XX DE Cys22 mutant tat amino acid sequence of HIV-1. XX HIV Tat protein; AIDS; tumour; HIV infection; dendritic cell; KW Kaposi's sarcoma cell; activated endothelial cell; KW cytokine-activated endothelial cell; vaccine. XX Human immunodeficiency virus type 1. OS PN WO9927958-A2.





CC syndromes and symptoms associated with HIV infection. A biologically  
CC active Tat protein, fragments and/or mutants and/or Tat DNA which is  
CC capable of entering and localizing in the nuclei of activated endothelial  
CC cells or dendritic cells and/or activating the proliferation, migration  
CC and invasion of Kaposi's sarcoma (KS) cells and cytokine-activated  
CC endothelial cells, is used as a vaccine. HIV-1 Tat or its mutants  
CC in a biologically active form is able to induce a very strong immune  
CC response against HIV, able to prevent infection or the development of  
CC the disease and to permit efficient therapeutic strategies in  
CC HIV-1-infected individuals.

XX  
SQ Sequence 83' AA;

Query Match 82.9%; Score 457.5; DB 20; Length 83;  
Best Local Similarity 95.3%; Pred. No. 2.le-40;  
Matches 82; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 1 MEPVDPRLEPWKHPGSPQKTACTNICYKCKCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
Db 1 mepvdprlepwkhpqsgpqtactnycyckckcfhcqvcfittalgisysgrkrrrrppq 60  
Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKE 86  
Db 61 gsqthqvslskqptsqs---ptgpk 83

Search completed: August 26, 2002, 08:12:31  
Job time: 240 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 08:10:41 ; Search time 38.46 Seconds  
(without alignments)  
60.334 Million cell updates/sec

Title: US-09-509-239-23  
Perfect score: 552  
Sequence: 1 MEVPDRLEPWKHPGSPQPKT.....QSKGPTGPKETSGHHHHH 95

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	478	86.6	86	1	US-08-450-257-1
2	478	86.6	86	1	US-08-450-246-1
3	478	86.6	86	1	US-08-450-098-1
4	478	86.6	86	1	US-08-451-233-1
5	478	86.6	86	1	US-08-450-236-1
6	478	86.6	86	3	US-07-808-452-1
7	478	86.6	86	3	US-09-030-613-19
8	478	86.6	86	4	US-09-124-900-6
9	478	86.6	86	4	US-09-451-905-19
10	478	86.6	86	4	US-08-235-403-1
11	478	86.6	86	5	PCT-US92-10770-1
12	478	86.6	86	5	PCT-US95-06077-2
13	462	83.7	86	2	US-08-505-210-1
14	462	83.7	86	4	US-09-089-333-1
15	447	81.0	82	1	US-08-053-079A-15
16	408	73.9	72	3	US-09-030-613-17
17	408	73.9	72	4	US-09-451-905-17
18	384	69.6	72	2	US-08-893-853-1
19	384	69.6	72	4	US-09-113-921-1
20	360.5	65.3	312	1	US-08-094-128A-27
21	360.5	65.3	312	1	US-08-455-674-27
22	360.5	65.3	312	1	US-08-455-992-27
23	360.5	65.3	312	1	US-08-455-972-27
24	360.5	65.3	312	5	PCT-US92-00652-27
25	351	63.6	72	1	US-07-910-867B-2
26	330	59.8	72	1	US-07-910-867B-5
27	324	58.7	72	1	US-07-910-867B-3

28	310	56.2	72	1	US-07-910-867B-1	Sequence 1, Appl
29	276	50.0	56	1	US-08-450-257-7	Sequence 7, Appl
30	276	50.0	56	1	US-08-450-246-7	Sequence 7, Appl
31	276	50.0	56	1	US-08-450-098-7	Sequence 7, Appl
32	276	50.0	56	1	US-08-451-233-7	Sequence 7, Appl
33	276	50.0	56	1	US-08-450-236-7	Sequence 7, Appl
34	276	50.0	56	4	US-08-235-403-7	Sequence 7, Appl
35	188	34.1	37	1	US-07-724-500B-22	Sequence 22, Appl
36	181	32.8	36	1	US-08-450-257-2	Sequence 2, Appl
37	181	32.8	36	1	US-08-450-246-2	Sequence 2, Appl
38	181	32.8	36	1	US-08-450-098-2	Sequence 2, Appl
39	181	32.8	36	1	US-08-451-233-2	Sequence 2, Appl
40	181	32.8	36	1	US-08-450-236-2	Sequence 2, Appl
41	181	32.8	36	4	US-08-235-403-2	Sequence 2, Appl
42	181	32.8	36	4	US-09-336-093-6	Sequence 6, Appl
43	180.5	32.7	157	1	US-08-450-257-60	Sequence 60, Appl
44	180.5	32.7	157	1	US-08-450-246-60	Sequence 60, Appl
45	180.5	32.7	157	1	US-08-450-098-60	Sequence 60, Appl

#### ALIGNMENTS

RESULT 1  
US-08-450-257-1  
; Sequence 1, Application US/08450257  
; Patent No. 5652122  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: PABO, Carl  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: FAWELL, Stephen E.  
; APPLICANT: PEPINSKY, R. B.  
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450.257  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/235,403  
; FILING DATE: 28-APR-1994  
; APPLICATION NUMBER: US 07/934,375  
; FILING DATE: 21-AUG-1992  
; APPLICATION NUMBER: US 07/098,766  
; FILING DATE: 28-JUL-1993  
; APPLICATION NUMBER: PCT/US93/07833  
; FILING DATE: 19-AUG-1993  
; APPLICATION NUMBER: US 07/454,450  
; FILING DATE: 21-DEC-1989  
; APPLICATION NUMBER: US 07/636,662  
; FILING DATE: 02-JAN-1991  
; APPLICATION NUMBER: US 08/158,015  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B170 CIP 2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090

TELEX: 14-8367  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 86 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: human immunodeficiency virus  
 STRAIN: type 1  
 US-08-450-257-1

Query Match 86.6%; Score 478; DB 1; Length 86;  
 Best Local Similarity 96.5%; Pred. No. 5.4e-46;  
 Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 MEPVDPRLEPKHSGSQPKTACTNCKYKCCFHCQVCFITAAAGISYGRKKRRRRPPQ 60  
 Db 1 MEPVDPRLEPKHSGSQPKTACTNCKYKCCFHCQVCFITAAAGISYGRKKRRRRPPQ 60  
 Qy 61 GSQTHQVSLSKOPTSQSGKEPTGPK 86  
 Db 61 GSQTHQVSLSKOPTSQSGKEPTGPK 86

RESULT 2  
 US-08-450-246-1  
 ; Sequence 1, Application US/08450246  
 ; Patent No. 5670617  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FRANKEL, Alan  
 ; APPLICANT: PABO, Carl  
 ; APPLICANT: BARSOUM, James G.  
 ; APPLICANT: FAWELL, Stephen E.  
 ; APPLICANT: PEPINSKY, R. B.  
 ; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 69  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FISH & NEAVE  
 ; STREET: 1251 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10020  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/450.246  
 ; FILING DATE: 25-MAY-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/235,403  
 ; FILING DATE: 28-APR-1994  
 ; APPLICATION NUMBER: US 07/934,375  
 ; FILING DATE: 21-AUG-1992  
 ; APPLICATION NUMBER: US 07/098,766  
 ; FILING DATE: 28-JUL-1993  
 ; APPLICATION NUMBER: PCT/US93/07833  
 ; FILING DATE: 19-AUG-1993  
 ; APPLICATION NUMBER: US 07/454,450  
 ; FILING DATE: 21-DEC-1989  
 ; APPLICATION NUMBER: US 07/636,662  
 ; FILING DATE: 02-JAN-1991  
 ; APPLICATION NUMBER: US 08/158,015  
 ; FILING DATE: 24-NOV-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Haley Jr., James F.  
 ; REGISTRATION NUMBER: 27,794  
 ; REFERENCE/DOCKET NUMBER: B170 CIP 2

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 596-9000  
 TELEFAX: (212) 596-9090  
 TELEX: 14-8367  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 86 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: human immunodeficiency virus  
 STRAIN: type 1  
 US-08-450-246-1  
 Query Match 86.6%; Score 478; DB 1; Length 86;  
 Best Local Similarity 96.5%; Pred. No. 5.4e-46;  
 Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 MEPVDPRLEPKHSGSQPKTACTNCKYKCCFHCQVCFITAAAGISYGRKKRRRRPPQ 60  
 Db 1 MEPVDPRLEPKHSGSQPKTACTNCKYKCCFHCQVCFITAAAGISYGRKKRRRRPPQ 60  
 Qy 61 GSQTHQVSLSKOPTSQSGKEPTGPK 86  
 Db 61 GSQTHQVSLSKOPTSQSGKEPTGPK 86  
 RESULT 3  
 US-08-450-098-1  
 ; Sequence 1, Application US/08450098  
 ; Patent No. 5674980  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FRANKEL, Alan  
 ; APPLICANT: PABO, Carl  
 ; APPLICANT: BARSOUM, James G.  
 ; APPLICANT: FAWELL, Stephen E.  
 ; APPLICANT: PEPINSKY, R. B.  
 ; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 69  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FISH & NEAVE  
 ; STREET: 1251 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10020  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/450.098  
 ; FILING DATE: 25-MAY-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/235,403  
 ; FILING DATE: 28-APR-1994  
 ; APPLICATION NUMBER: US 07/934,375  
 ; FILING DATE: 21-AUG-1992  
 ; APPLICATION NUMBER: US 07/098,766  
 ; FILING DATE: 28-JUL-1993  
 ; APPLICATION NUMBER: PCT/US93/07833  
 ; FILING DATE: 19-AUG-1993  
 ; APPLICATION NUMBER: US 07/454,450  
 ; FILING DATE: 21-DEC-1989  
 ; APPLICATION NUMBER: US 07/636,662  
 ; FILING DATE: 02-JAN-1991  
 ; APPLICATION NUMBER: US 08/158,015  
 ; FILING DATE: 24-NOV-1993  
 ; ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: human immunodeficiency virus  
STRAIN: type 1  
US-08-450-098-1

Query Match 86.6%; Score 478; DB 1; Length 86;  
Best Local Similarity 96.5%; Pred. No. 5.4e-46;  
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHKGSPKTKACTNCKYCKKCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
Db 1 MEPVDPRLEPKHKGSPKTKACTNCKYCKKCFHCQVCFITKALGISYGRKKRRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSQSGEPTGPKE 86  
Db 61 GSQTHQVSLSKOPTSQSGDPTGPKE 86

RESULT 4  
US-08-451-233-1  
; Sequence 1, Application US/08451233  
; Patent No. 5747641  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: PABO, Carl  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: FAWELL, Stephen E.  
; APPLICANT: PEPINSKY, R. B.  
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/451,233  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/235,403  
; FILING DATE: 28-APR-1994  
; APPLICATION NUMBER: US 07/934,375  
; FILING DATE: 21-AUG-1992  
; APPLICATION NUMBER: US 07/098,766  
; FILING DATE: 28-JUL-1993  
; APPLICATION NUMBER: PCT/US93/07833  
; FILING DATE: 19-AUG-1993  
; APPLICATION NUMBER: US 07/454,450  
; FILING DATE: 21-DEC-1989  
; APPLICATION NUMBER: US 07/636,662  
; FILING DATE: 02-JAN-1991

APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: human immunodeficiency virus  
STRAIN: type 1  
US-08-451-233-1

Query Match 86.6%; Score 478; DB 1; Length 86;  
Best Local Similarity 96.5%; Pred. No. 5.4e-46;  
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHKGSPKTKACTNCKYCKKCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
Db 1 MEPVDPRLEPKHKGSPKTKACTNCKYCKKCFHCQVCFITKALGISYGRKKRRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSQSGEPTGPKE 86  
Db 61 GSQTHQVSLSKOPTSQSGDPTGPKE 86

RESULT 5  
US-08-450-236-1  
; Sequence 1, Application US/08450236  
; Patent No. 5804604  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: PABO, Carl  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: FAWELL, Stephen E.  
; APPLICANT: PEPINSKY, R. B.  
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,236  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/235,403  
; FILING DATE: 28-APR-1994  
; APPLICATION NUMBER: US 07/934,375  
; FILING DATE: 21-AUG-1992  
; APPLICATION NUMBER: US 07/098,766  
; FILING DATE: 28-JUL-1993  
; APPLICATION NUMBER: PCT/US93/07833  
; FILING DATE: 19-AUG-1993  
; APPLICATION NUMBER: US 07/454,450



Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKE 86  
|||||  
Db 61 GSQTHQVSLSKOPTSQSRGDDTGPKE 86

## RESULT 8

US-09-124-900-6  
; Sequence 6, Application US/09124900  
; Patent No. 6268484  
; GENERAL INFORMATION:  
; APPLICANT: KATINGER, Hermann  
; APPLICANT: BUCHACHER, Andrea  
; APPLICANT: ERNST, Wolfgang  
; APPLICANT: BALLAUN, Claudia  
; APPLICANT: PURTSCHER, Martin  
; APPLICANT: TRKOLA, Alexandra  
; APPLICANT: PREDL, Renate  
; APPLICANT: SCHMATZ, Christine  
; APPLICANT: KLIMA, Annelies  
; APPLICANT: STEINDL, Franz  
; APPLICANT: MUSTER, Thomas  
; TITLE OF INVENTION: HIV-Vaccines  
; FILE REFERENCE: 1939-112P  
; CURRENT APPLICATION NUMBER: US/09/124,900  
; CURRENT FILING DATE: 1998-07-30  
; PRIOR APPLICATION NUMBER: PCT/EP95/01481  
; PRIOR FILING DATE: 1995-04-19  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-124-900-6

Query Match 86.6%; Score 478; DB 4; Length 86;  
Best Local Similarity 96.5%; Pred. No. 5.4e-46;  
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHGPSQPKTACTNCKYKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
|||||  
Db 1 MEPVDPRLEPKHGPSQPKTACTNCKYKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKE 86  
|||||  
Db 61 GSQTHQVSLSKOPTSQSRGDDTGPKE 86

## RESULT 9

US-09-451-905-19  
; Sequence 19, Application US/09451905  
; Patent No. 6306613  
; GENERAL INFORMATION:  
; APPLICANT: Robert Z. Florkiewicz  
; APPLICANT: Andrew Baird  
; APPLICANT: Dale E. Warnock  
; TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT  
; FILE REFERENCE: 200124.402C4  
; CURRENT APPLICATION NUMBER: US/09/451,905  
; CURRENT FILING DATE: 1999-12-01  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-451-905-19

Query Match 86.6%; Score 478; DB 4; Length 86;

Best Local Similarity 96.5%; Pred. No. 5.4e-46;  
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MEPVDPRLEPKHGPSQPKTACTNCKYKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
|||||  
Db 1 MEPVDPRLEPKHGPSQPKTACTNCKYKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKE 86  
|||||  
Db 61 GSQTHQVSLSKOPTSQSRGDDTGPKE 86

## RESULT 10

US-08-235-403-1  
; Sequence 1, Application US/08235403  
; Patent No. 6316003  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: PABO, Carl  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: FAWELL, Stephen E.  
; APPLICANT: PEPINSKY, R. B.  
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/235,403  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/934,375  
; FILING DATE: 21-AUG-1992  
; APPLICATION NUMBER: US 07/098,766  
; FILING DATE: 28-JUL-1993  
; APPLICATION NUMBER: PCT/US93/07833  
; FILING DATE: 19-AUG-1993  
; APPLICATION NUMBER: US 07/454,450  
; FILING DATE: 21-DEC-1989  
; APPLICATION NUMBER: US 07/636,662  
; FILING DATE: 02-JAN-1991  
; APPLICATION NUMBER: US 08/158,015  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B170 CIP 2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 86 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: human immunodeficiency virus  
; STRAIN: type 1  
US-08-235-403-1

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Query Match      86.6%; Score 478; DB 4; Length 86;
Best Local Similarity 96.5%; Pred. No. 5.4e-46;
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPEPKHSGSQPKTACTNCKKCCFHCQVCFITKALGISYGRKKRRRRPPQ 60
Db 1 MEPVDPRLPEPKHSGSQPKTACTNCKKCCFHCQVCFITKALGISYGRKKRRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSQSKGEPTGPKE 86
Db 61 GSQTHQVSLSKOPTSQSKGEPTGPKE 86

RESULT 11
PCT-US92-10770-1
; Sequence 1, Application PC/TUS9210770
; GENERAL INFORMATION:
; APPLICANT: Jayasena, Suredha D.
; APPLICANT: Johnston, Brian H.
; TITLE OF INVENTION: Antiviral Reagents Based on
; TITLE OF INVENTION: RNA-Binding Proteins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SRI International
; STREET: 333 Ravenswood Avenue
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10770
; FILING DATE: 19921211
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,452
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: P-2962
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 859-4550
; TELEFAX: (415) 859-3880
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: the sequence of the TAT protein of
; INDIVIDUAL ISOLATE: HIV-1
PCT-US92-10770-1

Query Match      86.6%; Score 478; DB 5; Length 86;
Best Local Similarity 96.5%; Pred. No. 5.4e-46;
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPEPKHSGSQPKTACTNCKKCCFHCQVCFITKALGISYGRKKRRRRPPQ 60
Db 1 MEPVDPRLPEPKHSGSQPKTACTNCKKCCFHCQVCFITKALGISYGRKKRRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSQSKGEPTGPKE 86
Db 61 GSQTHQVSLSKOPTSQSKGEPTGPKE 86
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RESULT 12
PCT-US95-06077-2
; Sequence 2, Application PC/TUS9506077
; GENERAL INFORMATION:
; APPLICANT: Immunobiology Research, Institute Inc.
; TITLE OF INVENTION: Vaccine Interdiction of Extracellular
; TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
; TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar
; TITLE OF INVENTION: Inter-cellular Transactivating Strategies
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06077
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/247,991
; FILING DATE: 23-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: IRI44PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-06077-2

Query Match      86.6%; Score 478; DB 5; Length 86;
Best Local Similarity 96.5%; Pred. No. 5.4e-46;
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPEPKHSGSQPKTACTNCKKCCFHCQVCFITKALGISYGRKKRRRRPPQ 60
Db 1 MEPVDPRLPEPKHSGSQPKTACTNCKKCCFHCQVCFITKALGISYGRKKRRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSQSKGEPTGPKE 86
Db 61 GSQTHQVSLSKOPTSQSKGEPTGPKE 86

RESULT 13
US-08-505-210-1
; Sequence 1, Application US/08505210
; Patent No. 5981258
; GENERAL INFORMATION:
; APPLICANT: MEHTALI, Majid
; APPLICANT: GUSS, Tania
; TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS
; TITLE OF INVENTION: OF VIRAL PROTEINS FOR OBTAINING AN ANTIVIRAL EFFECT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
```



CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: United States  
 ZIP: 22314-2756  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/505,210  
 FILING DATE: 14-AUG-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/215,248  
 FILING DATE: 21-MAR-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/FR94/01457  
 FILING DATE: 13-DEC-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dadio, Susan M.  
 REGISTRATION NUMBER: 40,373  
 REFERENCE/DOCKET NUMBER: 017753-066  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 836-6620  
 TELEFAX: (703) 836-2021  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 86 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Human immunodeficiency virus type 1  
 STRAIN: Lai  
 INDIVIDUAL ISOLATE: sequence of the TAT protein of HIV-1  
 US-08-505-210-1  
 Query Match 83.7%; Score 462; DB 2; Length 86;  
 Best Local Similarity 93.0%; Pred. No. 3.2e-44;  
 Matches 80; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MEPVDPRLPEPKHPSQPKTACTNCYCKKCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
 Db 1 MEPVDPRLPEPKHPSQPKTACTTCYCKKCFHCQVCFITKALGISYGRKKRRRRPPQ 60  
 QY 61 GSQTHQVLSLKOPTSQSGKEPTGPKE 86  
 Db 61 GSQTHQVLSLKOPTSQPRGDTGPKE 86  
 RESULT 14  
 US-09-099-333-1  
 ; Sequence 1, Application US/09099333A  
 ; Patent No. 6228369  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GUSS, Tania  
 ; APPLICANT: MEHTALI, Majid  
 ; TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS OF VIRAL  
 ; TITLE OF INVENTION: PROTEINS FOR OBTAINING AN ANTI-VIRAL EFFECT  
 ; FILE REFERENCE: 017753-091  
 ; CURRENT APPLICATION NUMBER: US/09/099,333A  
 ; CURRENT FILING DATE: 1998-06-18  
 ; EARLIER APPLICATION NUMBER: FR 93 14914  
 ; EARLIER FILING DATE: 1993-12-13  
 ; EARLIER APPLICATION NUMBER: US 08/215,248  
 ; EARLIER FILING DATE: 1994-03-21  
 ; EARLIER APPLICATION NUMBER: US 08/505,210  
 ; EARLIER FILING DATE: 1995-08-14  
 Query Match 81.0%; Score 447; DB 1; Length 82;  
 Best Local Similarity 95.1%; Pred. No. 1.4e-42;  
 Matches 78; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MEPVDPRLPEPKHPSQPKTACTNCYCKKCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
 Db 1 MEPVDPRLPEPKHPSQPKTACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRPPQ 60  
 QY 61 GSQTHQVLSLKOPTSQSGKEPT 82  
 Db 61 GSQTHQVLSLKOPTSQSGKEPT 82



RESULT 19  
US-09-113-921-1  
; Sequence 1, Application US/09113921  
; Patent No. 6193981  
; GENERAL INFORMATION:  
; APPLICANT: Goldstein, Gideon  
; TITLE OF INVENTION: Methods and Compositions for Impairing  
; TITLE OF INVENTION: Multiplication of HIV-1  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Spring House Corporate Cntr., P.O. Box 457  
; CITY: Spring House  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/113.921  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/893.853  
; FILING DATE: 11-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bak, Mary E.  
; REGISTRATION NUMBER: 31,215  
; REFERENCE/DOCKET NUMBER: GGP2AUSA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-540-9200  
; TELEFAX: 215-540-5818  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 72 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-113-921-1  
  
Query Match 69.6%; Score 384; DB 4; Length 72;  
Best Local Similarity 93.1%; Pred. No. 1.le-35;  
Matches 67; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 MEPVDPRLPKHSGSQPKTACTNCKKCCPHCCVCFITAAALGISYGRKKRRRPPQ 60  
Db 1 MEPVDPRLPKHSGSQPKTACTNCKKCCPHCCVCFITAAALGISYGRKKRRRPPQ 60  
  
QY 61 GSQTHQVSLSKQ 72  
Db 61 DSQTHQVSLSKQ 72  
  
RESULT 20  
US-08-094-128A-27  
; Sequence 27, Application US/08094128A  
; Patent No. 5595884  
; GENERAL INFORMATION:  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: ANDROPHY, Elliot J.  
; TITLE OF INVENTION: PAPILLOMAVIRUS E2 TRANS-ACTIVATION  
; TITLE OF INVENTION: REPRESSORS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York

STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/094.128A  
FILING DATE: 24-SEP-1993  
CLASSIFICATION: 517  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/646.998  
FILING DATE: 28-JAN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/00652  
FILING DATE: 28-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B156CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-094-128A-27  
  
Query Match 65.3%; Score 360.5; DB 1; Length 312;  
Best Local Similarity 70.2%; Pred. No. 2.3e-32;  
Matches 66; Conservative 6; Mismatches 13; Indels 9; Gaps 2;  
  
QY 1 MEPVDPRLPKHSGSQPKTACTNCKKCCPHCCVCFITAAALGISYGRKKRRRPPQ 60  
Db 1 MEPVDPRLPKHSGSQPKTACTNCKKCCPHCCVCFITAAALGISYGRKKRRRPPQ 60  
  
QY 61 GSQTHQVSLSKQPKTACTNCKKCCPHCCVCFITAAALGISYGRKKRRRPPQ 91  
Db 61 GSSMAGAGRIYYSR-----FGDEAARFTTGHY 88  
  
RESULT 21  
US-08-455-674-27  
; Sequence 27, Application US/08455674  
; Patent No. 5616559  
; GENERAL INFORMATION:  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: ANDROPHY, Elliot J.  
; TITLE OF INVENTION: PAPILLOMAVIRUS E2 TRANS-ACTIVATION  
; TITLE OF INVENTION: REPRESSORS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455.674  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION: 514

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/094,128
; FILING DATE: 24-SEP-1993
; APPLICATION NUMBER: US 07/646,998
; FILING DATE: 28-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00652
; FILING DATE: 28-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B156CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9030
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-455-674-27

```

```

Query Match      55.3%; Score 360.5; DB 1; Length 312;
Best Local Similarity 70.2%; Pred. No. 2.3e-32;
Matches 66; Conservative 6; Mismatches 13; Indels 9; Gaps 2;

QY 1 MEPVDRPLEPKWKGPSGPKTACTNCCYCKCCFHCQVCFITAAALGISYGRKKRRQRRPPQ 60
      |||||
Db 1 MEPVDRPLEPKWKGPSGPKTACTNCCYCKCCFHCQVCFITAAALGISYGRKKRRQRRPPQ 60
      |||||

QY 61 GSQ---THQVSLSKOPTSQSKGPTGPKETSGHH 91
      |||  |||
Db 61 GSSMAGAGRTVYSR-----FGDEAARFSTTGHV 88
      |||  |||

```

RESULT 22  
US-08-455-992-27  
; Sequence 27, Application US/08455992  
; Patent No. 5656599  
; GENERAL INFORMATION:  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: ANDROPHY, Elliot J.  
; TITLE OF INVENTION: PAPILLOMAVIRUS E2 TRANS-ACTIVATION  
; TITLE OF INVENTION: REPRESSORS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455.992  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/094,128  
; FILING DATE: 24-SEP-1993  
; APPLICATION NUMBER: US 07/646,998  
; FILING DATE: 28-JAN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/00652  
; FILING DATE: 28-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.

```

; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B156CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-455-992-27

Query Match          65.3%; Score 360.5; DB 1; Length
Best Local Similarity 70.2%; Pred. No. 2.3e-32;
Matches 66; Conservative 6; Mismatches 13; Indels

QY 1 MEVDPRLPEWHPGSPQKACTNCKYKCCFHCQVCFITAAALGISYGRKKI
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MEVDPRLPEWHPGSPQKACTNCKYKCCFHCQVCFITAAALGISYGRKKI
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 GSQ---THQVSLSKQPTSQSKGEPTGPRETSQHH 91
   | | : : : | : | : | : | : | : | : | : | : | : | : | : |
Db 61 GSSMAGAGRIIYSR-----FGDEAARFTTGHY 88

RESULT 23
US-08-455-972-27
; Sequence 27, Application US/08455972
; Patent No. 5667965
; GENERAL INFORMATION:
; APPLICANT: BARSOUM, James G.
; APPLICANT: ANDROPHY, Elliot J.
; TITLE OF INVENTION: PAPILLOMAVIRUS E2 TRANS-ACTIVATION
; TITLE OF INVENTION: REPRESSORS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,972
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/094,128
; FILING DATE: 24-SEP-1993
; APPLICATION NUMBER: US 07/646,998
; FILING DATE: 28-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00652
; FILING DATE: 28-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B156CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```

RESULT 23  
US-08-455-972-27  
: Sequence 27, Application US/08455972  
: Patent No. 5667965  
: GENERAL INFORMATION:  
: APPLICANT: BARSOOM, James G.  
: APPLICANT: ANDROPHY, Elliot J.  
: TITLE OF INVENTION: PAPILLOMAVIRUS E2 TRANS-ACTIVATION  
: TITLE OF INVENTION: REPRESSORS  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: FISH & NEAVE  
: STREET: 1251 Avenue of the Americas  
: CITY: New York  
: STATE: New York  
: COUNTRY: USA  
: ZIP: 10020  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent In Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/455,972  
: FILING DATE: 31-MAY-1995  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/094,128  
: FILING DATE: 24-SEP-1993  
: APPLICATION NUMBER: US 07/646,998  
: FILING DATE: 28-JAN-1991  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: PCT/US92/00652  
: FILING DATE: 28-JAN-1992  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Haley Jr., James F.  
: REGISTRATION NUMBER: 27,794  
: REFERENCE/DOCKET NUMBER: B1566C1P  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (212) 596-9000  
: TELEFAX: (212) 596-9090  
: INFORMATION FOR SEQ ID NO: 27:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 312 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-455-972-27

Query Match 65.3%; Score 360.5; DB 1; Length 312;  
Best Local Similarity 70.2%; Pred. No. 2.3e-32;  
Matches 66; Conservative 6; Mismatches 13; Indels 9; Gaps 2;  
Qy 1 MEPVDPRLPEPKHPSQPKTACTNCKYKCCFHCQVCFITKALGISYGRKKRRRRPQ 60  
Db 1 MEPVDPRLPEPKHPSQPKTACTNCKYKCCFHCQVCFITKALGISYGRKKRRRRPQ 60  
Qy 61 GSQ---THQVLSKOPTSQSGKEPTGPKETSGHH 91  
Db 61 GSSMAGAGRIYYR-----FGDEAARFSTTGHY 88

RESULT 24  
PCT-US92-00652-27  
Sequence 27, Application PC/TUS9200652  
GENERAL INFORMATION:  
APPLICANT: BIOGEN, INC.  
APPLICANT: NEW ENGLAND MEDICAL CENTER,  
APPLICANT: HOSPITALS, INC.  
APPLICANT: BARSOUM, James G. (US only)  
APPLICANT: ANDROPHY, Elliot J. (US only)  
TITLE OF INVENTION: PAPILLOMAVIRUS E2 TRANS-ACTIVATION  
TITLE OF INVENTION: REPRESSORS  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 875 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022-6250  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/00652  
FILING DATE: 19920128  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B156CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)715-0600  
TELEFAX: (212)715-0673  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US92-00652-27

Query Match 65.3%; Score 360.5; DB 5; Length 312;  
Best Local Similarity 70.2%; Pred. No. 2.3e-32;  
Matches 66; Conservative 6; Mismatches 13; Indels 9; Gaps 2;  
Qy 1 MEPVDPRLPEPKHPSQPKTACTNCKYKCCFHCQVCFITKALGISYGRKKRRRRPQ 60  
Db 1 MEPVDPRLPEPKHPSQPKTACTNCKYKCCFHCQVCFITKALGISYGRKKRRRRPQ 60  
Qy 61 GSQ---THQVLSKOPTSQSGKEPTGPKETSGHH 91  
Db 61 GSSMAGAGRIYYR-----FGDEAARFSTTGHY 88

RESULT 25  
US-07-910-867B-2  
Sequence 2, Application US/07910867B  
Patent No. 5597895  
GENERAL INFORMATION:  
APPLICANT: Gaynor, Richard B.  
APPLICANT: Garcia, Joseph A.  
APPLICANT: Harrich, David  
TITLE OF INVENTION: Transdominant Tat Mutants and Uses  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: US  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/910,867B  
FILING DATE: 02-JUL-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mayfield, Denise L.  
REGISTRATION NUMBER: 33,732  
REFERENCE/DOCKET NUMBER: UTSD:263/MAY  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 72 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-910-867B-2

Query Match 63.6%; Score 351; DB 1; Length 72;  
Best Local Similarity 83.3%; Pred. No. 4.8e-32;  
Matches 60; Conservative 1; Mismatches 11; Indels 0; Gaps 0;  
Qy 1 MEPVDPRLPEPKHPSQPKTACTNCKYKCCFHCQVCFITKALGISYGRKKRRRRPQ 60  
Db 1 MEPVDPRLPEPKHPSQPKTACTNCKYKCCFHCQVCFITKALGISYGRKKRRRRPQ 60  
Qy 61 GSQTHQVLSKQ 72  
Db 61 DSQTHQVLSKQ 72

RESULT 26  
US-07-910-867B-5  
Sequence 5, Application US/07910867B  
Patent No. 5597895  
GENERAL INFORMATION:  
APPLICANT: Gaynor, Richard B.  
APPLICANT: Garcia, Joseph A.  
APPLICANT: Harrich, David  
TITLE OF INVENTION: Transdominant Tat Mutants and Uses  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee

```
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: US
;; ZIP: 77210
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/910,867B
;; FILING DATE: 02-JUL-1992
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mayfield, Denise L.
;; REGISTRATION NUMBER: 33,732
;; REFERENCE/DOCKET NUMBER: UTSD:263/MAY
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 512/418-3000
;; TELEFAX: 512/474-7577
;; TELEX: N/A
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 72 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-07-910-867B-5

Query Match 59.8%; Score 330; DB 1; Length 72;
Best Local Similarity 79.2%; Pred. No. 1e-29;
Matches 57; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

QY 1 MEPVDPRLPEPKHGPSQPKTACTNCKKCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 1 MEPVDPNLEPKHGPSQPKTACNNCKKCFHCYACFTRKGLGISYGRKKRRAGGQP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 61 GSQTHQVSLSKQ 72
   ||||| |||||
Db 61 DSQTHQASLSKQ 72
   ||||| |||||

RESULT 27
US-07-910-867B-3
; Sequence 3, Application US/07910867B
; Patent No. 5597895
; GENERAL INFORMATION:
; APPLICANT: Gaynor, Richard B.
; APPLICANT: Garcia, Joseph A.
; APPLICANT: Harrich, David
; TITLE OF INVENTION: Transdominant Tat Mutants and Uses
; TITLE OF INVENTION: Theeof
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/910,867B
; FILING DATE: 02-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTSD:263/MAY
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 72 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-910-867B-1

STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/910,867B
FILING DATE: 02-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:263/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-910-867B-3

Query Match 58.7%; Score 324; DB 1; Length 72;
Best Local Similarity 77.8%; Pred. No. 4.7e-29;
Matches 56; Conservative 1; Mismatches 15; Indels 0; Gaps 0;

QY 1 MEPVDPRLPEPKHGPSQPKTACTNCKKCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 1 MEPVDPNLEPKHGPSQPKTACNNCKKCFHCYACFTRKGLGISYGRKKRRAGGAPQ 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 61 GSQTHQVSLSKQ 72
   ||||| |||||
Db 61 DSQTHQASLSKQ 72
   ||||| |||||

RESULT 28
US-07-910-867B-1
; Sequence 1, Application US/07910867B
; Patent No. 5597895
; GENERAL INFORMATION:
; APPLICANT: Gaynor, Richard B.
; APPLICANT: Garcia, Joseph A.
; APPLICANT: Harrich, David
; TITLE OF INVENTION: Transdominant Tat Mutants and Uses
; TITLE OF INVENTION: Theeof
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/910,867B
; FILING DATE: 02-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTSD:263/MAY
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 72 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-910-867B-1
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Query Match 56.2%; Score 310; DB 1; Length 72;  
Best Local Similarity 75.0%; Pred. No. 1.7e-27;  
Matches 56; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

QY 1 MEPVDPLPDKHSGSQPKTACTNCKKCCFHQVCFITAAALGISYGRKKRRRRPPQ 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||  
Db 1 MEPVDPLPDKHSGSQPKTACTNCKKCCFHQVCFITAAALGISYGRKKRRRRPPQ 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||  
QY 61 GSQTHQVLSKQ 72  
||||| ||||||| ||  
Db 61 DSQTHQVLSKQ 72  
||||| ||||||| ||

RESULT 29  
US-08-450-257-7  
; Sequence 7, Application US/08450257  
; Patent No. 5652122  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: PABO, Carl  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: FAWELL, Stephen E.  
; APPLICANT: PEPINSKY, R. B.  
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,257  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/235,403  
; FILING DATE: 28-APR-1994  
; APPLICATION NUMBER: US 07/934,375  
; FILING DATE: 21-AUG-1992  
; APPLICATION NUMBER: US 07/098,766  
; FILING DATE: 28-JUL-1993  
; APPLICATION NUMBER: PCT/US93/07833  
; FILING DATE: 19-AUG-1993  
; APPLICATION NUMBER: US 07/454,450  
; FILING DATE: 21-DEC-1989  
; APPLICATION NUMBER: US 07/636,662  
; FILING DATE: 02-JAN-1991  
; APPLICATION NUMBER: US 08/158,015  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B170 CIP 2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 56 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-450-257-7

Query Match 50.0%; Score 276; DB 1; Length 56;  
Best Local Similarity 76.4%; Pred. No. 7.1e-24;  
Matches 55; Conservative 0; Mismatches 1; Indels 16; Gaps 1;

QY 1 MEPVDPLPDKHSGSQPKTACTNCKKCCFHQVCFITAAALGISYGRKKRRRRPPQ 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||  
Db 1 MEPVDPLPDKHSGSQPKTA-----FITKALGISYGRKKRRRRPPQ 44  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||  
QY 61 GSQTHQVLSKQ 72  
||||| ||||||| ||  
Db 45 GSQTHQVLSKQ 56  
||||| ||||||| ||

RESULT 30  
US-08-450-246-7  
; Sequence 7, Application US/08450246  
; Patent No. 5670617  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: PABO, Carl  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: FAWELL, Stephen E.  
; APPLICANT: PEPINSKY, R. B.  
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,246  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/235,403  
; FILING DATE: 28-APR-1994  
; APPLICATION NUMBER: US 07/934,375  
; FILING DATE: 21-AUG-1992  
; APPLICATION NUMBER: US 07/098,766  
; FILING DATE: 28-JUL-1993  
; APPLICATION NUMBER: PCT/US93/07833  
; FILING DATE: 19-AUG-1993  
; APPLICATION NUMBER: US 07/454,450  
; FILING DATE: 21-DEC-1989  
; APPLICATION NUMBER: US 07/636,662  
; FILING DATE: 02-JAN-1991  
; APPLICATION NUMBER: US 08/158,015  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B170 CIP 2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 56 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-450-246-7

```

Query Match      50.0%; Score 276; DB 1; Length 56;
Best Local Similarity 76.4%; Pred. No. 7.1e-24;
Matches 55; Conservative 0; Mismatches 1; Indels 16; Gaps 1;

QY 1 MEVDPRLEPWKHPGSOPTACTNCKKCCFHCQVGFITAAIGISYGRKKRRRRPPQ 60
   |||||
Db 1 MEVDPRLEPWKHPGSOPTACTNCKKCCFHCQVGFITAAIGISYGRKKRRRRPPQ 60
   |||||
QY 61 GSQTHQVSLSKQ 72
   |||||
Db 45 GSQTHQVSLSKQ 56
   |||||

```

Search completed: August 26, 2002, 08:10:41  
Job time: 130 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2002, 08:13:23 ; Search time 50.45 seconds  
(without alignments)  
180.941 Million cell updates/sec

Title: US-09-509-239-23  
Perfect score: 552  
Sequence: 1 MEPVDPRLPWHKPGSQPKT.....QSKGPTGPKETSGHHHHH 95

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.71.\*

1: Pirl.\*

2: Pirl.\*

3: Pirl.\*

4: Pirl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	478	86.6	86	2 S33982	trans-activating t
2	470	85.1	95	1 TNLJ12	trans-activating t
3	462	83.7	86	2 A25700	trans-activating t
4	429	77.7	101	2 T09446	tat protein - huma
5	426	77.2	101	1 E44001	trans-activating t
6	403	73.0	86	2 JC5591	transactivator pro
7	400	72.5	86	1 TNLJ2R	trans-activating t
8	400	72.5	86	2 S34381	tat protein - huma
9	395	71.6	86	1 TNLJND	trans-activating t
10	387.5	70.2	87	2 T01665	tat protein - huma
11	364	65.9	72	1 TNLJH4	trans-activating t
12	353	63.9	71	2 T09384	trans-activating t
13	315.5	57.2	100	1 TNLJST	trans-activating t
14	175.5	31.8	130	1 TNLJGG	trans-activating t
15	170.5	30.9	130	1 TNLJST	trans-activating t
16	170.5	30.9	130	2 S53096	tat protein - huma
17	163.5	29.6	130	1 TNLJG2	trans-activating t
18	161.5	29.3	133	1 TNLJCA	trans-activating t
19	161	29.2	130	2 S12157	trans-activating t
20	151	27.4	129	1 TNLJG3	trans-activating t
21	149	27.0	106	1 TNLJG2	trans-activating t
22	148.5	26.9	96	2 S08440	trans-activating t
23	142	25.7	100	1 TNLJG4	trans-activating t
24	139.5	25.3	119	2 A46356	tat protein - simi
25	138.5	25.1	132	2 T11564	tat protein - simi
26	133.5	24.2	131	2 T11557	trans-activating t
27	123	22.3	116	1 A48344	trans-activating t
28	114.5	20.7	145	1 TNLJBT	trans-activating t
29	112	20.3	73	2 S46349	trans-activating t

30 88 15.9 1001 2 T28897  
31 85.5 15.5 617 2 T23197  
32 85 15.4 1477 2 T13797  
33 82.5 14.9 346 2 F96785  
34 82.5 14.9 3942 2 T42730  
35 78 14.1 439 2 T46375  
36 77 13.9 174 2 G84600  
37 77 13.9 944 1 S48821  
38 76 13.8 354 2 S39406  
39 76 13.8 355 2 S35345  
40 76 13.8 1802 2 T00020  
41 76 13.8 2273 2 T46477  
42 76 13.8 2424 2 T46480  
43 75.5 13.7 3938 2 T42761  
44 75 13.6 355 2 T56547  
45 75 13.6 1069 2 T43280

#### ALIGNMENTS

RESULT 1

S33982

trans-activating transcription regulator - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 06-Oct-1994 #sequence\_revision 23-Feb-1996 #text\_change 20-Sep-1999

C:Accession: S33982; S26385; S19864

R:Carlini, F.

submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33982

A:Molecule type: DNA

A:Residues: 1-86 <CAR>

A:Cross-references: EMBL:Z11530; NID:960192; PIDN:CAA77625.1; PID:960196

R:Stiderovski, D.P.; Matsuyama, T.; Frigerio, E.; Chui, S.; Min, X.; Erfle, H.; Sumner

Nucleic Acids Res. 20, 5311-5320, 1992

A:Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activator

A:Reference number: S26385; MUID:93065196

A:Accession: S26385

A:Molecule type: nucleic acid

A:Residues: 1-86 <SID>

A:Cross-references: EMBL:X64650; NID:960144; PIDN:CAA45921.1; PID:960145

C:Genetics:

A:Gene: tat

A:Introns: 72/2

C:Superfamily: AIDS trans-activating transcription regulator

C:Keywords: AIDS; immunodeficiency

Query Match 86.6%; Score 478; DB 2; Length 86;

Best Local Similarity 96.5%; Pred. No. 2e-37; Mismatches 1; Indels 0; Gaps 0;

Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPVDPRLPWHKPGSQPKTACTNCYCKKCCFHCQVCFTAAALGISYGRKKRRRRPQ 60

DB 1 MEPVDPRLPWHKPGSQPKTACTNCYCKKCCFHCQVCFTAAALGISYGRKKRRRRPQ 60

QY 61 GSQTHQVSLSKOPTSOSKGEPTGPKE 86

DB 61 GSQTHQVSLSKOPTSOSKGEPTGPKE 86

RESULT 2

TNLJ12

trans-activating transcription regulator - human immunodeficiency virus type 1 (isola

C:Species: human immunodeficiency virus type 1, HIV-1

A>Note: host Homo sapiens (man)

C:Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 02-Jul-1998

C:Accession: A04017

R:Arya, S.K.; Gallo, R.C.

Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986

A:Title: Three novel genes of human T-lymphotropic virus type III: Immune reactivity

A:Reference number: A94093; MUID:86177573

A:Accession: A04017

A:Molecule type: DNA

A:Residues: 1-95 <ARY>

C:Genetics:

A:Gene: tat

C:Superfamily: AIDS trans-activating transcription regulator

C:Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 85.1%; Score 470; DB 1; Length 95;

Best Local Similarity 95.3%; Pred. No. 1.2e-36;

Matches 82; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60

Db 10 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 69

Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKE 86

Db 70 GSQTHQVSLSKOPTSQSKGPTGPKE 95

#### RESULT 3

A25700

trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 28-Sep-1987 #sequence\_revision 28-Sep-1987 #text\_change 02-Jul-1998

C:Accession: A25700

R:Sodroski, J.; Patarca, R.; Rosen, C.; Wong-Staal, F.; Haseltine, W.

Science 229, 74-77, 1985

A:Reference number: A25700; MUID:85244627

A:Accession: A25700

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-86 <SOD>

C:Superfamily: AIDS trans-activating transcription regulator

Query Match 83.7%; Score 462; DB 2; Length 86;

Best Local Similarity 93.0%; Pred. No. 6e-36;

Matches 80; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60

Db 1 MEPVDPRLPEPKHGPSQPKTACTTCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKE 86

Db 61 GSQTHQVSLSKOPTSQSKGPTGPKE 86

#### RESULT 4

T09446

tat protein - human immunodeficiency virus type 1 (strain JRFL)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 26-Aug-1999

C:Accession: T09446

R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,

submitted to the EMBL Data Library, July 1996

A:Reference number: Z16673

A:Accession: T09446

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-101 <PAN>

A:Cross-references: EMBL:U63632; NID:g1465777; PID:g1465783

C:Genetics:

A:Gene: tat

A:Introns: 72/2

C:Superfamily: AIDS trans-activating transcription regulator

Query Match 77.7%; Score 429; DB 2; Length 101;

Best Local Similarity 85.1%; Pred. No. 7.6e-33;

Matches 74; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60

Db 1 MEPVDPRLPEPKHGPSQPKTACTTCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKE 87

Db 61 GSQTHQVSLSKOPTSQSKGPTGPKE 87

#### RESULT 5

E44001

trans-activating transcription regulator - human immunodeficiency virus type 1 (stra

N:Alternate names: tat protein

C:Species: human immunodeficiency virus type 1, HIV-1

A>Note: host Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 02-Jul-1998

C:Accession: E44001

R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6587-6600, 1992

A:Title: Complete nucleotide sequence, genome organization, and biological properties

A:Reference number: A44001; MUID:93021387

A:Accession: E44001

A:Molecule type: DNA

A:Residues: 1-101 <LIY>

A:Cross-references: GB:M93258

C:Genetics:

A:Gene: tat

A:Introns: 72/2

C:Superfamily: AIDS trans-activating transcription regulator

C:Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 77.2%; Score 426; DB 1; Length 101;

Best Local Similarity 83.9%; Pred. No. 1.4e-32;

Matches 73; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60

Db 1 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKE 87

Db 61 GSQTHQVSLSKOPTSQSKGPTGPKE 87

#### RESULT 6

JC5591

transactivator protein - human immunodeficiency virus type 1

N:Alternate names: tat protein

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 17-Mar-1999

C:Accession: JC5591

R:Hoffmann, S.; Willbold, D.

Biochem. Biophys. Res. Commun. 235, 806-811, 1997

A:Title: A selection system to study protein-RNA interactions: Functional display of

A:Reference number: JC5591; MUID:97350867

A:Accession: JC5591

A:Molecule type: Protein

A:Residues: 1-86 <HO2>

C:Comment: This protein is a key regulatory protein in the viral replication cycle a

C:Superfamily: AIDS trans-activating transcription regulator

F:22-31/Region: cysteine-rich

Query Match 73.0%; Score 403; DB 2; Length 86;

Best Local Similarity 77.9%; Pred. No. 1.7e-30;

Matches 67; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60

Db 1 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60

```

Qy 61 GSQTHQVSLSKOPTSOSKGEPTGPKE 86
      1:|||||:|||||:|||||:|||||
Db 61 GGQTHQDPIPKQPSQPRGDTGPKE 86

RESULT 7
TNLJZR
trans-activating transcription regulator - human immunodeficiency virus Zr-6
C:Species: human immunodeficiency virus Zr-6
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C:Accession: C26192
R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu
Gene 52, 71-82, 1987
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti
A:Reference number: A26192; MUID:87248097
A:Accession: C26192
A:Molecule type: DNA
A:Residues: 1-86 <SRI>
A:Cross-references: GB:K03458; GB:M16322; NID:G329398; PIDN:AAA45377.1; PID:G329400
C:Genetics:
A:Gene: tat
C:Introns: 72/3
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 72.5%; Score 400; DB 1; Length 86;
Best Local Similarity 77.9%; Pred. No. 3.2e-30;
Matches 67; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
      1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MDPVDPNLEPNHPSQPKTACNCRCKKCCYHCQVCFITKGLGISYGRKKRRRRPSQ 60

Qy 61 GSQTHQVSLSKOPTSOSKGEPTGPKE 86
      1:|||||:|||||:|||||:|||||
Db 61 GGQTHQDPIPKQPSQPRGDTGPKE 86

RESULT 8
S54381
tat protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
C:Accession: S54381
R:Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A:Reference number: S54377
A:Accession: S54381
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-86 <THE>
A:Cross-references: EMBL:M22639; NID:G329377; PIDN:AAA45363.1; PID:G329378
C:Genetics:
A:Introns: 72/2
C:Superfamily: AIDS trans-activating transcription regulator

Query Match 72.5%; Score 400; DB 2; Length 86;
Best Local Similarity 76.7%; Pred. No. 3.2e-30;
Matches 66; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
      1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MDPVDPNLEPNHPSQPKTACNCRCKKCCYHCQVCFITKGLGISYGRKKRRRRPSQ 60

Qy 61 GSQTHQVSLSKOPTSOSKGEPTGPKE 86
      1:|||||:|||||:|||||:|||||
Db 61 GGQTHQDPIPKQPSQPRGDTGPKE 86

RESULT 9
trans-activating transcription regulator - human immunodeficiency virus type 1 (isola
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 02-Jul-1998
C:Accession: B25523
R:Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devar
```

```

TNLJND
trans-activating transcription regulator - human immunodeficiency virus type 1 (isola
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: J00071
R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe,
Gene 81, 275-284, 1989
A:Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human imm
A:Reference number: J00065; MUID:90034200
A:Accession: J00071
A:Molecule type: DNA
A:Residues: 1-86 <SP>
A:Cross-references: GB:M27323; NID:G328154; PIDN:AAA44866.1; PID:G328155
C:Genetics:
A:Gene: tat
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS; immunodeficiency; transcription

Query Match 71.6%; Score 395; DB 1; Length 86;
Best Local Similarity 74.4%; Pred. No. 9.1e-30;
Matches 64; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
      1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MDPVDPNLEPNHPSQPKTACNCRCKKCCYHCQVCFITKGLGISYGRKKRRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSOSKGEPTGPKE 86
      1:|||||:|||||:|||||:|||||
Db 61 GDOAHQVPIPEQPSQSRGDTGPKE 86

RESULT 10
T01665
tat protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000
C:Accession: T01665
R:Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two 1
A:Reference number: 214389; MUID:86245056
A:Accession: T01665
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-87 <ALI>
A:Cross-references: EMBL:K03456; NID:G60228; PIDN:CAA28015.1; PID:G60233
C:Genetics:
A:Introns: 72/2
C:Superfamily: AIDS trans-activating transcription regulator

Query Match 70.2%; Score 387.5; DB 2; Length 87;
Best Local Similarity 74.7%; Pred. No. 4.5e-29;
Matches 65; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

Qy 1 MEPVDPRLEPKHPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
      1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MDPVDPNLEPNHPSQPKTACNCRCKKCCYHCQVCFITKGLGISYGRKKRRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSOSKGEPTGPKE 86
      1:|||||:|||||:|||||:|||||
Db 61 GNOAHQDPLPEQPSQHRGDTGPKE 87

RESULT 11
TNLJH4
trans-activating transcription regulator - human immunodeficiency virus type 1 (isola
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 02-Jul-1998
C:Accession: B25523
R:Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devar
```

PROC. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986  
 A:Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human  
 A:Reference number: A94136; MUID:87041461  
 A:Accession: B25523  
 A:Molecule type: DNA  
 A:Residues: 1-72 <DES>  
 A:Cross-references: GB:M13137; NID:g326460  
 A:Note: the GenBank entry ADRE3AA PID:g209908 differs from the published sequence in tra  
 C:Gene: tat  
 C:Superfamily: AIDS trans-activating transcription regulator  
 C:Keywords: transcription regulation

Query Match 65.9%; Score 364; DB 1; Length 72;  
 Best Local Similarity 88.9%; Pred. No. 5.7e-27;  
 Matches 64; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 Qy 1 MEPVDPRLPEPKHPGSPKPTACTNCYCKKCCFHCOVCFITAAALGISYGRKKRRRPPQ 60  
 Db 1 MEPVDPRLPEPKHPGSPKPTACTNCYCKKCCFHCOVCFITAAALGISYGRKKRRRRAHQ 60  
 Qy 61 GSQTHQVLSLKQ 72  
 Db 61 DSONHOASLSKQ 72

RESULT 12  
 T09384  
 trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
 C:Accession: T09384  
 R:Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.; Bie  
 J. Virol. 69, 4228-4236, 1995  
 A:Title: Defective accessory genes in a human immunodeficiency virus type 1-infected lon  
 A:Reference number: 216654; MUID:95287475  
 A:Accession: T09384  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-71 <MC>  
 A:Cross-references: EMBL:U24451; NID:9829440; PIDN:AAA79576.1; PID:g829444  
 C:Gene: tat  
 C:Superfamily: AIDS trans-activating transcription regulator  
 C:Keywords: transcription

Query Match 63.9%; Score 353; DB 2; Length 71;  
 Best Local Similarity 83.1%; Pred. No. 5.9e-26;  
 Matches 59; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 Qy 1 MEPVDPRLPEPKHPGSPKPTACTNCYCKKCCFHCOVCFITAAALGISYGRKKRRRPPQ 60  
 Db 1 MEPVDPRLPEPKHPGSPKPTACTNCYCKKCCFHCOVCFITAAALGISYGRKKRRRPPQ 60  
 Qy 61 GSQTHQVLSLKQ 71  
 Db 61 DSEAHQASLSE 71

RESULT 13  
 TNLJST  
 trans-activating transcription regulator - simian immunodeficiency virus SIVcpz  
 C:Species: simian immunodeficiency virus SIVcpz  
 A:Note: host Pan troglodytes (chimpanzee)  
 C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999  
 C:Accession: S09987  
 R:Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.  
 Nature 345, 356-359, 1990  
 A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.  
 A:Reference number: S09983; MUID:90259077  
 A:Accession: S09987

A>Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-100 <HUE>  
 A:Cross-references: EMBL:X52154; NID:g58866; PIDN:CAA36404.1; PID:g763084  
 C:Gene: tat  
 A:Introns: 73/2  
 A:Superfamily: AIDS trans-activating transcription regulator  
 C:Keywords: AIDS; immunodeficiency; transcription

Query Match 57.2%; Score 315.5; DB 1; Length 100;  
 Best Local Similarity 60.7%; Pred. No. 2.2e-22;  
 Matches 54; Conservative 12; Mismatches 22; Indels 1; Gaps 1;  
 Qy 1 MEPVDPRLPEPKHPGSPKPTACTNCYCKKCCFHCOVCFITAAALGISYGRKKRRRPP 59  
 Db 1 MDPIDPDLPEPKHPGSPKPTVCNCCYKACCCYHCYCTKKGLGISYGRKKRTTTRTAP 60  
 Qy 60 QGSOHQVLSLKQTSOSKGEPTGPKETS 88  
 Db 61 AGSKNODSIPKQPLSQSRGNKEGSEKST 89

RESULT 14  
 TNLJGG  
 trans-activating transcription regulator - human immunodeficiency virus type 2 (isol:  
 N:Alternate names: tat protein  
 C:Species: human immunodeficiency virus type 2, HIV-2  
 A:Note: host Homo sapiens (man)  
 C:Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 16-Jul-1999  
 C:Accession: J50332  
 R:Hasegawa, A.; Tsujimoto, H.; Maki, N.; Ishikawa, K.; Miura, T.; Fukasawa, M.; Miki  
 AIDS Res. Hum. Retroviruses 5, 593-604, 1989  
 A:Title: Sequence of a distinct HIV-2 isolate from Ghana showing significant diverge  
 A:Reference number: J50327; MUID:90122350  
 A:Accession: J50332  
 A:Molecule type: DNA  
 A:Residues: 1-130 <HAS>  
 A:Cross-references: GB:M30895; GB:D00477; NID:g325709; PIDN:AAA3929.1; PID:g325710  
 A:Note: this sequence was submitted to JIPID, October 1989  
 C:Gene: tat  
 A:Gene: tat  
 A:Introns: 99/2  
 C:Superfamily: AIDS trans-activating transcription regulator  
 C:Keywords: AIDS; transcription regulation

Query Match 31.8%; Score 175.5; DB 1; Length 130;  
 Best Local Similarity 49.3%; Pred. No. 2.2e-09;  
 Matches 35; Conservative 9; Mismatches 24; Indels 3; Gaps 2;  
 Qy 17 QPKTACTN-CYCKKCCFHCOVCFITAAALGISYGRKKRRRPPQSGQTHQVLSLKQPTS 75  
 Db 45 RPLEACTNSCYCKQCSFHCQLGKGLGIWYAKSR--RRTPRKTKTHSSASDKSIS 102  
 Qy 76 QSKGEPTGPK 86  
 Db 103 TRTGDQSPTKE 113

RESULT 15  
 TNLJST  
 trans-activating transcription regulator - human immunodeficiency virus type 2 (isol:  
 N:Alternate names: tat protein  
 C:Species: human immunodeficiency virus type 2, HIV-2  
 A:Note: host Homo sapiens (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Jul-1999  
 C:Accession: F33943  
 R:Kumar, P.; Hui, H.; Kappes, J.C.; Haggarty, B.S.; Hoxie, J.A.; Arya, S.K.; Shaw, G  
 J. Virol. 64, 890-901, 1990  
 A:Title: Molecular characterization of an attenuated human immunodeficiency virus ty  
 A:Reference number: A33943; MUID:90112662

A;Gene: tat  
A;Introns: 99/3  
C;Superfamily: AIDS trans-activating transcription regulator  
C;Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 29.6%; Score 163.5; DB 1; Length 130;  
Best Local Similarity 42.7%; Pred. NO. 2.8e-08;  
Matches 35; Conservative 10; Mismatches 24; Indels 13; Gaps 4;

QY 17 QPKTACTN-CYCKKCCFHCVCPTTAALGISYGRKKRRRPPQGSGQTH-----QVSLS 70  
          ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 45 RPLETNNSCYKRCCYCHCOMFLNKGLGICYERKGR--RRRTPKTKTHPSPTPKSIS 102  
          ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 71 -----KQPTSQSKEPTGPKE 87  
          ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 103 TRTGDSOPTKKQKTVEATVET 124  
          ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 18  
TNLJCA  
trans-activating transcription regulator - human immunodeficiency virus type 2 (isla  
N;Alternate names: tat protein  
C;Species: human immunodeficiency virus type 2, HIV-2  
A;Note: host Homo sapiens (man)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Jun-2000  
C;Accession: I38475; JQ0981  
R;Tristem, M.; Hill, F.; Karpas, A.  
J. Gen. Virol. 72, 721-724, 1991  
A;Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus  
A;Reference number: A38475; MUID:91170959  
A;Accession: I38475  
A;Molecule type: DNA  
A;Residues: 1-133 <TRI>  
A;Cross-references: GB:D00835; NID:g3153166; PIDN:BAA00714.1; PID:g221467  
C;Genetics:  
A;Gene: tat  
A;Introns: 102/2  
C;Superfamily: AIDS trans-activating transcription regulator  
C;Keywords: transcription

Query Match 29.3%; Score 161.5; DB 1; Length 133;  
Best Local Similarity 43.8%; Pred. NO. 4.4e-08;  
Matches 32; Conservative 8; Mismatches 20; Indels 13; Gaps 3;

QY 17 QPKTACTN-CYCKKCCFHCVCPTTAALGISYGRKKRRRPPQGSGQTHQVSLS----- 70  
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 48 QPLEEDCNYSYCRCCYHCLKGLGICYDRKGR--RRRTPKKAHAHSSASDKSIS 105  
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 71 -----KQPTSQSK 78  
          ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 106 TTRNSOPAKKQK 118  
          ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 19  
SL2157  
trans-activating transcription regulator - human immunodeficiency virus type 2  
C;Species: human immunodeficiency virus type 2, HIV-2  
C;Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Sep-1999  
C;Accession: SL2157  
R;Kuehnelt, H.; Kreutz, R.; Ruebsamen-Waigmann, H.  
Nucleic Acids Res. 18, 6142, 1990  
A;Title: Nucleotide sequence of HIV-2(D194), an isolate from a Gambian case of 'Neuro  
A;Reference number: SL2152; MUID:91045094  
A;Accession: SL2157  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Molecule type: DNA  
A;Residues: 1-130 <KUE>  
A;Cross-references: EMBL:X52223; NID:g60155; PIDN:CANA36459.1; PID:g763106  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1990  
C;Genetics:  
A;Introns: 99/2



Qy	17	OPKTACTN-CYCKKCCFHCQVCITAAALGISTSYGKKRRRRPPQCSQTHOYVLSLKQPTS	75
Db	48	RPLEPCYNKCYKRCYHCQHCFLKKGLGICY----EQHRRRTPKTKTNPLPASNRRSL	103
Qy	76	QSKGEPTGPKE	86
Db	104	STRTRNQPKK	114

trans-activating transcription regulator - bovine immunodeficiency virus (isolate 127  
C/Species: bovine immunodeficiency virus  
C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 02-Jul-1998  
C/Accession: D34742

R:Garvey, K.J.; Oberste, M.S.; Else, J.E.; Braun, M.J.; Gonda, M.A.  
Virology 175, 391-409, 1990

A:Title: Nucleotide sequence and genome organization of biologically active proviruses of  
A:Reference number: A34742; MUID:90223985

A:Accession: D34742

A:Molecule type: genomic RNA

A:Residues: 1-145 <GAR>

A:Cross-references: GB:M32690

C:Genetics:

A:Gene: tat

A:Introns: 103/3

C:Superfamily: AIDS trans-activating transcription regulator

C:Keywords: AIDS; immunodeficiency; transcription

Query Match 20.7%; Score 114.5; DB 1; Length 145;  
Best Local Similarity 32.9%; Pred. No. 0.001;  
Matches 23; Conservative 10; Mismatches 28; Indels 9; Gaps 1;

Qy 18 PKTACTNCCYCKKCFHCOVCFITAAALGTSYGR-----KKRQRPRPQGSOTHOVS 68

Db 34 PRDCPHCCPCISWHCOLCEFLQNLGNYGSPRPRTRGKGRIRRTASGGDQRREAD 93

Qy 69 LSKOPTSQSK 78

Db 94 SORSFTNMDQ 103

RESULT 29

S46349

trans-activating transcription regulator - simian immunodeficiency virus SIVagm (isolate

N:Alternate names: tat protein

C:Species: simian immunodeficiency virus SIVagm

A:Variety: isolate SAB-1

C:Date: 25-Dec-1994 #sequence\_revision 14-Feb-1997 #text\_change 20-Sep-1999

C:Accession: S46349

R:Jin, M.J.; Hui, H.; Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; Hirsch, V.M.;

EMBO J. 13, 2935-2947, 1994

A:Title: Mosaic genome structure of simian immunodeficiency virus from West African green

A:Reference number: S46335; MUID:94298785

A:Accession: S46349

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-73 <JIN>

A:Cross-references: EMBL:U04005; NID:9466229; PIDN:AAA21507.1; PID:9466233

A:Experimental source: isolate SAB-1; sabaesus monkey

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993

C:Genetics:

A:Gene: tat

C:Superfamily: AIDS trans-activating transcription regulator

Query Match 20.3%; Score 112; DB 2; Length 73;  
Best Local Similarity 46.3%; Pred. No. 0.001;  
Matches 25; Conservative 6; Mismatches 19; Indels 4; Gaps 2;

Qy 17 OPKTACTN-CYCKKCFHCOVCFITAAALGTSYGRKKRQRPRPQGSOTHOVS 69

Db 21 RPLQACDNTCFCKVCCFHCILCFHKKALGIRYVPR---PRRASKKISHNQVSL 71

RESULT 30

T28897

hypothetical protein T17H7.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C:Accession: T28897

R:Favella, A.

submitted to the EMBL Data Library, January 1996

A:Description: The sequence of C. elegans cosmid T17H7.

A:Reference number: Z20340

A:Accession: T28897

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1001 <FAV>

A:Cross-references: EMBL:U42841; PIDN:AA48171.1; GSPDB:GN00021; CESP:T17H7.5

A:Experimental source: strain Bristol N2; clone T17H7

C:Genetics:

A:Gene: CESP:T17H7.5

A:Map position: 3

A:Introns: 50/3; 140/3; 762/3; 795/3; 840/3; 942/3

Query Match 15.9%; Score 88; DB 2; Length 1001;

Best Local Similarity 38.2%; Pred. No. 1.3;

Matches 21; Conservative 5; Mismatches 15; Indels 14; Gaps 2;

Qy 42 ALGISYGRKKRRRRRPPQGSQ--THQVSLSKQPTSQSKGEPTGPKETSGHHHHH 95

Db 856 SLMIPIHHRQSRSDSRGPPQMSRAASSIPLSPQTPQ-----HHHHHH 897

Search completed: August 26, 2002, 08:13:24

Job time: 293 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 08:15:43 ; Search time 40.39 Seconds  
(without alignments)  
91.071 Million cell updates/sec

Title: US-09-509-239-23

Perfect score: 552

Sequence: 1 MEPVDPRLPQKHPGSPQKT.....QSKGPTGPKTSGHHHHH 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	478	86.6	86	1 TAT_HV1B1	P04606 human immun
2	473	85.7	86	1 TAT_HV1P2	P04607 human immun
3	470	85.1	86	1 TAT_HV112	P04326 human immun
4	462	83.7	86	1 TAT_HV1B1R	P04610 human immun
5	453	82.1	102	1 TAT_HV1RH	P05908 human immun
6	446	80.8	86	1 TAT_HV1H2	P04608 human immun
7	438	79.3	101	1 TAT_HV1JR	P08079 human immun
8	430	77.9	101	1 TAT_HV1SI	P19553 human immun
9	429	77.7	101	1 TAT_HV1SC	P05906 human immun
10	427	77.4	101	1 TAT_HV1C4	P05907 human immun
11	426	77.2	101	1 TAT_HV1V2	P35965 human immun
12	423	76.6	101	1 TAT_HV1MN	P05905 human immun
13	423	76.6	101	1 TAT_HV1S3	P19552 human immun
14	411	74.5	101	1 TAT_HV1A2	P04614 human immun
15	411	74.5	101	1 TAT_HV1OY	P08093 human immun
16	400	72.5	86	1 TAT_HV122	P12506 human immun
17	400	72.5	86	1 TAT_HV126	P04609 human immun
18	395	71.6	86	1 TAT_HV1ND	P18804 human immun
19	387.5	70.2	87	1 TAT_HV1MA	P04613 human immun
20	384	69.6	99	1 TAT_HV1EL	P04611 human immun
21	342	62.0	101	1 TAT_HV1U4	P24738 human immun
22	324	58.7	58	1 TAT_HV1B5	P04612 human immun
23	315.5	57.2	100	1 TAT_SIVCZ	P17285 chimpanzee
24	175.5	31.8	130	1 TAT_HV2G1	P18044 human immun
25	174	31.5	130	1 TAT_HV2KR	P04124 human immun
26	170.5	30.9	130	1 TAT_HV2ST	P20880 human immun
27	163.5	29.6	130	1 TAT_HV2RO	P04605 human immun
28	161.5	29.3	133	1 TAT_HV2CA	P24109 human immun
29	161	29.2	130	1 TAT_HV2D1	P17759 human immun
30	159.5	28.9	130	1 TAT_HV2M1	P05911 simian immun
31	158.5	28.7	130	1 TAT_HV2BE	P18098 human immun
32	158.5	28.7	130	1 TAT_HV2N2	P05909 human immun
33	153.5	27.8	130	1 TAT_HV2SB	P12453 human immun

## ALIGNMENTS

### RESULT 1

ID	TAT_HV1B1	STANDARD;	PRT;	86 AA.
AC	P04606;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	TAT protein (Transactivating regulatory protein).			
GN	TAT			
OS	Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1), and			
OS	Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).			
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11678, 11707;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ISOLATE BH10;			
RX	MEDLINE=8511123; PubMed=2578615;			
RA	Ratner L., Haseitine W., Patarca R., Livak K.J., Starcich B.R.,			
RA	Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,			
RA	Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,			
RA	Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,			
RA	Wong-Staal F.;			
RT	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";			
RL	Nature 313:277-284(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ISOLATE HXB3;			
RX	MEDLINE=85228248; PubMed=2988795;			
RA	Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,			
RA	Shaw G.M., Wong-Staal F., Reddy E.P.;			
RT	"HTLV-III env gene products synthesized in E. coli are recognized by			
RL	antibodies present in the sera of AIDS patients.";			
RL	Cell 41:979-986(1985).			
CC	-1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE			
CC	TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND			
CC	ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR			
CC	PROMOTER.			
CC	-1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.			
CC	-1- MISCELLANEOUS: THE TWO ISOLATES TAT SEQUENCE ARE IDENTICAL.			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; M14100; AAA44676.1; -			
DR	EMBL; M15654; AAA44199.1; -			
DR	HIV; M15654; TAT\$BHI02.			
DR	HIV; M14100; TAT\$HXB3.			
DR	InterPro; IPR001831; HIV_Tat.			
DR	Pfam; PF00539; Tat; 1.			
DR	PRINTS; PR00055; HIVTATDOMAIN.			

P11263 simian immu  
P15835 human immu  
Q02838 simian immu  
P05910 simian immu  
P19507 simian immu  
P05913 simian immu  
P27982 simian immu  
P12513 simian immu  
P27975 simian immu  
P22384 simian immu  
P36340 simian immu  
P12507 human immu

```
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 86 AA; 9784 MW; 4DD609415FAF9015 CRC64;

Query Match 86.6%; Score 478; DB 1; Length 86;
Best Local Similarity 96.5%; Pred. No. 1.6e-39;
Matches 83; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHPSQKPTACTNCYCKKCCFHCQVCFITAAIGISYGRKKRRRPPQ 60
    |||||||
Db 1 MEPVDPRLEPKHPSQKPTACTNCYCKKCCFHCQVCFITAAIGISYGRKKRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSQSGKEPTGPKE 86
    |||||||
Db 61 GSQTHQVSLSKOPTSQSGKEPTGPKE 86

RESULT 2
TAT_HV1PV
ID TAT_HV1PV STANDARD; PRT; 86 AA.
AC P04607;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11700;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511157; PubMed=2982104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
RT AIDS/lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC
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CC
CC EMBL; M11840; AAB59870.1;
CC PIR; A04017; TNLJ12.
CC HIV; M11840; TATSPV22.
CC InterPro: IPR001831; HIV_Tat.
CC Pfam; PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
CC KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 86 AA; 9794 MW; 4DD5C6415FAF9015 CRC64;

Query Match 85.7%; Score 473; DB 1; Length 86;
Best Local Similarity 95.3%; Pred. No. 4.9e-39;
Matches 82; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHPSQKPTACTNCYCKKCCFHCQVCFITAAIGISYGRKKRRRPPQ 60
    |||||||
Db 1 MEPVDPRLEPKHPSQKPTACTNCYCKKCCFHCQVCFITAAIGISYGRKKRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSQSGKEPTGPKE 86
    |||||||
Db 61 GSQTHQVSLSKOPTSQSGKEPTGPKE 86
```

```
|||||
Db 61 GSQTHQVSLSKOPTSQSGKEPTGPKE 86

RESULT 3
TAT_HV112
ID TAT_HV112 STANDARD; PRT; 86 AA.
AC P04326;
DT 20-MAR-1987 (Rel. 04, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (clone 12) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11679;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177573; PubMed=3008154;
RA Arya S.K., Gallo R.C.;
RT "Three novel genes of human T-lymphotropic virus type III: immune
RT reactivity of their products with sera from acquired immune
RT deficiency syndrome patients.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC
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CC
CC EMBL; M11840; AAA44999.1;
CC PIR; A04017; TNLJ12.
CC HIV; M11840; TATSPCV12.
CC InterPro: IPR001831; HIV_Tat.
CC Pfam; PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
CC KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 86 AA; 9758 MW; 4DD609414FBE9115 CRC64;

Query Match 85.1%; Score 470; DB 1; Length 86;
Best Local Similarity 95.3%; Pred. No. 9.5e-39;
Matches 82; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHPSQKPTACTNCYCKKCCFHCQVCFITAAIGISYGRKKRRRPPQ 60
    |||||||
Db 1 MEPVDPRLEPKHPSQKPTACTNCYCKKCCFHCQVCFITAAIGISYGRKKRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSQSGKEPTGPKE 86
    |||||||
Db 61 GSQTHQVSLSKOPTSQSGKEPTGPKE 86

RESULT 4
TAT_HV1BR
ID TAT_HV1BR STANDARD; PRT; 86 AA.
AC P04610;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
```

```

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8509333; PubMed=2981635;
RA Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
RT "Nucleotide sequence of the AIDS virus, LAV.";
RL Cell 40:9-17(1985).
RN [2]
RP SEQUENCE FROM N.A. (CLONE PNL4-3).
RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
RL Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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CC -----
CC EMBL; K02013; AAB59745.1; -
CC EMBL; M19921; AAA44985.1; -
CC HIV; K02013; TATSR0.
CC InterPro; IPR001831; HIV_Tat.
CC PRINTS; PR000539; Tat; 1.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC VARIANT 24 24 T -> N (IN CLONE PNL4-3).
CC VARIANT 39 39 T -> M (IN CLONE PNL4-3).
CC VARIANT 58 61 PQPG -> AHON (IN CLONE PNL4-3).
CC VARIANT 67 67 V -> A (IN CLONE PNL4-3).
CC VARIANT 77 77 P -> S (IN CLONE PNL4-3).
CC SEQUENCE 86 AA; 9769 MW; 9B1B4A915FA8A14 CRC64;
DR DR
DR EMBL; M19921; AAA44985.1; -
DR HIV; K02013; TATSR0.
DR InterPro; IPR001831; HIV_Tat.
DR PRINTS; PR000539; Tat; 1.
DR Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
FT VARIANT 24 24 T -> N (IN CLONE PNL4-3).
FT VARIANT 39 39 T -> M (IN CLONE PNL4-3).
FT VARIANT 58 61 PQPG -> AHON (IN CLONE PNL4-3).
FT VARIANT 67 67 V -> A (IN CLONE PNL4-3).
FT VARIANT 77 77 P -> S (IN CLONE PNL4-3).
SQ SEQUENCE 86 AA; 9769 MW; 9B1B4A915FA8A14 CRC64;

Query Match 83.7%; Score 462; DB 1; Length 86;
Best Local Similarity 93.0%; Pred. No. 5.5e-38;
Matches 80; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHGPSQPKTACTCYCKKCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Db 1 MEPVDPRLEPKHGPSQPKTACTCYCKKCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Qy 61 GSQTHQVSLSKQPTSQSGKEPTGPK 86
Db 61 GSQTHQVSLSKQPTSQSGKEPTGPK 86

RESULT 5
TAT_HVIRH
ID TAT_HVIRH STANDARD; PRT; 102 AA.
AC P05908;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (RH/HAT isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11701;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86218077; PubMed=2423250;
RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S.,

Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8509333; PubMed=2981635;
RA Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
RT "Nucleotide sequence of the AIDS virus, LAV.";
RL Cell 40:9-17(1985).
RN [2]
RP SEQUENCE FROM N.A. (CLONE PNL4-3).
RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
RL Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K02013; AAB59745.1; -
CC EMBL; M19921; AAA44985.1; -
CC HIV; K02013; TATSR0.
CC InterPro; IPR001831; HIV_Tat.
CC PRINTS; PR000539; Tat; 1.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC VARIANT 24 24 T -> N (IN CLONE PNL4-3).
CC VARIANT 39 39 T -> M (IN CLONE PNL4-3).
CC VARIANT 58 61 PQPG -> AHON (IN CLONE PNL4-3).
CC VARIANT 67 67 V -> A (IN CLONE PNL4-3).
CC VARIANT 77 77 P -> S (IN CLONE PNL4-3).
CC SEQUENCE 86 AA; 9769 MW; 9B1B4A915FA8A14 CRC64;
DR DR
DR EMBL; K02013; AAB59745.1; -
DR EMBL; M19921; AAA44985.1; -
DR HIV; K02013; TATSR0.
DR InterPro; IPR001831; HIV_Tat.
DR PRINTS; PR000539; Tat; 1.
DR Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
FT VARIANT 24 24 T -> N (IN CLONE PNL4-3).
FT VARIANT 39 39 T -> M (IN CLONE PNL4-3).
FT VARIANT 58 61 PQPG -> AHON (IN CLONE PNL4-3).
FT VARIANT 67 67 V -> A (IN CLONE PNL4-3).
FT VARIANT 77 77 P -> S (IN CLONE PNL4-3).
SQ SEQUENCE 86 AA; 9769 MW; 9B1B4A915FA8A14 CRC64;

Query Match 82.1%; Score 453; DB 1; Length 102;
Best Local Similarity 88.5%; Pred. No. 4.7e-37;
Matches 77; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHGPSQPKTACTCYCKKCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Db 1 MEPVDPRLEPKHGPSQPKTACTCYCKKCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Qy 61 GSQTHQVSLSKQPTSQSGKEPTGPK 87
Db 61 GSQTHQVSLSKQPTSQSGKEPTGPK 87

RESULT 6
TAT_HVIRH
ID TAT_HVIRH STANDARD; PRT; 86 AA.
AC P04608; O09778;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
RT virus.";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]
RP REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.

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RESULT 9
TAT_HV1SC
ID TAT_HV1SC STANDARD; PRT; 101 AA.
AC P05906;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Farrel K., Gao H.-G., Franchini G., Aldovini A., Collalti E.,
RA Garrell C., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC
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CC
CC EMBL; M17450; AAA45060.1; -
CC HIV; M17450; TATSSC.
CC InterPro: IPR001831; HIV_Tat.
CC Pfam: PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC SEQUENCE 101 AA; 11426 MW; C91090B938D15788 CRC64;

Query Match 77.7%; Score 429; DB 1; Length 101;
Best Local Similarity 83.9%; Pred. No. 9.2e-35;
Matches 73; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRPPQ 60
Db 1 MDPVDPRLPEPKHGPSQPKAACKTSCYCKKCCFHCQVCFITKGLGISYGRKKRRRAPQ 60

Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKET 87
Db 61 DSQTHQVSLPKOPASQARGDPTGPRES 87

RESULT 10
TAT_HV1C4
ID TAT_HV1C4 STANDARD; PRT; 101 AA.
AC P05907;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11687;
RN [1]
RP SEQUENCE FROM N.A.

MEDLINE=87041461; PubMed=3490666;
Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
Andersen P.R., Devare S.G.;
RT "Molecular cloning and primary nucleotide sequence analysis of a
RT distinct human immunodeficiency virus isolate reveal significant
RT divergence in its genomic sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC
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CC
CC EMBL; M13137; AAA44309.1; -
CC HIV; M13137; TATSCDC45.
CC InterPro: IPR001831; HIV_Tat.
CC Pfam: PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC SEQUENCE 101 AA; 11594 MW; 817D915F3FB1C7FA CRC64;

Query Match 77.4%; Score 427; DB 1; Length 101;
Best Local Similarity 86.0%; Pred. No. 1.4e-34;
Matches 74; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRPPQ 60
Db 1 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRAHQ 60

Qy 61 GSQTHQVSLSKOPTSQSKGPTGPK 86
Db 61 DSQNHQASLSKQPSQTRGDPTGPKE 86

RESULT 11
TAT_HV1Y2
ID TAT_HV1Y2 STANDARD; PRT; 101 AA.
AC P35965;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=36377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93021387; PubMed=1404605;
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
RA Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological
RT properties of human immunodeficiency virus type 1 in vivo: evidence
RT for limited defectiveness and complementation.";
RL J. Virol. 66:6587-6600(1992).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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Db 61 SSQHDSLSKQPSQSRGDPGTPKES 87

RESULT 14
TAT_HV1A2
ID TAT_HV1A2 STANDARD; PRT; 101 AA.
AC P04614;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85090453; PubMed=2578227;
RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
RA Stempien M.M., Brown-Shiner S.L., Gee W.W., Renard A., Randolph A.,
RA Levy J.A., Dina D., Luciw P.A.;
RT Nucleotide sequence and expression of an AIDS-associated retrovirus
RT (ARV-2).;
RL Science 227:484-492(1985).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A
CC HEALTHY GABONESE INDIVIDUAL.
CC -1- MISCELLANEOUS: THE SINGLE C -> S SUBSTITUTION AT RESIDUE 22 OF THE
CC OVI TAT PROTEIN RENDERS IT INACTIVE, BUT MAY NOT ACCOUNT FOR THE
CC AVIRENCE OF THE VIRUS.
CC -----
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CC -----
CC EMBL; M26727; AA83395.1; -
CC HIV; M26727; TATSOYI.
CC InterPro; IPR001831; HIV_Tat.
CC Pfam; PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC SEQUENCE 101 AA; 11561 MW; 83ACAC36CC4C87AD CRC64;

Query Match 74.5%; Score 411; DB 1; Length 101;
Best Local Similarity 81.6%; Pred. No. 4.9e-33;
Matches 71; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHKGSPQKTCNCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Db 1 MEPVDPRLEPKHKGSPQKTCNCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Qy 61 GSQTHQVLSKQPTSQSKGEGTGPKE 87
Db 61 DSKTHQVLSKQPASQPRGDPGTPKES 87

RESULT 16
TAT_HV122
ID TAT_HV122 STANDARD; PRT; 86 AA.
AC P12506;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (22/CDC-234 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11683;
RN [1]
RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
RL Submitted (NOV-1988) to the HIV data bank.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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Db 1 MDPVDPNLESHNPGSQRTACNCKCHCKKCCYHCQVCFITKGLGISYGRKKRRRPPQ 60
Qy 61 GSQTHQVLSKOPTSQSGKEPTGPK 86
Db 61 GQAHQVPIPEQPSQSQRGDPGPK 86

RESULT 19
TAT_HV1MA STANDARD; PRT; 87 AA.
ID TAT_HV1MA
AC P04613;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11697;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86245056; PubMed=2424612;
RA Alison M., Main-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus; nucleotide sequence analysis
of two isolates from African patients.";
RL Cell 46:63-74(1986).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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CC -----
DR EMBL; X04415; CRA28015.1; -
DR HIV; K03456; TAT$MAL.
DR InterPro; IPR001831; HIV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 87 AA; 10036 MW; 3832412849D5BICE CRC64;
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-Query Match 70.2%; Score 387.5; DB 1; Length 87;
Best Local Similarity 74.7%; Pred. No. 7.6e-31;
Matches 65; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

Qy 1 MEPVDPRLPKNHPSQKPTACTNCKKCCPHCCQVCFITAGLISYGRKKRRRPPQ 60
Db 1 MDPVDPNLEPNHPSQKPTPCNCKKCCYHCQVCFITKGLGISYGRKKRRRPPQ 60
Qy 61 GSQTHQVLSKOPTSQSGKE-PTGPK 86
Db 61 GQAHQVPIPEQPSQSQRGDPGPK 87

RESULT 20
TAT_HV1EL STANDARD; PRT; 99 AA.
ID TAT_HV1EL
AC P04611;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
```

```
GN TAT.
OS Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86245056; PubMed=2424612;
RA Alison M., Main-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus; nucleotide sequence analysis
of two isolates from African patients.";
RL Cell 46:63-74(1986).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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CC -----
DR EMBL; K03454; AAA44322.1; -
DR HIV; K03454; TAT$ELI.
DR InterPro; IPR001831; HIV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 99 AA; 11081 MW; B0ECD5199874A762 CRC64;

Query Match 69.6%; Score 384; DB 1; Length 99;
Best Local Similarity 72.1%; Pred. No. 1.8e-30;
Matches 62; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPKNHPSQKPTACTNCKKCCPHCCQVCFITAGLISYGRKKRRRPPQ 60
Db 1 MDPVDPNLEPNHPSQKPTPCNCKKCCYHCQVCFITKGLGISYGRKKRRRPPQ 60
Qy 61 GSQTHQVLSKOPTSQSGKEPTGPK 86
Db 61 GQAHQVPIPEQPSQSQRGDPGPK 86

RESULT 21
TAT_HV1U4 STANDARD; PRT; 101 AA.
ID TAT_HV1U4
AC P24738;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (strain Ugandan / isolate U455)
(HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11703;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91090981; PubMed=2265025;
RA Oram J.D., Downing R.G., Roff M., Clegg J.C.S., Serwadda D.,
RA Carswell J.W.;
RT "Nucleotide sequence of a Ugandan HIV-1 provirus reveals genetic
diversity from other HIV-1 isolates.";
RL AIDS Res. Hum. Retroviruses 6:1073-1078(1990).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC
```

```
CC CC PROMOTER.
CC CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC CC
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CC CC
CC CC EMBL; M62320; AAA75021.1; -.
CC CC InterPro: IPR001831; HIV_Tat.
CC CC Pfam; PF00539; Tat; 1.
CC CC PRINTS; PR00055; HIVTATDOMAIN.
CC CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC CC AIDS.
CC CC SEQUENCE 101 AA; 11378 MW; 3C782A8055DAB249 CRC64;

Query Match 62.0%; Score 342; DB 1; Length 101;
Best Local Similarity 65.5%; Pred. No. 2e-26;
Matches 57; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCFHCQVCFITAAALGISYGRKKRRRPPQ 60
DB 1 MEPVDNLEPKHGPSQPTTACSCYCKVCCWHCOLCFLLKGLGISYGRKKRPRGPPQ 60
QY 61 GSQTHQVSLSKOPTSQSGKEPTGPKET 87
DB 61 GSKDHQTLIPKPLQSRVSGQEE 87

RESULT 22
TAT_HV1B5
ID TAT_HV1B5 STANDARD; PRT; 58 AA.
AC P04612;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (BH5 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11682;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85111123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).
CC CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC CC PROMOTER.
CC CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC CC
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CC CC
CC CC EMBL; K02012; AAA44656.1; -.
CC CC HIV; K02012; TAT5BH5.
```

```
DR InterPro: IPR001831; HIV_Tat.
DR Pfam; PF00539; Tat; 1.
DR Transcription regulation; Activator; RNA-binding; Nuclear protein;
DR AIDS.
DR FT NON_TER 58
DR SEQUENCE 58 AA; 6800 MW; E36C21F8FFD813E3 CRC64;

Query Match 58.7%; Score 324; DB 1; Length 58;
Best Local Similarity 96.5%; Pred. No. 6.3e-25;
Matches 55; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCFHCQVCFITAAALGISYGRKKRRR 57
DB 1 MEPVDPRLEPKHGPSQPKTACTTCYCKKCFHCQVCFITAAALGISYGRKKRRR 57

RESULT 23
TAT_SIVCZ
ID TAT_SIVCZ STANDARD; PRT; 100 AA.
AC P17285;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90259077; PubMed=2188136;
RA Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
RT "Genetic organization of a chimpanzee lentivirus related to HIV-1.";
RL Nature 345:356-359(1990).
CC CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC CC PROMOTER.
CC CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC CC
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CC CC
CC CC EMBL; X52154; CAA36404.1; -.
CC CC HIV; X52154; TATSCP2.
CC CC InterPro: IPR001831; HIV_Tat.
CC CC Pfam; PF00539; Tat; 1.
CC CC PRINTS; PR00055; HIVTATDOMAIN.
CC CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC CC AIDS.
CC CC SEQUENCE 100 AA; 11209 MW; 1B78830B90EED50E CRC64;

Query Match 57.2%; Score 315.5; DB 1; Length 100;
Best Local Similarity 60.7%; Pred. No. 6.7e-24;
Matches 54; Conservative 12; Mismatches 22; Indels 1; Gaps 1;

QY 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCFHCQVCFITAAALGISYGRKKRRR-PP 59
DB 1 MDPTDPRLEPKHGPSQPTTVCNICYKACCYHCICYFTKGLGISYGRKKRTTRRAP 60
QY 60 QGSOHQVSLSKOPTSQSGKEPTGPKETS 88
DB 61 AGSKNNQDSIPKQPLSQSRGNKGESEKT 89
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RESULT 24
TAT_HV2G1
ID TAT_HV2G1 STANDARD; PRT; 130 AA.
AC P18044;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 2 (isolate Ghana-1) (HIV-2).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=1171;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=90122350; PubMed=2611042;
RA Hasegawa A., Tsujimoto H., Maki N., Ishikawa K.I., Miura T.,
RA Fukasawa M., Miki K., Hayami M.;
RT *Genomic divergence of HIV-2 from Ghana.*;
RL AIDS Res. Hum. Retroviruses 5:593-604(1989).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U22047; AAA64580.1; -
CC InterPro; IPR001831; HIV_Tat.
CC Pfam; PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC
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CC
CC EMBL; M30895; AAA43929.1; -
CC PIR; J50332; TNLJGG.
CC HIV; M30895; TAT$2GH1.
CC InterPro; IPR001831; HIV_Tat.
CC Pfam; PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 130 AA; 14580 MW; 95F308B537027D67 CRC64;

Query Match 31.88; Score:175.5; DB 1; Length 130;
Best Local Similarity 49.38; Pred. No. 2.2e-10;
Matches 35; Conservative 9; Mismatches 24; Indels 3; Gaps 2;

Oy 17 OPKTACTN-CYCKKCCFHCQVCFFTAALGISVGRKKRRRPPGQSTHOVSLSKQPTS 75
   .| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 45 RPLEACTNSCYCKQCSFHCQVCFFTAALGISVGRKKRRRPPGQSTHOVSLSKQPTS 75
   .| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 76 OSKGEPTGPK 86
   |: ||
Db 103 TRTGSQPTKE 113

RESULT 25
TAT_HV2KR
ID TAT_HV2KR STANDARD; PRT; 130 AA.
AC Q74124;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 2 (isolate KF) (HIV-2).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=73484;
RN [1]
SEQUENCE FROM N.A.

Kraus G.K., Talbott R., Leavitt M., Luznick L., Schmidt A.,
Badel P., Bartz C., Morton W., Wong-Staal F., Looney D.J.;
Submitted (APR-1995) to the EMBL/GenBank/DBJ databases
-1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
PROMOTER.
-1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC
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CC
CC EMBL; U22047; AAA64580.1; -
CC InterPro; IPR001831; HIV_Tat.
CC Pfam; PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 130 AA; 14440 MW; 2E328084003CC6E0 CRC64;

Query Match 31.58; Score 174; DB 1; Length 130;
Best Local Similarity 49.38; Pred. No. 3e-10;
Matches 36; Conservative 8; Mismatches 25; Indels 4; Gaps 3;

Oy 17 OPKTACTN-CYCKKCCFHCQVCFFTAALGISVGRKKRRRPPGQSTHOVSLSKQPTS 75
   || || || || || || || || || || || || || || || || || || ||
Db 45 QPLEACNPNCKKCCYHCQVCFFTAALGISVGRKKRRRPPGQSTHOVSLSKQPTS 102
   || || || || || || || || || || || || || || || || || || ||

Oy 76 OSKG-EPTGPKET 87
   | | | | |
Db 103 TRTGSQTEKQKT 115

RESULT 26
TAT_HV2ST
ID TAT_HV2ST STANDARD; PRT; 130 AA.
AC P20880;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 2 (isolate ST) (HIV-2).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11721;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=90112662; PubMed=2296086;
RA Kumar P., Hui H., Kappes J.C., Haggarty B.S., Hoxie J.A., Arya S.K.,
RA Shaw G.M., Hahn B.H.;
RT *Molecular characterization of an attenuated human immunodeficiency
RT virus type 2 isolate.*;
RL J. Virol. 64:890-901(1990).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC
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CC
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QY 71 -----KOPTSQSK 78
Db 106 TRTRANSQPAKKQK 118

RESULT 29
TAT_HV2D1
ID TAT_HV2D1 STANDARD; PRT; 130 AA.
AC P17759;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 2 (isolate D194) (HIV-2).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11713;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89184631; PubMed=2467304;
RA Kuehnel H., von Briesen H., Dietrich U., Adamski M., Mix D.,
RA Blesert L., Kreutz R., Immanuel A., Henco K., Melchsnr C.,
RA Andresen R., Gelderblom H., Ruebsamen-Waigmann H.;
RT "Molecular cloning of two west African human immunodeficiency virus
RT type 2 isolates that replicate well in macrophages: a Gambian
RT isolate, from a patient with neurologic acquired immunodeficiency
RT syndrome, and a highly divergent Ghanaian isolate.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:2383-2387(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91045094; PubMed=2235509;
RA Kuehnel H., Kreutz R., Ruebsamen-Waigmann H.;
RT "Nucleotide sequence of HIV-2D194, an isolate from a Gambian case of
RT 'neuro-AIDS', which showed excellent growth in macrophages.";
RL Nucleic Acids Res. 18:6142-6142(1990).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -!- MISCELLANEOUS: THIS ISOLATE IS FROM A GAMBIAN CASE OF
CC 'NEURO-AIDS'.
CC
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CC
CC EMBL; J04542; AAA76845.1; -
CC DR EMBL; X52223; CAA36469.1; -
CC DR PIR; S12157; S12157.
CC DR HIV; J04542; TAT52D194.
CC DR InterPro; IPR001831; HIV_Tat.
CC DR Pfam; PF00539; Tat; 1.
CC DR PRINTS; PR00055; HIVTATDOMAIN.
CC KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC SEQUENCE 130 AA; 14597 MW; 1A659CB2F933C537 CRC64;

Query Match 29.2%; Score 161; DB 1; Length 130;
Best Local Similarity 33.9%; Pred. No. 5.3e-09;
Matches 39; Conservative 12; Mismatches 26; Indels 38; Gaps 5;

QY 2 EPVDRPLEPWHKPGS-----QPKTACTN-CYCKKCCFHQV 36
Db 7 EP-ESLESYNEPSSCTSERDVTAGRAKQGBELLALHRLPLEACTNSCYKQCSYHCQL 65
QY 37 CFITAAALGISYGRKKRRRRPPQSQTHQVSLSS-----KQPTSQSKGEP 81

Db 66 CFLKAGLGIWYARQGR--RRTPRKTKTHPPASPDKSISRTGDSQPTKKQKTP 118

RESULT 30
TAT_SIVM1
ID TAT_SIVM1 STANDARD; PRT; 130 AA.
AC P05911;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Simian immunodeficiency virus (Wm142-83 isolate) (SIV-MAC).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11733;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87287230; PubMed=3649576;
RA Chakrabarti L., Guvader M., Alison M., Daniel M.D., Destosiers R.C.,
RA Tiollais P., Sonigo P.;
RT "Sequence of simian immunodeficiency virus from macaque and its
RT relationship to other human and simian retroviruses.";
RL Nature 328:543-547(1987).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -!- MISCELLANEOUS: THIS IS A MACAQUE ISOLATE.
CC
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CC
CC EMBL; Y00277; CAB46521.1; -
CC DR PIR; F28887; TNLJG3.
CC DR HIV; M16403; TATSM142.
CC DR InterPro; IPR001831; HIV_Tat.
CC DR Pfam; PF00539; Tat; 1.
CC DR PRINTS; PR00055; HIVTATDOMAIN.
CC KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC SEQUENCE 130 AA; 14545 MW; DA133BC4BAB7F521 CRC64;

Query Match 28.9%; Score 159.5; DB 1; Length 130;
Best Local Similarity 50.0%; Pred. No. 7.3e-09;
Matches 29; Conservative 10; Mismatches 16; Indels 3; Gaps 2;

QY 17 QPKTACTN-CYCKKCCFHQVCFITAAALGISYGRKKRRRRPPQSQTHQVSLSKQP 73
Db 45 RPLEACYNTCYCKKCCYHCQFCFLKKGISY--BKSHRRRRTPKKAKANTSSASNEP 100

Search completed: August 26, 2002, 08:15:43
Job time: 347 sec
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 08:14:57 ; Search time 86.53 Seconds  
(without alignments)  
189.929 Million cell updates/sec

Title: US-09-509-239-23  
Perfect score: 552  
Sequence: 1 MEPVDRLEPWKHGSPQKT.....QSKGPTGPKETSGHHHHH 95

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mic:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	450	81.5	86	15	Q74087 human immun
2	448	81.2	86	15	Q900A7 human immun
3	446	80.8	86	15	Q99BV4 human immun
4	446	80.8	101	15	Q9DRA9 human immun
5	445	80.6	101	15	Q92880 human immun
6	443	80.3	86	15	Q99BV5 human immun
7	443	80.3	101	15	Q9DH20 human immun
8	442	80.1	86	15	O57293 simian-huma
9	441	79.9	101	15	Q99BV7 human immun
10	440	79.7	86	15	Q99BV6 human immun
11	440	79.7	86	15	Q99BV3 human immun
12	439	79.5	86	15	Q99BW1 human immun
13	439	79.5	86	15	Q99BW0 human immun
14	439	79.5	101	15	O92885 human immun
15	439	79.5	101	15	O92899 human immun
16	438	79.3	101	15	O56318 simian-huma

#### ALIGNMENTS

RESULT 1

Q74087	17	438	79.3	101	15	O92893
ID	Q74087					O99BV8
AC	Q74087					Q9DQ29
DT	01-NOV-1996 (TRENBLrel. 01, Created)					Q902U5
DT	01-NOV-1996 (TRENBLrel. 01, Last sequence update)					Q93022
DT	01-DEC-2001 (TRENBLrel. 19, Last annotation update)					Q77688
DE	TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).					P90265
GN	TAT.					Q04191
OS	Human immunodeficiency virus type 1.					O40219
OC	Viruses; Retroviridae; Lentivirus.					Q90257
OX	NCBI_TaxID=11676;					O11405
RN	[1]					O92895
RP	SEQUENCE FROM N.A.					Q74810
RC	STRAIN=PM213;					Q80270
RX	MEDLINE=90101366; PubMed=1688473;					O9WJY2
RA	Cloyd M.W., Moore B.E.;					O99BV9
RT	"Spectrum of Biological Properties of Human Immunodeficiency Virus (HIV-1) Isolates."					O75758
RL	Virology 174:103-116(1990).					O92902
RN	[2]					Q73370
RP	SEQUENCE FROM N.A.					Q93199
RC	STRAIN=PM213;					O9WJY7
RX	MEDLINE=90101366; PubMed=1688473;					O9WJY9
RA	Cloyd M.W., Moore B.E.;					Q04192
RT	"Spectrum of Biological Properties of Human Immunodeficiency Virus (HIV-1) Isolates."					Q9Q6V3
RL	Virology 174:103-116(1990).					Q74747
RN	[2]					Q902H8
RP	SEQUENCE FROM N.A.					Q91BN6

RA Iwatani Y.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER (BY SIMILARITY).

CC EMBL: D86069; BAA13000.1; -.

DR InterPro: IPR001831; HIV\_Tat.

DR Pfam: PF00539; Tat; 1.

DR PRINTS: PR00055; HIVTATDOMAIN.

KW Activator; Nuclear protein; RNA-binding; Transcription regulation.

SQ SEQUENCE 86 AA; 9865 MW; 4DDC56CICE269115 CRC64;

Query Match 81.5%; Score 450; DB 15; Length 86;  
Best Local Similarity 91.9%; Pred. No. 2.2e-47;

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Matches 79; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEPVDPRLPEPKHGPSQPKTACTNCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Db 1 MEPVDPRLPEPKHGPSQPKTACTNCKKCCFHCQVCFITAAALGISYGRKKRRRRRAHQ 60

QY 61 GSQTHQVSLSKOPTSQSKGPTGPKE 86
Db 61 NSQTHQVSLSKOPTSQSRGPTGPKE 86

RESULT 2
Q900A7 PRELIMINARY; PRT; 86 AA.
AC Q900A7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PI2.2;
RA Aldhous M.C.; Schwager M., Mok J.Y.Q., Yirell D.L., Leigh Brown A.J.,
RA Froebel K.S.;
RT "The natural history of pediatric HIV infection suggests an
RT association between the specificity of the cytotoxic T cells and
RT clinical outcome.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AF324449; AAK14291.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat. 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription regulation.
KW SEQUENCE 86 AA; 9842 MW; 60C7F0727C482F49 CRC64;
SQ SEQUENCE 86 AA; 9842 MW; 60C7F0727C482F49 CRC64;

Query Match 80.8%; Score 446; DB 15; Length 86;
Best Local Similarity 89.5%; Pred. No. 6.8e-47;
Matches 77; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MEPVDPRLPEPKHGPSQPKTACTNCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Db 1 MEPVDPRLPEPKHGPSQPKTACTNCKKCCFHCQVCFITAAALGISYGRKKRRRRSPQ 60

QY 61 GSQTHQVSLSKOPTSQSKGPTGPKE 86
Db 61 SSQTHQVSLSKOPTSQSRGPTGPKE 86

RESULT 4
Q9DHA9 PRELIMINARY; PRT; 101 AA.
AC Q9DHA9;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20457217; PubMed=11000225;
RA Yuste E., Lopez-Galindez C., Domingo E.;
RT "Unusual Distribution of Mutations Associated with Serial Bottleneck
RT Passages of Human Immunodeficiency Virus Type 1.";
RL J. Virol. 74:9546-9552(2000).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AF256210; AAG16839.1; -.
DR EMBL: AF256209; AAG16831.1; -.
DR InterPro; IPR001831; HIV_Tat.

Matches 79; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEPVDPRLPEPKHGPSQPKTACTNCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Db 1 MEPVDPRLPEPKHGPSQPKTACTNCKKCCFHCQVCFITAAALGISYGRKKRRRRRAHQ 60

QY 61 GSQTHQVSLSKOPTSQSKGPTGPKE 86
Db 61 NSQTHQVSLSKOPTSQSRGPTGPKE 86

RESULT 2
Q900A7 PRELIMINARY; PRT; 86 AA.
AC Q900A7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95074930; PubMed=7983770;
RA Fang H., Pincus S.H.;
RA "Unique insertion sequence and pattern of CD4 expression in variants
RT selected with immunotoxins from human immunodeficiency virus type 1-
RT infected T cells.";
RL J. Virol. 69:75-81(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Fang H., Pincus S.H.;
RT "Spontaneous activation of human immunodeficiency virus type 1 in an
RT immunotoxin-resistant variant T cell line.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NL4-3;
RX MEDLINE=96036482; PubMed=7483282;
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
RA Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes
RT from primary virus cultures using the polymerase chain reaction.";
RL Virology 213:80-86(1995)..
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=NL4-3;
RX MEDLINE=86281827; PubMed=3016298;
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
RA Martin M.A.;
RT "Production of acquired immunodeficiency syndrome-associated
RT retrovirus in human and nonhuman cells transfected with an infectious
RT molecular clone.";
RL J. Virol. 59:284-291(1986).
DR EMBL: AF070521; AAC28449.1; -.
DR EMBL: U26942; AAB60575.1; -.
SQ SEQUENCE 86 AA; 9845 MW; 26B2281979769110 CRC64;

Query Match 81.2%; Score 448; DB 15; Length 86;
Best Local Similarity 90.7%; Pred. No. 3.9e-47;
Matches 78; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEPVDPRLPEPKHGPSQPKTACTNCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Db 1 MEPVDPRLPEPKHGPSQPKTACTNCKKCCFHCQVCFITAAALGISYGRKKRRRRRAHQ 60

QY 61 GSQTHQVSLSKOPTSQSKGPTGPKE 86
Db 61 NSQTHQVSLSKOPTSQSRGPTGPKE 86
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DR Pfam: PF00539; Tat: 1.
DR PRINTS: PR00055: HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 101 AA; 11425 MW; 1A1E45C93960630E CRC64;

Query Match 80.8%; Score 446; DB 15; Length 101;
Best Local Similarity 89.7%; Pred. No. 8e-47; 7; Indels 0; Gaps 0;
Matches 78; Conservative 2; Mismatches 0;

Qy 1 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Db 1 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKET 87
Db 61 DSQTHQVSLSKOPTSQSKGPTGPKES 87

RESULT 5
Q92880 PRELIMINARY; PRT; 101 AA.
ID O92880;
AC O92880;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MBC200;
RA Oelrichs R.B., Lawson V.A., Coates K.M., Chatfield C., Deacon N.J.,
RA McPhee D.A.;
RT "Rapid full-length genomic sequencing of two cytopathically
RT heterogeneous Australian primary HIV-1 isolates.";
RL J. Biomed. Sci. 7:128-135(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MBC200;
RA Oelrichs R.B., McPhee D.A., Deacon N.J.;
RT "Biological cloning and full-length sequence of two Australian HIV-1
RT primary clinical isolates with distinct cellular tropism and
RT cytopathicity.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AF042100; AAD03194.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat: 1.
DR PRINTS: PR00055: HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 101 AA; 11593 MW; A9F467BD68399235 CRC64;

Query Match 80.6%; Score 445; DB 15; Length 101;
Best Local Similarity 89.5%; Pred. No. 1.1e-46;
Matches 77; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Db 1 MEPVDPRLPEPKHGPSQPKTACTTCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKET 86
Db 61 DSETHQVSLSKOPTSQHRGDTGPKET 86
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RESULT 6
Q99BV5 PRELIMINARY; PRT; 86 AA.
ID Q99BV5;
AC Q99BV5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PI2.1;
RA Aldhous M.C., Schwager M., Mok J.Y.Q., Virrell D.L., Leigh Brown A.J.,
RA Froebel K.S.;
RT "The natural history of pediatric HIV infection suggests an
RT association between the specificity of the cytotoxic T cells and
RT clinical outcome.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AF324448; AAK14290.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat: 1.
DR PRINTS: PR00055: HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 86 AA; 9828 MW; C1C6E1727D928438 CRC64;

Query Match 80.3%; Score 443; DB 15; Length 86;
Best Local Similarity 88.4%; Pred. No. 1.6e-46;
Matches 76; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Db 1 MDPVDPRLPEPKHGPSQPKTACTTCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKET 86
Db 61 SSQTHQVSLSKOPTSQPRGDTGPKET 86

RESULT 7
Q9DH20 PRELIMINARY; PRT; 101 AA.
ID Q9DH20;
AC Q9DH20;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20457217; PubMed=11000225;
RA Yuste E., Lopez-Galindez C., Domingo E.;
RT "Unusual Distribution of Mutations Associated with Serial Bottleneck
RT Passages of Human Immunodeficiency Virus Type 1.";
RL J. Virol. 74:9546-9552(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yuste E., Lopez-Galindez C., Domingo E.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
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DR EMBL: AF256211; AAG16848.1; -.
DR EMBL: AF256204; AAG16788.1; -.
DR EMBL: AF256205; AAG16797.1; -.
DR EMBL: AF256206; AAG16805.1; -.
DR EMBL: AF256207; AAG16814.1; -.
DR EMBL: AF256208; AAG16822.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat. 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 101 AA; 11453 MW; 831E576C7E82C649 CRC64;

Query Match 80.3%; Score 443; DB 15; Length 101;
Best Local Similarity 88.5%; Pred. No. 1.9e-46;
Matches 77; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAAGISYGRKKRRRPPQ 60
DB 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCCFHCQVCFITKGLGISYGRKKRRRPPQ 60
QY 61 GSQTHQVSLSKQPTSQSKGPTGPKET 87
DB 61 DSQTHQVSLSKQASQPGDPTGPKES 87

RESULT 8
O57293 PRELIMINARY; PRT; 86 AA.
AC O57293;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]
RP SEQUENCE FROM N.A.
RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,
RA Halloran M., Axthelsson M.W., Letvin N.L., Sodroski J.G.;
RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SHIV-4, AND HXB2;
RX MEDLINE=92309177; PubMed=1613662;
RA Li J., Lord C.I., Haseltine W., Letvin N.L., Sodroski J.;
RT "Infection of cynomolgus monkeys with a chimeric HIV-1/SIVmac virus
RT that expresses the HIV-1 envelope glycoproteins.";
RL J. Acquir. Immune Defic. Syndr. 5:639-646(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-SHIV-4, AND HXB2;
RA Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P.,
RA Lin W., Montefiori D.C., Lee-Parritz D.E., Lu F., Collman R.G.,
RA Sodroski J., Letvin N.L.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AF041850; AAD12139.1; -.
DR EMBL: AF038399; AAB99973.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat. 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 86 AA; 9837 MW; 5132A4D9796364F5 CRC64;

Query Match 80.1%; Score 442; DB 15; Length 86;
Best Local Similarity 89.5%; Pred. No. 2.1e-46;

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Matches 77; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAAGISYGRKKRRRPPQ 60
DB 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCCFHCQVCFITKGLGISYGRKKRRRRAH 60
QY 61 GSQTHQVSLSKQPTSQSKGPTGPKET 86
DB 61 NSQTHQASLSKQPTSQPRGDTGPKET 86

RESULT 9
Q99BV7 PRELIMINARY; PRT; 101 AA.
AC Q99BV7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-P9.2;
RA Aldhous M.C., Schwager M., Mok J.Y.Q., Yirrell D.L., Leigh Brown A.J.,
RA "The natural history of pediatric HIV infection suggests an
RT association between the specificity of the cytotoxic T cells and
RT clinical outcome.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AF324446; AAK14288.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat. 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 101 AA; 11517 MW; 03AB48CC28C9DE2 CRC64;

Query Match 79.9%; Score 441; DB 15; Length 101;
Best Local Similarity 88.5%; Pred. No. 3.3e-46;
Matches 77; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAAGISYGRKKRRRPPQ 60
DB 1 MEPVDPRLEPKHGPSQPKTACTPCYCKKCCFHCQVCFITKGLGISYGRKKRRRAPQ 60
QY 61 GSQTHQVSLSKQPTSQSKGPTGPKET 87
DB 61 DSQTHQVSLSKQPTSQPRGDTGPKES 87

RESULT 10
Q99BV6 PRELIMINARY; PRT; 86 AA.
AC Q99BV6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-P9.3;
RA Aldhous M.C., Schwager M., Mok J.Y.Q., Yirrell D.L., Leigh Brown A.J.,

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RA Froebel K.S.;  
RT "the natural history of pediatric HIV infection suggests an  
RT association between the specificity of the cytotoxic T cells and  
RT clinical outcome."  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE  
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND  
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR  
CC PROMOTER (BY SIMILARITY).  
DR EMBL: AF324447; AAK14289.1; -  
DR InterPro: IPR001831; HIV\_Tat.  
DR Pfam: PF00539; Tat; 1.  
DR PRINTS: PR00055; HIVTATDOMAIN.  
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.  
SQ SEQUENCE 86 AA; 9726 MW; 276EB488E3291174 CRC64;

Query Match 79.7%; Score 440; DB 15; Length 86;  
Best Local Similarity 89.5%; Pred. No. 3.7e-46;  
Matches 77; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPQKHPGSPKTCCTCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||  
Db 1 MEPVDPRLPQKHPGSPKTCCTCYCKKCCFHCQVCFITKGLGISYGRKKRRRRAPQ 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

Qy 61 GSQTHQVSLSKQPTSSQSGEPTGPKE 86  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||  
Db 61 DSQTHQVSLSKQPTSSQSGEPTGPKE 86  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

RESULT 11  
Q99BV3 ID Q99BV3 PRELIMINARY; PRT; 86 AA.  
AC Q99BV3;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).  
GN TAT.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=P2.3;  
RA Aldhous M.C.; Schwager M., Mok J.Y.Q., Yirrell D.L., Leigh Brown A.J.,  
RA Froebel K.S.;  
RT "The natural history of pediatric HIV infection suggests an  
RT association between the specificity of the cytotoxic T cells and  
RT clinical outcome."  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE  
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND  
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR  
CC PROMOTER (BY SIMILARITY).  
DR EMBL: AF324447; AAK14289.1; -  
DR InterPro: IPR001831; HIV\_Tat.  
DR Pfam: PF00539; Tat; 1.  
DR PRINTS: PR00055; HIVTATDOMAIN.  
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.  
SQ SEQUENCE 86 AA; 9726 MW; 30CDFA726F6910F2 CRC64;

Query Match 79.7%; Score 440; DB 15; Length 86;  
Best Local Similarity 88.4%; Pred. No. 3.7e-46;  
Matches 76; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPQKHPGSPKTCCTCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||  
Db 1 MEPVDPRLPQKHPGSPKTCCTCYCKKCCFHCQVCFITKGLGISYGRKKRRRRAPQ 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

Qy 61 GSQTHQVSLSKQPTSSQSGEPTGPKE 86  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||  
Db 61 GSQTHQVSLSKQPTSSQSGEPTGPKE 86  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

RESULT 13  
Q99BW0 ID Q99BW0 PRELIMINARY; PRT; 86 AA.  
AC Q99BW0;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).  
GN TAT.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=P6.1;  
RA Aldhous M.C.; Schwager M., Mok J.Y.Q., Yirrell D.L., Leigh Brown A.J.,  
RA Froebel K.S.;  
RT "The natural history of pediatric HIV infection suggests an  
RT association between the specificity of the cytotoxic T cells and  
RT clinical outcome."  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE  
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND  
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR  
CC PROMOTER (BY SIMILARITY).  
DR EMBL: AF324450; AAK14292.1; -  
DR InterPro: IPR001831; HIV\_Tat.  
DR Pfam: PF00539; Tat; 1.  
DR PRINTS: PR00055; HIVTATDOMAIN.  
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.  
SQ SEQUENCE 86 AA; 9792 MW; 30CDFA726F6910F2 CRC64;

Db 61 SSQTHQVSLSKQPTSSQSGEPTGPKE 86  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

RESULT 12  
Q99BW1 ID Q99BW1 PRELIMINARY; PRT; 86 AA.  
AC Q99BW1;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).  
GN TAT.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=P2.2;  
RA Aldhous M.C.; Schwager M., Mok J.Y.Q., Yirrell D.L., Leigh Brown A.J.,  
RA Froebel K.S.;  
RT "The natural history of pediatric HIV infection suggests an  
RT association between the specificity of the cytotoxic T cells and  
RT clinical outcome."  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE  
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND  
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR  
CC PROMOTER (BY SIMILARITY).  
DR EMBL: AF324440; AAK14283.1; -  
DR InterPro: IPR001831; HIV\_Tat.  
DR Pfam: PF00539; Tat; 1.  
DR PRINTS: PR00055; HIVTATDOMAIN.  
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.  
SQ SEQUENCE 86 AA; 9725 MW; 3A1C9D314983A7A8 CRC64;

Query Match 79.5%; Score 439; DB 15; Length 86;  
Best Local Similarity 88.4%; Pred. No. 4.8e-46;  
Matches 76; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MEPVDPRLPQKHPGSPKTCCTCYCKKCCFHCQVCFITAAALGISYGRKKRRRRPPQ 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||  
Db 1 MDPVDPRLPQKHPGSPKTCCTCYCKKCCFHCQVCFITKGLGISYGRKKRRRRAPQ 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

Qy 61 GSQTHQVSLSKQPTSSQSGEPTGPKE 86  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||  
Db 61 GSQTHQVSLSKQPTSSQSGEPTGPKE 86  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

RESULT 13  
Q99BW0 ID Q99BW0 PRELIMINARY; PRT; 86 AA.  
AC Q99BW0;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).  
GN TAT.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=P6.1;  
RA Aldhous M.C.; Schwager M., Mok J.Y.Q., Yirrell D.L., Leigh Brown A.J.,  
RA Froebel K.S.;  
RT "The natural history of pediatric HIV infection suggests an  
RT association between the specificity of the cytotoxic T cells and  
RT clinical outcome."  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE  
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND  
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR

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CC PROMOTER (BY SIMILARITY).
DR EMBL: AF324442; AAK14285.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 86 AA; 9803 MW; 9B0D8E524AEC1B0E CRC64;

Query Match 79.5%; Score 439; DB 15; Length 86;
Best Local Similarity 89.5%; Pred. No. 4.8e-46;
Matches 77; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 MEPVDPRLEPWKHPGSOPTACTNCYCKCCFHCQVCFITAAALGISYGRKKRRRPPQ 60
Db 1 MEPVDPRLEPWKHPGSOPTACTNCYCKCCFHCQVCFITKALGISYGRKKRRRTPP 60
QY 61 GSQTHQVSLSKQTSQSKEGPTGPK 86
Db 61 DSQTHQVSLSKQTSQSRGPTGPK 86

RESULT 14
ID O92885 PRELIMINARY; PRT; 101 AA.
AC O92885;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=MBCD36;
RA Oelrichs R.B., McPhee D.A., Deacon N.J.;
RT Cohort of long term non-progressors.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
CC EMBL: AF042105; AAD03203.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 101 AA; 11576 MW; 9335253792B3FB2 CRC64;

Query Match 79.5%; Score 439; DB 15; Length 101;
Best Local Similarity 87.4%; Pred. No. 5.7e-46;
Matches 76; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 MEPVDPRLEPWKHPGSOPTACTNCYCKCCFHCQVCFITAAALGISYGRKKRRRPPQ 60
Db 1 MEPVDPRLEPWKHPGSOPTACTPCYCKCCFHCQVCFITKALGISYGRKKRRRAPQ 60
QY 61 GSQTHQVSLSKQTSQSKEGPTGPK 87
Db 61 DSQTHQVSLSKQTSQSRGPTGPK 87

RESULT 15
ID O92899 PRELIMINARY; PRT; 101 AA.
AC O92899;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=MBCD36;
RA Oelrichs R.B., McPhee D.A., Deacon N.J.;
RT Cohort of long term non-progressors.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
CC EMBL: AF042105; AAD03236.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 101 AA; 11512 MW; 440B807D4F48738E CRC64;

Query Match 79.5%; Score 439; DB 15; Length 101;
Best Local Similarity 85.1%; Pred. No. 5.7e-46;
Matches 74; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEPVDPRLEPWKHPGSOPTACTNCYCKCCFHCQVCFITAAALGISYGRKKRRRPPQ 60
Db 1 MEPVDPRLEPWKHPGSOPTACTSCYCKCCFHCQVCFITKGLGISYGRKKRRRPPQ 60
QY 61 GSQTHQVSLSKQTSQSKEGPTGPK 87
Db 61 DNQTHQVSLSKQSPSRGPTGPK 87

RESULT 16
ID O56318 PRELIMINARY; PRT; 101 AA.
AC O56318;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]
RC STRAIN=SHIV-89.6;
RA Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P.,
RA Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G.,
RA Sodroski J., Letvin N.L.;
RT "An env gene derived from a primary human immunodeficiency virus type
RT 1 isolate confers high in vivo replicative capacity to a chimeric
RT simian/human immunodeficiency virus in rhesus monkeys.;"
RL J. Virol. 70:3198-3206(1996).
RN [2]
RC STRAIN=SHIV-89.6;

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RA Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P.,  
RA Lin W., Montefiore D.C., Lee-Parritz D.E., Lu Y., Collman R.G.,  
RA Sodroski J., Levin N.L.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.  
RC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE  
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND  
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR  
CC PROMOTER (BY SIMILARITY).  
CC EMBL: AF038398; AAB99963.1; -.  
DR InterPro: IPR001831; HIV\_Tat.  
DR Pfam: PF00359; Tat; 1.  
DR PRINTS: PR00055; HIVTATDOMAIN.  
DR Activator; Nuclear protein; RNA-binding; Transcription regulation.  
KW SEQUENCE 101 AA; 11629 MW; ACC85C209970DDE9 CRG64;

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Query Match          79.3%; Score 438; DB 15; Length 101;
Best Local Similarity 88.4%; Pred. No. 7.6e-46;
Matches 76; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPWKHPGSPKPTACTNCKYCKCFHCQVCFITAAALGISYGRKKRRRRRPPQ 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MEPVDPRLEPWKHPGSPKPTACTNCKYCKCFHCQVCFITKALGISYGRKKRRRRRAHQ 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 GSQTHQVLSKQPTSSQSGEPTGPKE 86
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NSQTHQASLSKQSPSPRGDPTGPKE 86
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 17
O92893 PRELIMINARY; PRT; 101 AA.
AC O92893;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSCRIPTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MBCC54;
RA Oelrichs R.B., McPhee D.A., Deacon N.J.;
RT "Genomic sequence of HIV-1 from four members of the Sydney Blood Bank Cohort of long term non-progressors.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER (BY SIMILARITY).
CC EMBL; AF042103; AAD03220.1; -.
DR InterPro; IPR001831; HIV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR KW SEQUENCE; Nucleic protein; RNA-binding; Transcription regulation.
SO ACCESSION 101 AA: 11509 MW: 974357617DBDEF30 CRC64:

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[illegible]

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RESULT 18
Q99BV8 PRELIMINARY; PRT: 101 AA.
AC Q99BV8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P6.3;
RA Aldous M.C.; Schwager M., Mok J.Y.Q., Yirrell D.L., Leigh Brown A.J.
RA Froebel K.S.;
RT "the natural history of pediatric HIV infection suggests an
RT association between the specificity of the cytotoxic T cells and
RT clinical outcome.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
CC EMBL: AF324444; AAK14287.1; -.
CC InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 101 AA; 111615 MW; 5F80827F08100F03 CRC64;

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Query Match      79.3%; Score 438; DB 15; Length 101;
Best Local Similarity 87.4%; pred. No. 7.6e-46;
Matches 76; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHPSQPKTACTNCYKCKCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MEPVDPRLEPKHPSQPKTACTNCYKCKCFHCQVCFITAAALGISYGRKKRRRRPPQ 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 GSQTHQVSLSKQPTSQSKGPTGPKET 87
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 DSQTHQVSLSKQSTSQPRGDPGPKES 87
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT	19
Q9DQ29	
ID	Q9DQ29 PRELIMINARY; PRT; 101 AA.
AC	Q9DQ29;
DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN	TAT.
OS	Human immunodeficiency virus type 1.
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX	NCBI_TaxId=11676;
RN	[1]
RP	SEQUENCE FROM N.A.

RA MEDLINE 20304/79; Pubmed-11112460;  
RA Salminen M.O., Ehrenberg P.K., Mascola J.R., Dayhoff D.E., Merling R.,  
RA Blake B., Lounder M., Hegerich S., Polonis V.R., Birk D.L., Robb M.L.,  
RA McCutchan F.E., Michael N.L.;  
RT "Construction and biological characterization of infectious molecular  
RT clones of HIV-1 subtypes B and E (CRF01-AE) generated by the  
RT polymerase chain reaction.";  
RL Virology 278:103-110(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-WR27;  
RA Salminen M.O., Ehrenberg P.K., Mascola J.R., Dayhoff D.E., Merling R.,

```
RA Blake B., Louder M., Hegerich S., Polonis V.R., Birk D.L., Robb M.L.,
RA McCutchan F.E., Michael N.L.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
CC EMBL: AF286365; AAG30119.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 101 AA; 11572 MW; 41F97B5162E3C813 CRC64;

Query Match 79.2%; Score 437; DB 15; Length 101;
Best Local Similarity 86.2%; Pred. No. 1e-45;
Matches 75; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAAGLSYGRKKRRRRPPQ 60
Db 1 MDPVDPRLEPKHGPSQPKTACTNCYCKKCCFHCQVCFITKGLISYGRKKRRRRAPQ 60

Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKET 87
Db 61 EGQTHQVPLSKQPSQPRGDTGPKES 87

RESULT 20
ID Q902U5 PRELIMINARY; PRT; 101 AA.
AC Q902U5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=ARCH014;
RA Carr J.K., Avila M., Gomez-Carrillo M., Salomon H., Hierholzer J.,
RA Watanaveeradej V., Pando M., Negrete M., Russell K.L., Sanchez J.,
RA Birk D.L., Andrade R., Vinholes J., McCutchan F.E.;
RT "Diverse BF Recombinants have spread widely since the introduction of
RT HIV-1 into South America.";
RL AIDS 0:0-0(2001).
DR EMBL: AY037266; AAL12635.1; -.
SQ SEQUENCE 101 AA; 11478 MW; 34432B8FD16F5DFC CRC64;

Query Match 79.2%; Score 437; DB 15; Length 101;
Best Local Similarity 87.4%; Pred. No. 1e-45;
Matches 76; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAAGLSYGRKKRRRRPPQ 60
Db 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCCFHCQVCFITKGLISYGRKKRRRRPPQ 60

Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKET 87
Db 61 DSQTHQVSLSKOPTSQSKGPTGPKES 87

RESULT 21
ID O93022 PRELIMINARY; PRT; 101 AA.
AC O93022;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=89ES061;
RA Lopez-galindez C.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RC STRAIN=89ES061;
RX MEDLINE=9905865; PubMed=9870318;
RA Olivares I., Casado C., Iglesias-Ussel M.D., Dietrich U.,
RA Lopez-galindez C.;
RT "Complete sequence of an infectious molecular clone derived from a
RT Spanish HIV type 1 isolate.";
RL AIDS Res. Hum. Retroviruses 14:1649-1651(1998).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
CC EMBL: AJ006287; CAA06950.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 101 AA; 11512 MW; 831E576C7CA2E449 CRC64;

Query Match 78.6%; Score 434; DB 15; Length 101;
Best Local Similarity 87.4%; Pred. No. 2.3e-45;
Matches 76; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCCFHCQVCFITAAAGLSYGRKKRRRRPPQ 60
Db 1 MEPVDPRLEPKHGPSQPKTACTNCYCKKCCFHCQVCFITKGLISYGRKKRRRRAPQ 60

Qy 61 GSQTHQVSLSKOPTSQSKGPTGPKET 87
Db 61 DSQTHQVSLSKQPSQPRGDTGPKES 87

RESULT 22
ID Q77688 PRELIMINARY; PRT; 101 AA.
AC Q77688;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=CAMBRIDGE;
RA McIntosh A.A., Karpis A.;
RT "Nucleotide sequence of a Cambridge isolate of human immunodeficiency
RL virus type 1.";
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
CC EMBL: D10112; BAA00996.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 101 AA; 11430 MW; B76CF7B13E60C3EF CRC64;
```

```

[1] SEQUENCE FROM N.A.
RA Reitz M., Popovic M., Gartner S., Gallo R., Reed-Connole E.,
RA Beaver B.;
RL Submitted (JUN-1991) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TAT IS AN EFFECTOR OF AN AUTOSTIMULATORY PATHWAY THROUGH
CC INTERACTION WITH A POSITIVE CONTROL ELEMENT, THE TRANS-ACTIVATING
CC RESPONSIVE SEQUENCE (TAR).
CC -1- MISCELLANEOUS: DELETION MUTANTS IN THE TAT GENE ARE INCAPABLE OF
CC PROLIFIC REPLICATION AND EXHIBIT NO CYTOPATHIC EFFECTS IN T4+ CELL
CC LINES.
DR EMBL; M68893; AAA44188.1; -.
DR InterPro; IPR001831; HIV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Transcription regulation; AIDS.
SQ SEQUENCE 101 AA; 11547 MW; A76FAA123C098973 CRC64;

Query Match          78.4%; Score 433; DB 15; Length 101;
Best Local Similarity 85.1%; Pred. No. 2.3e-45;
Matches 74; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MEPVDPLEPKWPGSQPTACTNCYKKCFHCQVCFITAALGISYGRKRRRPPQ 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MEPVDPLKPKWPGSQPTACTTCYCKKCFHCQVCFTKGLGISYGRKRRRRAPQ 60

QY 61 GSQTHOVSLSQPTSQSKEPTGPKET 87
   |:|||||:|||||:|||||:|||||:
Db 61 DSETHOVSLSQPTSHRGDPTGPES 87

RESULT 25
O40219 PRELIMINARY; PRT: 101 AA.
AC O40219;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=AD8;
RX MEDLINE=96432129; PubMed=8835195;
RA Theodore T.S., Englund G., Buckler-White A., Buckler C.E.,
RA Martin M.A., Peden K.W.C.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL; AF004394; AAB64167.1; -.
DR InterPro; IPR001831; HIV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 101 AA; 11632 MW; 14FDB89C0421D0A1 CRC64;

Query Match          78.4%; Score 433; DB 15; Length 101;

```



Search completed: August 26, 2002, 08:14:58  
Job time: 386 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2002, 08:08:31 ; Search time 99.16 Seconds  
(without alignments)  
338.284 Million cell updates/sec

Title: US-09-509-239-13  
Perfect score: 1688  
Sequence: 1 MGGKWSKSSVVGWPTVRM.....QSRGDTGPKETSGHHHHH 302

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802:.\*  
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2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
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15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1688	100.0	302	20 AAY02351	A representative H
2	1688	100.0	302	22 AAG63233	Amino acid sequenc
3	1688	100.0	411	22 AAG63235	Amino acid sequenc
4	1688	100.0	413	20 AAY02355	A representative L
5	1688	100.0	413	22 AAG63237	Amino acid sequenc
6	1675	99.2	302	20 AAY02357	A representative H
7	1675	99.2	302	22 AAG63239	Amino acid sequenc
8	1675	99.2	411	20 AAY02353	A representative L
9	1139.5	67.5	215	20 AAY02349	A representative H
10	1139.5	67.5	215	22 AAG63231	Amino acid sequenc
11	1139.5	67.5	324	20 AAY02352	A representative L

12	1139.5	67.5	324	22 AAG63234	Amino acid sequenc
13	1139.5	67.5	326	20 AAY02354	A representative L
14	1139.5	67.5	326	22 AAG63236	Amino acid sequenc
15	1120	66.4	206	21 AAY50795	Human NEF protein/HIV-1 nef protein
16	1116	66.1	206	14 AAR38893	HIV-1 nef protein
17	1115	66.1	206	21 AAB10054	HIV-1 nef protein
18	1114	66.0	206	20 AAW89326	Sequence of E' pro
19	1111	65.8	206	7 AAP61515	Sequence of LAV v1
20	1107	65.6	216	7 AAP60423	HTLV-III E' protei
21	1092	64.7	206	20 AAW90179	HIV-1 jrl1 Nef pro
22	1011	59.9	216	22 AAE04960	Protein 6 containe
23	997	59.1	210	19 AAW53113	HIV-1 (ATCC CRL 85
24	997	59.1	210	21 AAY77299	HIV-1 jrl1 Nef (G2
25	996	59.0	217	22 AAE04962	HIV-1 strain Oxi o
26	983	58.2	210	12 AAR12262	Human tpa leader p
27	978	57.9	237	22 AAE04961	HIV-1 non-subtype
28	968	57.3	237	22 AAE04963	HIV-1 non-subtype
29	952	56.4	206	21 AAB69363	HIV-1 non-subtype
30	948.5	56.2	3025	22 AAB86169	HIV-1 non-subtype
31	934	55.3	206	21 AAB69361	Sequence encoded b
32	927.5	54.9	206	9 AAP81859	HIV-1 non-subtype
33	910.5	53.9	207	21 AAB69359	Sequence deduced f
34	903.5	53.5	207	11 AAR08407	HIV-1 non-subtype
35	901.5	53.4	207	21 AAB69364	HIV-1 non-subtype
36	895.5	53.1	219	21 AAB69356	HIV-1 non-subtype
37	895.5	53.1	219	21 AAB69362	HIV-1 non-subtype
38	893.5	52.9	217	21 AAB69365	HIV-1 non-subtype
39	885.5	52.5	207	21 AAB69366	HIV-1 non-subtype
40	878.5	52.0	207	21 AAB69357	HIV-1 non-subtype
41	867	51.4	206	21 AAB69358	HIV-1 non-subtype
42	860	50.9	206	21 AAB69360	HIV-1 non-subtype
43	834.5	49.4	209	19 AAW72998	HIV isolate LAV.MA
44	831.5	49.3	209	9 AAP81866	Sequence encoded b
45	796	47.2	212	19 AAW68481	HIV-1 strain YBF30

ALIGNMENTS

RESULT 1  
AAY02351  
ID AAY02351 standard; Protein; 302 AA.  
XX AC AAY02351;  
XX DT 09-JUL-1999 (first entry)  
XX DE A representative HIV-1 Nef-Tat-His protein.  
XX KW HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
XX KW vaccine; HIV infection; protein D.  
XX OS Synthetic.  
XX OS Human immunodeficiency virus type 1.  
XX PN WO9916884-A1.  
XX PD 08-APR-1999.  
XX PF 17-SEP-1998; 98WO-EF06040.  
XX PR 26-SEP-1997; 97GB-0020585.  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX Bruck C, Godart SAG, Marchand M;  
XX WPI; 1999-302282/25.  
XX DR N-PSDB; AAX35687.  
XX HIV Tat or Nef protein linked to a fusion partner  
XX Disclosure; Fig 2; 66pp; English.  
PS

XX The present sequence represents a representative HIV-1 Nef-Tat-His  
 CC protein. The protein is used in the creation of the fusion proteins of  
 CC the invention, in conjunction with a fusion partner (e.g. protein D).  
 CC The fusion protein can be used in a vaccine to prevent HIV infection.  
 XX Sequence 302 AA;

Query Match 100.0%; Score 1688; DB 20; Length 302;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-156;  
 Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVVGWPTVYRMRRAEPAADGGAASRDLEKHGATTSNTAATNAACAWLEA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 mggkwsksvvvgwptvremrraepaadvgaasrdlekhgaitssntaatnaacawlea 60

QY 61 QEEEEVGFPTQVPLRPMYTYAAVDLSHFLKEKGLGIIHSQRRQDILDWIYHTQGY 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 qeeeevgfptqpvlrmpmtkaavdlshflkekggleghsrrrqdildwihtqgy 120

QY 121 FPDWQNTPGGVRYPLTFGWCVKLVPEPDKVEEANKGENTSLHPVSLHGMDDPEREV 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 fpdwqntpggvrypltfgwcyklvppepdkveeankgentsllhpsvlhgmdperev 180

QY 181 LEWRFSRLAFHVARLHPEYFKNCTSEPVDPRLPEWPKHPSQPKTACTNCYCKKCCFH 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 lewrfsrlafhvarlhpeyfkntsepvdprrlepwhkpsqpkactactncycckccfh 240

QY 241 CQVCFITKALGISYGRKKRRRRPPQSGQTHQVSLSKQPTSQSRGDPGPKETSGHHHH 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 cqvcfitkalgisygrrrrppqsgqthqvsiskqptsrgdpgpketsgghhh 300

QY 301 HH 302  
 ||  
 Db 301 hh 302

RESULT 2  
 AAG63233  
 ID AAG63233 standard; Protein; 302 AA.  
 XX AC AAG63233;  
 XX 01-OCT-2001 (first entry)  
 XX Amino acid sequence of a His-tagged Nef-Tat linked protein of HIV.  
 XX HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.  
 XX Synthetic.  
 OS Human immunodeficiency virus.  
 OS Human immunodeficiency virus.  
 XX WO200154719-A2.  
 XX 02-AUG-2001.  
 XX 29-JAN-2001; 2001WO-EP00944.  
 XX 31-JAN-2000; 2000GB-0002200.  
 PR 14-APR-2000; 2000GB-0009336.  
 PR 06-JUN-2000; 2000GB-0013806.  
 PR 28-JUN-2000; 2000WO-EP05998.  
 XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX Voss G;  
 PI WPI: 2001-476172/51.  
 XX N-PSDB: AAH42877.  
 XX New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
 PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120

PT protein or polynucleotide for the manufacture of a vaccine -  
 XX Disclosure; Fig 1; 90pp; English.  
 PS The present sequence represents a His-tagged Nef-Tat linked protein of  
 CC HIV. The protein is expressed in the yeast Pichia pastoris, and is used  
 CC to produce the vaccine of the invention. The specification describes  
 CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the  
 CC manufacture of a vaccine. The vaccine is used for the prophylactic or  
 CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
 CC in synergy with gp120 in the treatment and prevention of HIV. The  
 CC vaccine reduces the HIV viral load in HIV infected humans and results  
 CC in a maintenance of CD4+ levels over those levels found in the absence  
 CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.  
 XX Sequence 302 AA;

Query Match 100.0%; Score 1688; DB 22; Length 302;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-156;  
 Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVVGWPTVYRMRRAEPAADGGAASRDLEKHGATTSNTAATNAACAWLEA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 mggkwsksvvvgwptvremrraepaadvgaasrdlekhgaitssntaatnaacawlea 60

QY 61 QEEEEVGFPTQVPLRPMYTYAAVDLSHFLKEKGLGIIHSQRRQDILDWIYHTQGY 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 qeeeevgfptqpvlrmpmtkaavdlshflkekggleghsrrrqdildwihtqgy 120

QY 121 FPDWQNTPGGVRYPLTFGWCVKLVPEPDKVEEANKGENTSLHPVSLHGMDDPEREV 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 fpdwqntpggvrypltfgwcyklvppepdkveeankgentsllhpsvlhgmdperev 180

QY 181 LEWRFSRLAFHVARLHPEYFKNCTSEPVDPRLPEWPKHPSQPKTACTNCYCKKCCFH 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 lewrfsrlafhvarlhpeyfkntsepvdprrlepwhkpsqpkactactncycckccfh 240

QY 241 CQVCFITKALGISYGRKKRRRRPPQSGQTHQVSLSKQPTSQSRGDPGPKETSGHHHH 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 cqvcfitkalgisygrrrrppqsgqthqvsiskqptsrgdpgpketsgghhh 300

QY 301 HH 302  
 ||  
 Db 301 hh 302

RESULT 3  
 AAG63235  
 ID AAG63235 standard; Protein; 411 AA.  
 XX AC AAG63235;  
 XX 01-OCT-2001 (first entry)  
 XX Amino acid sequence of a His tagged LipD-Nef-Tat linked protein.  
 DE HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.  
 XX Synthetic.  
 OS Human immunodeficiency virus.  
 OS Human immunodeficiency virus.  
 XX Key Location/Qualifiers  
 FT Peptide 1..109  
 FT /note= "ProtD fusion partner"  
 XX WO200154719-A2.  
 XX 02-AUG-2001.  
 XX 29-JAN-2001; 2001WO-EP00944.  
 XX 31-JAN-2000; 2000GB-0002200.

PR	14-APR-2000; 2000GB-0009336.	
PR	06-JUN-2000; 2000GB-0013806.	
PR	28-JUN-2000; 2000WO-EP05998.	
XX		
XX	(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.	
XX		
PI	Voss G;	
XX		
XX	WPI: 2001-476172/51.	
DR	N-PSDB; AAH42879.	
DR		
XX		
PT	New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef	
PT	linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120	
PT	protein or polynucleotide for the manufacture of a vaccine -	
PT		
XX	Disclosure; Fig 1; 90pp; English.	
XX		
CC	The present sequence represents a His-tagged Nef-Tat linked protein of	
CC	HIV, with a lipidation signal sequence (lipod) which is removed after	
CC	processing and a ProtD fusion partner. The protein is expressed in	
CC	Escherichia coli, and is used to produce the vaccine of the invention.	
CC	The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat;	
CC	and HIV gp120 in the manufacture of a vaccine. The vaccine is used for	
CC	the prophylactic or therapeutic immunization of humans against HIV.	
CC	Tat, Nef or Nef-Tat act in synergy with gp120 in the treatment and	
CC	prevention of HIV. The vaccine reduces the HIV viral load in HIV	
CC	infected humans and results in a maintenance of CD4+ levels over those	
CC	levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat	
CC	and HIV gp120.	
XX		
XX	Sequence 411 AA;	
SQ		

Query Match	100.0%;	Score 1688;	DB 22;	Length 411;
Best Local Similarity	100.0%;	Pred. No. 1.3e-155;		
Matches 302;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGGKWSVVGVGVTVERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA	60	
Db	110	mggkwsxvvvgvptvermrreaapaadgvaasrdlekghaicsncaatnaacawlea	169	
QY	61	QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRQDILDWIYHTQGY	120	
Db	170	qeeeevgfpvtpqvpplrpmtykaavdlshflkekgleglihsqrqaldwiyhtqgy	229	
QY	121	FPDQWNTPGGVRYPITFGWCYKLVPEPKVBEANKGENTSLHPVSLHGMDDPEREV	180	
Db	230	fpdwgnvtpggvrypitfgwcyklvppepkveeankgentsllhpvslhgmddperev	289	
QY	181	LEWRFDLSLAFHHVARELHPYFKNCSSEPVDPRLPEPKKHGPSQPKTACTNCYCKKCCFH	240	
Db	290	lewrfdsrlafhhvarelhpheyfknctsepvdprrlpewkhpqspktaactncyckkccfh	349	
QY	241	CQVCFIKALCISYGRKKRRORRPPQSGQTHQVSLSKOPTSQSRGDDTGPKEKTSGHUHH	300	
Db	350	cqvcfikalgisygrkkrrqrrppqsgsqthqvskskqpsqsrqddtgpketsghhhh	409	
QY	301	HH 302		
Db	410	hh 411		

RESULT	4	
AAV02355		
ID	AAV02355 standard; Protein; 413 AA.	
XX		
AC	AAV02355;	
XX		
DT	09-JUL-1999 (first entry)	
XX		
DE	A representative Lipod-Tat fusion protein.	
XX		
KW	HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;	

KW	vaccine; HIV infection; protein D.
XX	
OS	Synthetic.
OS	Human immunodeficiency virus type 1.
XX	
XX	
PN	WO9916884-A1.
XX	
XX	08-APR-1999.
PD	
XX	
XX	17-SEP-1998; 98WO-EF06040.
PF	
XX	
XX	26-SEP-1997; 97GB-0020585.
PR	
XX	
XX	
PA	(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX	
PI	Bruck C, Godart SAG, Marchand M;
XX	
XX	WPI; 1999-302282/25.
DR	N-PSDB; AAX35691.
DR	
XX	
PT	HIV Tat or Nef protein linked to a fusion partner
XX	
XX	Disclosure; Fig 2; 66pp; English.
PS	
XX	
CC	The present sequence represents a fusion protein comprising LipOD-HIV-1
CC	Tat. The protein is exemplifies the fusion proteins of
CC	the invention. The specification also describes fusion proteins
CC	comprising HIV-1 Nef protein. The fusion protein can be used in a
CC	vaccine to prevent HIV infection.
XX	
XX	
SO	Sequence 413 AA;

Query Match	100.0%;	Score 1688;	DB 20;	Length 413;
Best Local Similarity	100.0%;	Pred. NO. 1.3e-155;		
Matches 302;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGGKWSKSSVVGVTVTRMRRAEPAADGVCAASRDLEKHCAITSSNTAATNAACWLEA	60	
Db	112	mggkwsksvvgvvtvtrmreraepaadvgaasrdlekhgaitssntaataacwlea	171	
Qy	61	QEESEVGFPVTPQVPLRPMTYKAAVDLSHFLEKXGGLGLIHSQRRORDILDLIWYHTQGY	120	
Db	172	qeeevgfpvtcpvplrtpmtykaavdlshflekkgleglihsqrrddildliwhycqy	231	
Qy	121	FPDQNYTPGCVRYPLTFGWCYKLVPEVPDKEANKGENTSLHPVSLHGMDDPREV	180	
Db	232	fpdwgnytpgpgvcypltfwcycylvpvdpkveeankgentsllhpvslhgmddperev	291	
Qy	181	LEWFDLSLAFHHVARELHPDFYFNCTSEPVDPRLPEWKHPGSPKACTNCYCCKKCCFH	240	
Db	292	lewifdsrlafhhvarelhpdyfknctsepvdprlpwxhpgspkactncycckkccfh	351	
Qy	241	COVCFITKALGISYGRKKRRORRRPPGSGSOPHVSLSKQPTSQSGRPDTPGKETSGHHHH	300	
Db	352	cqvfcfitalgisyrkrrrrppgsgsqhqvslskqptsqsrqdpdtpgkpsghhhh	411	
Qy	301	HH 302		
Db	412	bb 413		

RESULT	5	
AAG63237		
ID	AAG63237 standard; Protein; 413 AA.	
XX		
XX	AAG63237;	
AC		
XX		
XX	01-OCT-2001 (first entry)	
DT		
XX		
XX	Amino acid sequence of a His tagged ProtD-Nef-Tat fusion protein.	
DE		
XX		
XX	HIV; nef gene; tat gene; vaccine; qpl20 gene; HIV viral load.	
KW		

XX Synthetic.  
 OS Human immunodeficiency virus.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..111  
 FT /note= "protD fusion partner"  
 XX WO200154719-A2.  
 XX PD 02-AUG-2001.  
 XX PF 29-JAN-2001; 2001WO-EP00944.  
 XX PR 31-JAN-2000; 2000GB-0002200.  
 XX PR 14-APR-2000; 2000GB-0009336.  
 XX PR 06-JUN-2000; 2000GB-0013806.  
 XX PR 28-JUN-2000; 2000WO-EP03998.  
 XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX PI Voss G;  
 XX DR WPI: 2001-476172/51.  
 XX DR N-PSDB; AAH42881.  
 XX PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
 PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
 PT protein or polynucleotide for the manufacture of a vaccine -  
 XX PS Disclosure; Fig 1; 90pp; English.  
 XX CC The present sequence represents a His-tagged ProTD-Nef-Tat fusion  
 CC protein. The protein is expressed in Escherichia coli, and is used to  
 CC produce the vaccine of the invention. The specification describes  
 CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the  
 CC manufacture of a vaccine. The vaccine is used for the prophylactic or  
 CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
 CC in synergy with gp120 in the treatment and prevention of HIV. The  
 CC vaccine reduces the HIV viral load in HIV infected humans and results  
 CC in a maintenance of CD4+ levels over those levels found in the absence  
 CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.  
 XX SQ Sequence 413 AA;

Query Match 100.0%; Score 1688; DB 22; Length 413;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-155;  
 Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVVGPTVRRMRRAEPADGVGAASRDLEKHGATSSNTAATNAACAWLEA 60  
 Db 112 mgkwsksvvgptvrermraepaadvgaaardlekghaltssntaatnaacawlea 171  
 QY 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRODILDLYHTQGY 120  
 Db 172 qeeeevgfvtqpvlrptmcykaavdlshflkekggleghlsqrrddildlyhtqgy 231  
 QY 121 FPDQNYTPGPGVRYPLTFCGCYKLVPEPDKVEEANKGENTSLHLPVSLHGMDDPEREY 180  
 Db 232 fpdqnytpgpgvrypltfgcycylvpvdpdkveeankgentsllhpsvslhgmddperey 291  
 QY 181 LEWRFSRLAFHHVARELHPEYFNKCTSEPVDPRLPEWKHPGSGQPKTACTNCYCKKCCFH 240  
 Db 292 lewrfdslafhhvarelhpeyfnkctsepvdprrlepwhpgsqpktactncycckccfh 351  
 QY 241 COVCFITKALGISYGRKKRRORRPPQSGSOTHVSLSKOPTSQSRGDPGTPKETSQHGH 300  
 Db 352 cqvcfitaalgisygrkrrrrppqsgsqthqvslskqpsqsrqgdpctgpketsghhhh 411  
 QY 301 HH 302  
 Db 412 hh 413

RESULT 6  
 AAY02357  
 ID AAY02357 standard; Protein; 302 AA.  
 XX AC AAY02357;  
 XX DT 09-JUL-1999 (first entry)  
 XX DE A representative HIV-1 mutant Tat-His protein.  
 XX KW HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
 KW vaccine; HIV infection; protein D.  
 XX OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX PN WO9916884-A1.  
 XX PD 08-APR-1999.  
 XX PF 17-SEP-1998; 98WO-EP06040.  
 XX PR 26-SEP-1997; 97GB-0020585.  
 XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX PI Bruck C, Godart SAG, Marchand M;  
 XX DR WPI: 1999-302282/25.  
 DR N-PSDB; AAX35693.  
 XX PT HIV Tat or Nef protein linked to a fusion partner  
 XX PS Disclosure; Fig 2; 66pp; English.  
 CC The present sequence represents a representative HIV-1 mutant Tat-His  
 CC protein. The protein is used in the creation of the fusion proteins of  
 CC the invention, in conjunction with a fusion partner (e.g. protein D).  
 CC The specification also describes fusion proteins, comprising HIV-1 Nef  
 CC protein. The fusion protein can be used in a vaccine to prevent HIV  
 CC infection.  
 XX SQ Sequence 302 AA;

Query Match 99.2%; Score 1675; DB 20; Length 302;  
 Best Local Similarity 99.0%; Pred. No. 1.5e-154;  
 Matches 299; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVVGPTVRRMRRAEPADGVGAASRDLEKHGATSSNTAATNAACAWLEA 60  
 Db 1 mgkwsksvvgptvrermraepaadvgaaardlekghaltssntaatnaacawlea 60  
 QY 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRODILDLYHTQGY 120  
 Db 61 qeeeevgfvtqpvlrptmcykaavdlshflkekggleghlsqrrddildlyhtqgy 120  
 QY 121 FPDQNYTPGPGVRYPLTFCGCYKLVPEPDKVEEANKGENTSLHLPVSLHGMDDPEREY 180  
 Db 121 fpdqnytpgpgvrypltfgcycylvpvdpdkveeankgentsllhpsvslhgmddperey 180  
 QY 181 LEWRFSRLAFHHVARELHPEYFNKCTSEPVDPRLPEWKHPGSGQPKTACTNCYCKKCCFH 240  
 Db 181 lewrfdslafhhvarelhpeyfnkctsepvdprrlepwhpgsqpktactncycckccfh 240  
 QY 241 COVCFITKALGISYGRKKRRORRPPQSGSOTHVSLSKOPTSQSRGDPGTPKETSQHGH 300  
 Db 241 cqvcfitaalgisygrkrrrrppqsgsqthqvslskqpsqsrqgdpctgpketsghhhh 300  
 QY 301 HH 302  
 Db 302 HH 302

Db 301 hh 302

RESULT 7

AAG63239

ID AAG63239 standard; Protein; 302 AA.

XX AC AAG63239;

XX 01-OCT-2001 (first entry)

XX DE Amino acid sequence of a His-tagged mutant His protein of HIV.

XX KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.

XX OS Synthetic.

XX OS Human immunodeficiency virus.

XX PN WO200154719-A2.

XX PD 02-AUG-2001.

XX PF 29-JAN-2001; 2001WO-EP00944.

XX PR 31-JAN-2000; 2000GB-0002200.

XX PR 14-APR-2000; 2000GB-0009336.

XX PR 06-JUN-2000; 2000GB-0013806.

XX PR 28-JUN-2000; 2000WO-EP05998.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Voss G;

XX WPI: 2001-476172/51.

XX DR N-PSDB; AAH42883.

XX PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120 protein or polynucleotide for the manufacture of a vaccine .

XX PS Disclosure; Fig 1; 90pp; English.

XX CC The present sequence represents a His-tagged mutant His protein of HIV. The protein is expressed in the yeast Pichia pastoris, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gp120 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.

XX SQ Sequence 302 AA;

Query Match 99.2%; Score 1675; DB 22; Length 302;

Best Local Similarity 99.0%; Pred. No. 1.5e-154;

Matches 299; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGKWKSSVVGWPTVRRMRRAEPAADVGAAASRDLEKHGALTSSNTAATNAACAWLEA 60

Db 1 mggkwsksvvgwptvrrmrtaepaadvgaasrdlekhgaltssntaataacawlea 60

QY 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGSLHSQRQDILDLYHTQGY 120

Db 61 qeevevgfvtppqvpplrmttykaadvlsflkekggleglihsqrrgdildlyhtqgy 120

QY 121 FPDWQNTPGVRYPLTGWCVKLYVPDPKVEEANKGENTSLLHPVSLHGMDPEREV 180

Db 121 fpdwqntpgpgrvrypltgwcvklyvpdpkveeankgentsllhpvslhgmdperev 180

QY 181 LEWRDLSRLAFHHVARELHPEYFKNCTSEFVDPRLPEFWKHPGSPQKTACTNCTCYKCCCFH 240

Db 181 lewrfdslrlafhhvarelhpeyfkntsefvpdrlefpwkhpsqpktaactnctcykcccfh 240

QY 241 CQVCFITKALGISYGRKKRRRRPQSGQTHQVLSUSKOPTSOSRGDPTGPKETSQHSHH 300

Db 241 cqvcfitaalgisygrkrrrrppqsgqthqvsiskgtskqsgkptgpketsghhhh 300

QY 301 HH 302

Db 301 hh 302

RESULT 8

AAV02353

ID AAY02353 standard; Protein; 411 AA.

XX AC AAY02353;

XX 09-JUL-1999 (first entry)

XX DE A representative Lipod-Tat-His fusion protein.

XX KW HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein; vaccine; HIV infection; protein D.

XX OS Synthetic.

XX OS Human immunodeficiency virus type 1.

XX PN WO9916884-A1.

XX PD 08-APR-1999.

XX PF 17-SEP-1998; 98WO-EP06040.

XX PR 26-SEP-1997; 97GB-0020585.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Bruck C, Godart SAG, Marchand M;

XX WPI: 1999-302282/25.

XX DR N-PSDB; AAX35689.

XX PT HIV Tat or Nef protein linked to a fusion partner

XX PS Disclosure; Fig 2; 66pp; English.

XX CC The present sequence represents a fusion protein comprising Lipod-HIV-1 Tat-His. The protein is exemplifies the fusion proteins of the invention. The specification also describes fusion proteins comprising HIV-1 Nef protein. The fusion protein can be used in a vaccine to prevent HIV infection.

XX SQ Sequence 411 AA;

Query Match 99.2%; Score 1675; DB 20; Length 411;

Best Local Similarity 99.7%; Pred. No. 2.4e-154;

Matches 301; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGKWKSSVVGWPTVRRMRRAEPAADVGAAASRDLEKHGALTSSNTAATNAACAWLEA 60

Db 110 mggkwsksvvgwptvrrmrtaepaadvgaasrdlekhgaltssntaataacawlea 169

QY 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGLGSLHSQRQDILDLYHTQGY 120

Db 170 qeevevgfvtppqvpplrmttykaadvlsflkekggleglihsqrrgdildlyhtqgy 229

QY 121 FPDWQNTPGVRYPLTGWCVKLYVPDPKVEEANKGENTSLLHPVSLHGMDPEREV 180

Db 230 fpdwqntpgpgrvrypltgwcvklyvpdpkveeankgentsllhpvslhgmdperev 289

QY 181 LEWRDLSRLAFHHVARELHPEYFKNCTSEFVDPRLPEFWKHPGSPQKTACTNCTCYKCCCFH 240

Db 290 lewrfdsrlafnhvarelhpeyfkntsepdvprlepwkhpqsgpaktactnycyckccfh 349  
 QY 241 CQVCFITKALGISYGRKKRRORRRPQSGTHQVLSLKOPTSQSRGDPGPKETSGHHH 300  
 Db 350 cqvcfittkalgisyrkrrrrppqsgthqvsksqptsqsrqdpckpsetsgghhh 409  
 QY 301 HH 302  
 Db 410 hh 411

RESULT 9  
 AAY02349  
 ID AAY02349 standard; Protein; 215 AA.  
 XX  
 AC AAY02349;  
 XX  
 DT 09-JUL-1999 (first entry)  
 XX  
 DE A representative HIV-1 Nef-His protein.  
 XX  
 KW HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
 KW vaccine; HIV infection; protein D.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO9916884-A1.  
 XX  
 PD 08-APR-1999.  
 XX  
 PF 17-SEP-1998; 98WO-EP06040.  
 XX  
 PR 28-SEP-1997; 97GB-0020585.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Bruck C, Godart SAG, Marchand M;  
 XX  
 DR WPI; 1999-302282/25.  
 DR N-PSDB; AAX35685.  
 XX  
 PT HIV Tat or Nef protein linked to a fusion partner  
 XX  
 PS Disclosure; Fig 2; 66pp; English.  
 XX  
 CC The present sequence represents a representative HIV-1 Nef-His protein.  
 CC The protein is used in the creation of the fusion proteins of  
 CC the invention, in conjunction with a fusion partner (e.g. protein D).  
 CC The specification also describes fusion proteins comprising HIV-1 Tat  
 CC protein. The fusion protein can be used in a vaccine to prevent HIV  
 CC infection.  
 XX  
 SQ Sequence 215 AA;

Query Match 67.5%; Score 1139.5; DB 20; Length 215;  
 Best Local Similarity 71.2%; Pred. No. 1.2e-102;  
 Matches 215; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGATSSNTAATNAACAWLEA 60  
 Db 1 mggkwsksvvgwptvrermraepaadvgaasrdlekhgaltssntaataacawlea 60  
 QY 61 QEEEEVGFPTPQVPLRPMYKAAVDLSHFLKEKGLGLHSORRODILDLWIYHTQGY 120  
 Db 61 qeeeevgfptpqvplrmpykaaavdlshflkekgglglhsqrrddldlwyhtqgy 120  
 QY 121 FPDQNTTPGPGVRYPLTTFGCYKLVPEPKVEANKGENTSLHPVSLHGMDDPEREV 180  
 Db 121 fpdqnytpgpgvrypltfgcylvppepkveeankgentslhpslhgmddperev 180

QY 181 LEWRDSDRLAFHHVARELHPEYFKNTSEPDVPRLEPWKHPQSQPKTACTNCKKCCFH 240  
 Db 181 lewrfdsralfhvharelhpeyfkntsepdvprlepwkhpqsgpaktactnycyckccfh 206  
 QY 241 CQVCFITKALGISYGRKKRRORRRPQSGTHQVLSLKOPTSQSRGDPGPKETSGHHH 300  
 Db 207 -----tsghhhh 213  
 QY 301 HH 302  
 Db 214 hh 215

RESULT 10  
 AAG63231  
 ID AAG63231 standard; Protein; 215 AA.  
 XX  
 AC AAG63231;  
 XX  
 DT 01-OCT-2001 (first entry)  
 XX  
 DE Amino acid sequence of a His-tagged Nef protein of HIV.  
 XX  
 KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus.  
 XX  
 PN WO200154719-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 29-JAN-2001; 2001WO-EP00944.  
 XX  
 PR 31-JAN-2000; 2000GB-0002200.  
 PR 14-APR-2000; 2000GB-0009336.  
 PR 06-JUN-2000; 2000GB-0013806.  
 PR 28-JUN-2000; 2000WO-EP03998.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX Voss G;  
 XX WPI; 2001-476172/51.  
 DR N-PSDB; AAH42875.  
 XX  
 PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
 PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
 PT protein or polynucleotide for the manufacture of a vaccine -  
 XX Disclosure; Fig 1; 90pp; English.

XX The present sequence represents a His-tagged Nef protein of HIV. The  
 CC protein is expressed in the yeast Pichia pastoris, and is used to  
 CC produce the vaccine of the invention. The specification describes  
 CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the  
 CC manufacture of a vaccine. The vaccine is used for the prophylactic or  
 CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
 CC in synergy with gp120 in the treatment and prevention of HIV. The  
 CC vaccine reduces the HIV viral load in HIV infected humans and results  
 CC in a maintenance of CD4+ levels over those levels found in the absence  
 CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.

XX Sequence 215 AA;

Query Match 67.5%; Score 1139.5; DB 22; Length 215;  
 Best Local Similarity 71.2%; Pred. No. 1.2e-102;  
 Matches 215; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGATSSNTAATNAACAWLEA 60  
 Db 1 mggkwsksvvgwptvrermraepaadvgaasrdlekhgaltssntaataacawlea 60

QY 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLIHSORQDILDLIWYHTQGY 120  
 |||||  
 Db 61 qeevevgfvtbpqvpLrpmtYkaavdlshflkekgleglIhsrrqrdildliwYhtqgy 120  
 |||||  
 QY 121 FPDWQNYTPGPGVRYPLTFTGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPEREV 180  
 |||||  
 Db 121 fpdwqnytpgpgvryplTftgwcYklvpEPdkveeankgentsllhpvsLhgmddperev 180  
 |||||  
 QY 181 LEWRDSRLAFHHVARELHPEYFKNCTSEPDVRLPEPWKHPGQPKTACTNVCYKCKCFH 240  
 |||||  
 Db 181 lewrdsrlafhhvarelhpeYfknC----- 206  
 |||||  
 QY 241 CQVCFITKALGISYGRKKRRRPPQSGQTHQVSLSKOPTSOSRGDPTGPKETSGHHH 300  
 |||||  
 Db 207 -----tsghhh 213  
 |||||  
 QY 301 HH 302  
 ||  
 Db 214 hh 215

RESULT 11  
 AAY02352  
 ID AAY02352 standard; Protein; 324 AA.  
 XX  
 AC AAY02352;  
 XX  
 DT 09-JUL-1999 (first entry)  
 XX  
 DE A representative LipD-Nef-His fusion protein.  
 XX  
 KW HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
 KW vaccine; HIV infection; protein D.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO9916884-A1.  
 XX  
 PD 08-APR-1999.  
 XX  
 PF 17-SEP-1998; 98WO-EP06040.  
 XX  
 PR 26-SEP-1997; 97GB-0020585.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Bruck C, Godart SAG, Marchand M;  
 XX  
 DR WPI; 1999-302282/25.  
 DR N-PSDB; AAX35688.  
 XX  
 PT HIV Tat or Nef protein linked to a fusion partner  
 XX  
 PS Disclosure; Fig 2; 66pp; English.  
 XX  
 CC The present sequence represents a fusion protein comprising LipD-HIV-1  
 CC Nef-His. The protein is exemplified the fusion proteins of  
 CC the invention. The specification also describes fusion proteins  
 CC comprising HIV-1 Tat protein. The fusion protein can be used in a  
 CC vaccine to prevent HIV infection.  
 XX  
 SQ Sequence 324 AA;

Query Match 67.5%; Score 1139.5; DB 20; Length 324;  
 Best Local Similarity 71.2%; Pred. No. 2.2e-102;  
 Matches 215; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 MGGKWSKSSVVGPTVRRMRRAEPAADGVGAASRDLEKHGATTSNTAATNAACAWLEA 60  
 |||||  
 Db 110 mggkwsksvvgptvrrmrreapadvggaasrdlekbgaltssntaataacawlea 169

QY 61 QEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLIHSORQDILDLIWYHTQGY 120  
 |||||  
 Db 170 qeevevgfvtbpqvpLrpmtYkaavdlshflkekgleglIhsrrqrdildliwYhtqgy 229  
 |||||  
 QY 121 FPDWQNYTPGPGVRYPLTFTGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDDPEREV 180  
 |||||  
 Db 230 fpdwqnytpgpgvryplTftgwcYklvpEPdkveeankgentsllhpvsLhgmddperev 289  
 |||||  
 QY 181 LEWRDSRLAFHHVARELHPEYFKNCTSEPDVRLPEPWKHPGQPKTACTNVCYKCKCFH 240  
 |||||  
 Db 290 lewrdsrlafhhvarelhpeYfknC----- 315  
 |||||  
 QY 241 CQVCFITKALGISYGRKKRRRPPQSGQTHQVSLSKOPTSOSRGDPTGPKETSGHHH 300  
 |||||  
 Db 316 -----tsghhh 322  
 |||||  
 QY 301 HH 302  
 ||  
 Db 323 hh 324

RESULT 12  
 AAG63234  
 ID AAG63234 standard; Protein; 324 AA.  
 XX  
 AC AAG63234;  
 XX  
 DT 01-OCT-2001 (first entry)  
 XX  
 DE Amino acid sequence of a His tagged LipD-Nef of HIV.  
 XX  
 KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..109  
 FT /note= "ProtD fusion partner"  
 XX  
 PN WO200154719-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 29-JAN-2001; 2001WO-EP00944.  
 XX  
 PR 31-JAN-2000; 2000GB-0002200.  
 PR 14-APR-2000; 2000GB-0009336.  
 PR 06-JUN-2000; 2000GB-0013806.  
 PR 28-JUN-2000; 2000WO-EP05998.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Voss G;  
 XX  
 DR WPI; 2001-476172/51.  
 DR N-PSDB; AAH42878.  
 XX  
 PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
 PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
 PT protein or polynucleotide for the manufacture of a vaccine .  
 XX  
 PS Disclosure; Fig 1; 90pp; English.  
 XX  
 CC The present sequence represents a His-tagged Nef protein of HIV, with  
 CC a lipidation signal sequence (Lipod) which is removed after processing.  
 CC The protein is expressed in Escherichia coli, and is used to  
 CC produce the vaccine of the invention. The specification describes  
 CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the  
 CC manufacture of a vaccine. The vaccine is used for the prophylactic or  
 CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
 CC in synergy with gp120 in the treatment and prevention of HIV. The

CC vaccine reduces the HIV viral load in HIV infected humans and results  
 CC in a maintenance of CD4+ levels over those levels found in the absence  
 CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.

XX  
 SQ Sequence 324 AA;

Query Match 67.5%; Score 1139.5; DB 22; Length 324;  
 Best Local Similarity 71.2%; Pred. No. 2.2e-102;  
 Matches 215; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 MGCKSKSSVVGPTVRRMRRAEPAADGVGAASRDLEKHGATTSNTAATNAACAWLEA 60  
 DB 110 mgdkwskssvvgptvrrmrreapadvgvaasrdlekhgaitssntaatnaacawlea 169  
 QY 61 QEEEEVGFPVTPVPLRPMTYKAAVDLSHFLKEKGLGSLHSORRQDILDWYHTQGY 120  
 DB 170 qeeeevgfvtppvplrpmtykaavdlshflkekgleglshsrrrqdildwiyhtqgy 229  
 QY 121 FPDQMYTPGPGVRYPLTFGWCYKLVPEPDKVEEANKGENTSLLHPVSLHGMDPEREV 180  
 DB 230 fpdqmytpgpgvrypltfgwcylvpvdpdkveeankgentsllhpvslhgmdperv 289  
 QY 181 LEWRFSRLAFHHVARELHPEYKNTSEVPDRLEPWKHPGQPKTACTNCYCKKCCFH 240  
 DB 290 lewrfsrlafhhvarelhpeyfknc----- 315  
 QY 241 CQVCFITKALGISYGRKKRRRRPQGSOTHOVSLSKPTQSQRGDPGTGPKETSGHHH 300  
 DB 316 -----tsghhh 322

QY 301 HH 302  
 DB 323 hh 324

## RESULT 13

AA02334  
 ID AAY02354 standard; Protein; 326 AA.

XX  
 AC AAY02354;  
 DT 09-JUL-1999 (first entry)

XX A representative Lipod-Nef fusion protein.

XX HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;  
 KW vaccine; HIV infection; protein D.

XX Synthetic.  
 OS Human immunodeficiency virus type 1.

XX WO9916884-A1.

XX 08-APR-1999.

XX 17-SEP-1998; 98WO-EP06040.

XX 26-SEP-1997; 97GB-0020585.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX Bruck C, Godart SAG, Marchand M;

XX WPI; 1999-302282/25.

XX N-PSDB; AAX35690.

XX HIV Tat or Nef protein linked to a fusion partner

XX Disclosure; Fig 2; 66pp; English.

XX The present sequence represents a fusion protein comprising Lipod-HIV-1  
 CC Nef. The protein is exemplified by the fusion proteins of

CC the invention. The specification also describes fusion proteins  
 CC comprising HIV-1 Tat protein. The fusion protein can be used in a  
 CC vaccine to prevent HIV infection.

XX  
 SQ Sequence 326 AA;

Query Match 67.5%; Score 1139.5; DB 20; Length 326;  
 Best Local Similarity 71.2%; Pred. No. 2.2e-102;  
 Matches 215; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 MGCKSKSSVVGPTVRRMRRAEPAADGVGAASRDLEKHGATTSNTAATNAACAWLEA 60  
 DB 112 mgdkwskssvvgptvrrmrreapadvgvaasrdlekhgaitssntaatnaacawlea 171  
 QY 61 QEEEEVGFPVTPVPLRPMTYKAAVDLSHFLKEKGLGSLHSORRQDILDWYHTQGY 120  
 DB 172 qeeeevgfvtppvplrpmtykaavdlshflkekgleglshsrrrqdildwiyhtqgy 231  
 QY 121 FPDQMYTPGPGVRYPLTFGWCYKLVPEPDKVEEANKGENTSLLHPVSLHGMDPEREV 180  
 DB 232 fpdqmytpgpgvrypltfgwcylvpvdpdkveeankgentsllhpvslhgmdperv 291  
 QY 181 LEWRFSRLAFHHVARELHPEYKNTSEVPDRLEPWKHPGQPKTACTNCYCKKCCFH 240  
 DB 292 lewrfsrlafhhvarelhpeyfknc----- 317  
 QY 241 CQVCFITKALGISYGRKKRRRRPQGSOTHOVSLSKPTQSQRGDPGTGPKETSGHHH 300  
 DB 318 -----tsghhh 324

QY 301 HH 302  
 DB 325 hh 326

## RESULT 14

AA063236  
 ID AAG63236 standard; Protein; 326 AA.

XX  
 AC AAG63236;

DT 01-OCT-2001 (first entry)

XX Amino acid sequence of a His tagged ProtD-Nef fusion protein.

XX HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.

XX Synthetic.

XX Human immunodeficiency virus.

XX Key Location/Qualifiers

FT Peptide 1..111

FT /note- "ProtD fusion partner"

XX WO200154719-A2.

XX 02-AUG-2001.

XX 29-JAN-2001; 2001WO-EP00944.

XX 31-JAN-2000; 2000GB-0002200.

XX 14-APR-2000; 2000GB-0009336.

XX 06-JUN-2000; 2000GB-0013806.

XX 28-JUN-2000; 2000WO-EP05998.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX Voss G;

XX WPI; 2001-476172/51.

XX N-PSDB; AAH42880.



PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef  
PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120  
XX protein or polynucleotide for the manufacture of a vaccine -  
XX  
PS Disclosure; Fig 1; 90pp; English.  
XX  
XX The present sequence represents a His-tagged ProT-D-Nef fusion protein.  
CC The protein is expressed in *Escherichia coli*, and is used to  
CC produce the vaccine of the invention. The specification describes  
CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the  
CC manufacture of a vaccine. The vaccine is used for the prophylactic or  
CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act  
CC in synergy with gp120 in the treatment and prevention of HIV. The  
CC vaccine reduces the HIV viral load in HIV infected humans and results  
CC in a maintenance of CD4+ levels over those levels found in the absence  
CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.  
XX  
XX Sequence 326 AA;  
SQ

Query Match 67.5%; Score 1139.5; DB 22; Length 326;  
Best Local Similarity 71.2%; Pred. No. 2.2e-102;  
Matches 215; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 MGKWSKSSVVGPTVRRMRRAEPAADGVGAASRDLEKHGATSSNTAATNAACAWLEA 60  
|||  
Db 112 mgkwsksvvgptvrermtaepaadvgaasrdlekghaitsntaataacawlea 171  
QY 61 QEEVEGFPVTPVPLRPMTYKAAVDLSHFLKEKGGLEGLHSQRQDILDLYHTQGY 120  
|||  
Db 172 qeeevgfpvtpvplrpmtykaavdlshflkekggleghsqrqdlldlyhtqgy 231  
QY 121 FPDQNYTTPGVRYPPLTFGWCKYKLVPEPDKVEEANKGENTSLHPVSLHGMDPEREV 180  
|||  
Db 232 fpdqnytpgvrppltfgwcyklypvepdkveeankgentslhpvslhgmdperev 291  
QY 181 LEWRFSRLAFHHVARELHPEYFKNC----- 317  
|||  
Db 292 lewrfsrlafhhvarelhpeyfknc-----tsghhhh 324  
QY 241 CQVCFITKALGISYGRKKRRRPPQSGTHQVSLSKQPTOSRGDTPGPKETSGHHH 300  
|||  
Db 318 -----tsghhhh 324

QY 301 HH 302  
||  
Db 325 hh 326

RESULT 15  
AAY50795  
ID AAY50795 standard; protein; 206 AA.  
XX  
AC AAY50795;  
XX  
DT 17-FEB-2000 (first entry)  
XX  
DE Human NEF protein/calmodulin binding inhibitor.  
DE  
DE NEF protein; calmodulin; negative factor protein; binding inhibitor;  
KW diagnosis; detection; infection; treatment; HIV.  
XX  
XX Homo sapiens.  
XX  
XX WO9557136-A2.  
XX  
XX PD 11-NOV-1999.  
XX  
XX 06-MAY-1999; 99WO-BP03105.  
XX  
XX 06-MAY-1998; 98DE-1020224.  
XX  
XX (SCHO/) SCHOTT M.  
PA

PA (SCHO/) SCHORR J.  
PA (ANTZ/) ANTZ C.  
XX  
PI Schott M, Schorr J, Antz C;  
XX  
XX WPI; 2000-038789/03.  
DR  
XX  
XX Binding agents used for treatment, prevention and diagnosis of human  
PT immune deficiency virus infection -  
PT  
XX  
XX Claim 3; Fig 1; 29pp; German.  
XX  
XX This invention describes novel binding partners (A) (i) for negative  
CC factor protein (Nef) that competitively inhibit binding of calmodulin (I)  
CC to Nef, or (ii) for (I) that competitively inhibit binding of Nef to (i).  
CC (A) are used for prevention, diagnosis (by specific detection of intra-  
CC and/or extra-cellular Nef, including staging of infection), and/or  
CC treatment of infections with human immune deficiency virus (HIV).  
XX  
XX Sequence 206 AA;  
SQ

Query Match 66.4%; Score 1120; DB 21; Length 206;  
Best Local Similarity 99.0%; Pred. No. 9.3e-101;  
Matches 204; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGKWSKSSVVGPTVRRMRRAEPAADGVGAASRDLEKHGATSSNTAATNAACAWLEA 60  
|||  
Db 1 mgkwsksvvgptvrermtaepaadvgaasrdlekghaitsntaataacawlea 60  
QY 61 QEEVEGFPVTPVPLRPMTYKAAVDLSHFLKEKGGLEGLHSQRQDILDLYHTQGY 120  
|||  
Db 61 qeeevgfpvtpvplrpmtykaavdlshflkekggleghsqrqdlldlyhtqgy 120  
QY 121 FPDQNYTTPGVRYPPLTFGWCKYKLVPEPDKVEEANKGENTSLHPVSLHGMDPEREV 180  
|||  
Db 121 fpdqnytpgvrppltfgwcyklypvepdkveeankgentslhpvslhgmdperev 180  
QY 181 LEWRFSRLAFHHVARELHPEYFKNC 206  
|||  
Db 181 lewrfsrlafhhvarelhpeyfknc 206

RESULT 16  
AAR38893  
ID AAR38893 standard; Protein; 206 AA.  
XX  
AC AAR38893;  
XX  
DT 10-NOV-1993 (first entry)  
XX  
DE Nef protein of HIV-1.  
XX  
XX AIDS; antibody; p25; gp110; gp41; assay; detection;  
KW immunity; vaccine.  
XX  
XX Human immunodeficiency virus-1.  
XX  
XX US5221610-A.  
PN  
XX  
PD 22-JUN-1993.  
XX  
XX 26-MAY-1988; 88US-0199143.  
XX  
XX 26-MAY-1988; 88US-0199143.  
PR  
XX 04-SEP-1991; 91US-0754300.  
XX  
XX (INRM ) INST NAT SANTE & RECH MEDICALE.  
PA (INSP ) INST PASTEUR.  
XX  
XX Bahraoui EM, Chamaret S, Ferris S, Granier C, Montagnier L;  
PI Rietschoten JV, Rochat H, Sabatier JM;  
XX

DR WPI; 1993-213434/26.  
 XX  
 XX Diagnosis of HIV infection - by detecting HIV antibodies using  
 PT antigenic polypeptide derived from nef protein of HIV-1  
 XX  
 XX Disclosure; Fig 2; 15pp; English.  
 PS  
 XX The nef protein comprises peptides which are expressed in vivo in HIV  
 CC infected patients before detectable amts. of p25, gp110 and gp41 are  
 CC expressed. Thus, they can be used in assays for early detection of HIV.  
 CC They can also be used to raise antibodies for use in detection,  
 CC to induce cellular immunity or to raise neutralising antibodies  
 CC that either inactivate the AIDS virus or reduce the viability of  
 CC the virus in vivo or destroy infected cells.  
 CC The peptides may be used in viral vaccines.  
 XX  
 XX Sequence 206 AA;  
 SQ

Query Match 66.1%; Score 1116; DB 14; Length 206;  
 Best Local Similarity 99.0%; Pred. No. 2.3e-100;  
 Matches 204; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MGKWSKSSVWGVPVTRMRRAEPAADGVGAASRDLEKHGALTSSNTAATNAACAWLEA 60  
 DB 1 mgkwsksvvgvptvtrmrreaepaadvgaasrdlekhgaltssntaataacawlea 60  
 QY 61 QEEEEVGFVPTQVPLRPMYKAADVLSHFLKEKGLIHSQRQDILDLMYHTQGY 120  
 DB 61 qeeeevfgvptqpvlrmpykaaavdlshflkekgleglihsqrrqdildlwyhtqgy 120  
 QY 121 FPDWQNTTGPVGRYPLTFGWCKYKLVPEPKVEEANKGENTSLLHPVSLHGMDPDEREV 180  
 DB 121 fpdwqnttgpvgvrypltfgwcyklypvepdkveeankgentsllhpvslnhgmdpder 180  
 QY 181 LEWRFDSRLAFHHVARELHPEYFKNC 206  
 DB 181 lewrfdsrlafhhvarelhpeyfknc 206

RESULT 17  
 AAB10054  
 ID AAB10054 standard; Protein; 206 AA.  
 XX  
 AC AAB10054;  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE HIV-1 nef protein.  
 XX  
 KW Glycoprotein; gag; pol; Gp-1; Gp-2; anti-HIV; cytostatic;  
 KW gene therapy; treatment; infectious disease; HIV; AIDS; neoplasm;  
 KW Carcinoma; melanoma; nef protein.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN EP1006196-A2.  
 XX  
 PD 07-JUN-2000.  
 XX  
 PF 25-NOV-1999; 99EP-0250415.  
 XX  
 PR 26-NOV-1998; 98DE-1056463.  
 XX  
 XX (PETTE-) PETTE INST HEINRICH.  
 XX  
 XX Von Laer MD;  
 PI  
 XX WPI; 2000-378268/33.  
 DR  
 DR N-PSDB; AAA40298, AAB10053, AAB10054.  
 XX  
 XX New retroviral packing cell useful as pharmaceutical carrier in gene  
 PT therapy for treatment of HIV and neoplasms, comprises retroviral genes  
 PT

PT and glycoproteins -  
 XX  
 PS Disclosure; Page 48; 69pp; German.  
 XX  
 CC This invention describes a novel retroviral packing cell (I), comprising  
 CC the retroviral genes gag, pol and glycoproteins GP-1 and GP-2 of the LCMV  
 CC coding gene gp, or a part of these. The products of the invention have  
 CC anti-HIV and cytostatic activity and can be used for gene therapy. (I) is  
 CC useful for in vitro infection of cells, especially hematopoietic stem  
 CC cells, for expression of transgenes in cells and as a pharmaceutical  
 CC carrier for gene therapy. (I) is therefore useful in the treatment of  
 CC infectious diseases (HIV or AIDS), neoplasms (carcinomas), melanomas and  
 CC other diseases. This sequence represents the Human immunodeficiency virus  
 CC (HIV-1) nef protein described in the method of the invention.  
 XX  
 XX Sequence 206 AA;  
 SQ

Query Match 66.1%; Score 1115; DB 21; Length 206;  
 Best Local Similarity 98.1%; Pred. No. 2.8e-100;  
 Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MGKWSKSSVWGVPVTRMRRAEPAADGVGAASRDLEKHGALTSSNTAATNAACAWLEA 60  
 DB 1 mgkwsksvvgvptvtrmrreaepaadvgaasrdlekhgaltssntaanaacawlea 60  
 QY 61 QEEEEVGFVPTQVPLRPMYKAADVLSHFLKEKGLIHSQRQDILDLMYHTQGY 120  
 DB 61 qeeeevfgvptqpvlrmpykaaavdlshflkekgleglihsqrrqdildlwyhtqgy 120  
 QY 121 FPDWQNTTGPVGRYPLTFGWCKYKLVPEPKVEEANKGENTSLLHPVSLHGMDPDEREV 180  
 DB 121 fpdwqnttgpvgvrypltfgwcyklypvepdkveeankgentsllhpvslnhgmdpder 180  
 QY 181 LEWRFDSRLAFHHVARELHPEYFKNC 206  
 DB 181 lewrfdsrlafhhvarelhpeyfknc 206

RESULT 18  
 AAW89326  
 ID AAW89326 standard; Protein; 206 AA.  
 XX  
 AC AAW89326;  
 XX  
 DT 01-JUN-1999 (first entry)  
 XX  
 DE HIV-1 nef protein sequence.  
 XX  
 KW Antigenic composition; primate; lentivirus; nef gene; vaccine;  
 KW infection; AIDS; HIV-1; nef protein.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN US5851813-A.  
 XX  
 PD 22-DEC-1998.  
 XX  
 PF 27-JAN-1994; 94US-0188583.  
 XX  
 PR 27-JAN-1994; 94US-0188583.  
 PR 12-JUL-1990; 90US-0551945.  
 PR 09-JUL-1991; 91US-0727494.  
 XX  
 XX (HARD ) HARVARD COLLEGE.  
 XX  
 XX Desrosiers RC;  
 PI  
 XX WPI; 1999-080408/07.  
 DR  
 DR N-PSDB; AAV81866.  
 XX  
 XX Lentivirus antigenic compositions - containing lentivirus with nef  
 PT gene deletion  
 PT

XX Disclosure; Fig 2A-R; 93pp; English.

PS The invention relates to an antigenic composition comprising an isolated

CC primate lentivirus whose genome contains an engineered non-reversible

CC null mutation in the nef gene, or an infectious DNA clone in a carrier.

CC The antigenic composition is used in vaccines against infection by the

CC lentivirus, e.g. AIDS.

XX Sequence 206 AA;

QY Query Match 66.0%; Score 1114; DB 20; Length 206;

CC Best Local Similarity 97.6%; Pred. No. 3.5e-100;

XX Matches 201; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVGVPTVRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60

DB 1 mggkwsksvlgvavrmrreapaaadvgaasrdlekghaltsntaannaacawlea 60

QY 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSORRODILDLIWYHTQGY 120

DB 61 qeeekvgfvtqvpvlrmpmtykaavdlshflkekgleglilhsqrrqldldliwhtqgy 120

QY 121 FPDWQNTYTPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180

DB 121 fpdwqnytpggyiryppltfgwcylvpvpdkveeankgentsllhpsvslhgmddperev 180

QY 181 LEWRDSDRLAFHHVARELHPEYFKNC 206

DB 181 lewrdsrlafhhvarelhpeyfknc 206

RESULT 19

AAP61515

ID AAP61515 standard; Protein; 206 AA.

XX AAP61515;

XX AC

DT 08-JUN-1991 (first entry)

DE Sequence of E' protein.

XX HIV; LAV; AIDS; diagnosis; vaccine.

XX HTLV-IIIB/H9 cells (ATCC CRL 8543).

XX EP187041-A.

XX 09-JUL-1986.

XX 23-DEC-1985; 85EP-0309454.

XX 24-DEC-1984; 84US-0685272.

PR 04-DEC-1985; 85US-0805069.

XX (GETH ) GENENTECH INC.

XX Capon DJ, Lasky LA;

XX WPI; 1986-177602/28.

DR N-PSDB; AAN60288.

XX Acquired immune deficiency syndrome polypeptide(s) - obtd. by

PT molecular cloning etc. and used for diagnosis and in vaccines

PT against virus disease

XX Example; fig 2; 125pp; English.

PS A comparison of AAN60287 with the cDNA of the HTLV-III genome

CC revealed one particular clone, designated p7.11 which contained a

CC DNA sequence encoding this peptide (AAP60308) sequence. This approx.

CC 2.2 kilobase covers the precursor gag region and encodes, 5' to 3',

CC p-12, p-15, p-24 a second p-15 protein, and approx. 300 extra base

CC pairs 3' to the gag region (see AAN60288).

XX Sequence 206 AA;

QY Query Match 65.8%; Score 1111; DB 7; Length 206;

CC Best Local Similarity 97.1%; Pred. No. 7e-100;

XX Matches 200; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVGVPTVRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60

DB 1 mggkwsksvlgvavrmrreapaaadvgaasrdlekghaltsntaannaacawlea 60

QY 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLEGLIHSORRODILDLIWYHTQGY 120

DB 61 qeeekvgfvtqvpvlrmpmtykaavdlshflkekgleglilhsqrrqldldliwhtqgy 120

QY 121 FPDWQNTYTPGVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180

DB 121 fpdwqnytpggyiryppltfgwcylvpvpdkveeankgentsllhpsvslhgmddperev 180

QY 181 LEWRDSDRLAFHHVARELHPEYFKNC 206

DB 181 lewrdsrlafhhvarelhpeyfknc 206

RESULT 20

AAP60423

ID AAP60423 standard; Protein; 216 AA.

XX AAP60423;

XX AC

DT 20-AUG-1991 (first entry)

DE Sequence of LAV virus ORF F protein.

XX AIDS vaccine; diagnosis; immunoassay; HIV; HTLV-III.

XX Lymphadenopathy virus.

XX WO8602383-A.

XX 24-APR-1986.

XX 18-OCT-1985; 85WO-EP00548.

XX 21-JAN-1985; 85GB-0001473.

PR 18-OCT-1984; 84FR-0016013.

PR 16-NOV-1984; 84GB-0029099.

XX (CNRS ) CNRS CENT NAT RECH SCI.

PA (INSP ) INST PASTEUR.

XX Montagnier L, Krust B, Chamaret S, Clavel F, Chermann J-C;

PI Barre-Sinoussi F, Alizon M, Sonigo P, Stewart C, Danos O;

PI Wain-Hobson S;

XX WPI; 1986-119166/18.

DR N-PSDB; AAN60365.

XX Purified glyco:protein and peptide(s) - are recognised by sera contg.

PT antibodies against lymphadenopathy virus and useful in detecting

PT AIDS antibodies or in vaccines

XX Disclosure; Fig 4; 75pp; English.

PS The inventors claim a polypeptide which is recognised by sera of

CC human origin contg. antibodies against the virus of

CC lymphadenopathies (LAV) or acquired immune deficiency syndrome

CC (AIDS). Also claimed are various peptides corresp. to the AA

CC sequences deducible from proteins encoded by LAV DNA, defined by

CC specific residues (e.g. 12-32, 37-46, 49-79, 88-153) in accordance

```
CC with a formula given in the specification.
XX
SQ Sequence 216 AA;

Query Match 65.68; Score 1107; DB 7; Length 216;
Best Local Similarity 98.1%; Pred. No. 1.8e-99;
Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGKWSKSVVGVPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60
   |||||||
Db 11 mggkwsksvvgwptvrrmtraepaahgvaaspdlkkgaitssntaataacawlea 70
   |||||||

Qy 61 QEEVEGVFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDWIYHTGGY 120
   |||||||
Db 71 qeevegvfpvtpqvpplrmpthykaavdlshflkekggleglshgrqrdildwihtggy 130
   |||||||

Qy 121 PPDQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180
   |||||||
Db 131 fpdwqnytpgpgvrypltfwgcyklvppepkveeankgentsllhpsvslhgmdpperev 190
   |||||||

Qy 181 LEWRDLSRLAFHHVARELHPYFKNC 206
   |||||||
Db 191 lewrfdslafhhvarelhpqyfknc 216

RESULT 21
AAW90179
ID AAW90179 standard; Protein; 206 AA.
AC AAW90179;
XX
DT 14-JUN-1999 (first entry)
XX
DE HTLV-III E' protein.
XX
KW AIDS; acquired immunodeficiency syndrome; viral infection; env protein;
KW fusion polypeptide; E' protein; gag protein; pol protein; P' protein;
KW gp signal peptide; detection; vaccination; etiological agent;
KW infection inhibitor; AIDS associated retrovirus; p24; gp41.
XX
OS Human lymphotropic virus type III.
XX
FH Key Location/Qualifiers
FT Misc-difference 11 /label= Val, Ile
FT Misc-difference 51 /label= Thr, Asn
FT Misc-difference 54 /label= Asp, Ala
FT Misc-difference 65 /label= Glu, Lys
FT Misc-difference 151 /label= Glu, Asp
FT Misc-difference 153 /label= Leu, Val
XX
PN US5853978-A.
XX
PD 29-DEC-1998.
XX
PF 29-JUL-1994; 94US-0282857.
XX
PR 08-MAY-1986; 86US-0861016.
PR 24-DEC-1984; 84US-0685272.
PR 04-DEC-1985; 85US-0805069.
PR 02-AUG-1988; 88US-0227568.
PR 19-NOV-1992; 92US-0979391.
PR 29-SEP-1993; 93US-0129009.
PR 29-JUL-1994; 94US-0282857.
XX
PA (GETH ) GENENTECH INC.
XX
```

```
PI Berman PW, Capon DJ, Lasky LA;
XX
DR WPI; 1999-094894/08.
DR N-PSDB; AAV74271.
XX
PT New AIDS-associated fusion polypeptide(s) - used for the detection
XX of AIDS or to inhibit infection by AIDS associated retrovirus or
XX dissemination of such retrovirus in infected individuals
XX
PS Example 1; Fig 2A-J; 47pp; English.
XX
CC This invention describes a novel fusion polypeptide which comprises
CC (a) a first polypeptide sequence of an AIDS associated E', env, or gag
CC polypeptide, that specifically binds complementary antibody and (b) a
CC second polypeptide sequence which is not an AIDS associated virus
CC polypeptide. Also described are (1) a fusion polypeptide having a
CC herpes simplex virus (HSV) gp signal peptide sequence fused in reading
CC frame with a polypeptide sequence other than HSV gp, (2) a nucleic acid
CC encoding a fusion polypeptide as in (1); (3) an expression vector
CC comprising a nucleic acid as in (2); (4) a host comprising a vector as
CC in (3). The AIDS-associated fusion polypeptides can be used in the
CC detection of and vaccination against viral etiological agents of AIDS.
CC They can also be administered as a pharmaceutical agent to inhibit
CC infection by AIDS associated retrovirus or dissemination of such
CC retrovirus in infected individuals.
XX
SQ Sequence 206 AA;

Query Match 64.7%; Score 1092; DB 20; Length 206;
Best Local Similarity 96.1%; Pred. No. 4.9e-98;
Matches 198; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MGGKWSKSVVGVPTVRRMRRAEPAADGVGAASRDLEKKGAISSNTAATNAACAWLEA 60
   |||||||
Db 1 mggkwsksvvgwptvrrmtraepaahgvaaspdlkkgaitssntaataacawlea 60
   |||||||

Qy 61 QEEVEGVFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLHSORRQDILDWIYHTGGY 120
   |||||||
Db 61 qeevegvfpvtpqvpplrmpthykaavdlshflkekggleglshgrqrdildwihtggy 120
   |||||||

Qy 121 PPDQNYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMDDPEREV 180
   |||||||
Db 121 fpdwqnytpgpgvrypltfwgcyklvppepkveeankgentsllhpsvslhgmdpperev 180
   |||||||

Qy 181 LEWRDLSRLAFHHVARELHPYFKNC 206
   |||||||
Db 181 lewrfdslafhhvarelhpqyfknc 206

RESULT 22
AAE04960
ID AAE04960 standard; Protein; 216 AA.
XX
AC AAE04960;
XX
DT 10-SEP-2001 (first entry)
XX
DE HIV-1 jrf1 Nef protein.
XX
KW DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV;
KW cell mediated immune response; cytotoxic T lymphocyte; CTL;
KW human immunodeficiency virus-1; HIV-1; mutant; muten.
XX
OS Human immunodeficiency virus type 1.
XX
SY Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 2 /note= "Myristylation site"
XX
PN WO200143693-A2.
XX
```

PD 21-JUN-2001.  
XX  
XX 15-DEC-2000; 2000WO-US34162.  
PF  
XX 17-DEC-1999; 99US-0172442.  
PR  
XX (MERI ) MERCK & CO INC.  
PA  
XX Shiver JW, Liang X, Fu T;  
PI  
XX WPI: 2001-417878/44.  
DR N-PSDB; AAD09603.  
XX  
XX Novel DNA vaccine useful for inducing cell mediated immune response  
PT against virulent strains of HIV, comprises DNA expression vector, and  
PT DNA containing codon optimized open reading frame encoding Nef protein  
PT  
XX  
XX Claim 5; Page 13; 84pp; English.  
PS  
XX  
XX The present invention relates to a DNA vaccine comprising a DNA  
CC expression vector, and a DNA molecule containing a codon optimised open  
CC reading frame encoding a Nef protein or its immunogenic derivative. The  
CC Nef protein or its derivative is expressed and generates an immune  
CC response which provides a substantial level of protection against HIV  
CC infection, upon administration of to a host. The DNA vaccine is useful  
CC for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL)  
CC response against infection or disease caused by virulent strains of HIV,  
CC by administering the DNA vaccine into the tissue of the vertebrate host,  
CC preferably human. It is also useful for lowering transmission rate to  
CC previously uninfected individuals and/or for reducing levels of viral  
CC loads within an infected individual, so as to prolong the asymptomatic  
CC phase of HIV infection. The present sequence is human immunodeficiency  
CC virus-1 (HIV-1) Jrf1 Nef protein. The different codon optimised nef  
CC constructs of the invention are used in the exemplification of the  
XX invention.  
XX  
SQ Sequence 216 AA;  
  
Query Match 59.9%; Score 1011; DB 22; Length 216;  
Best Local Similarity 83.8%; Pred. No. 4e-90;  
Matches 181; Conservative 15; Mismatches 10; Indels 10; Gaps 1;  
  
QY 1 MGKSKSSVVGWPTVRRMRRAEPAAD-----GVGAASRDLEKHGAISSNTAA 50  
DB 1 mggkswksrsvpgwstvrermrraeapaadrvttepaavgavsrdrlekghaltsntaa 60  
  
QY 51 TNAACWLEAQEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGLIHSORRQDIL 110  
DB 61 tnadcawleaqedeegvfvrpgvplrpmtkygavdlsflflekkgleglihsqkqdl 120  
  
QY 111 DLMIYHTQGYFPDQNYTPGPGVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSL 170  
DB 121 dlwvyhtqgyfpdqnytpgpgirfltfgwckfklvpepekeveanegenncillhpsmq 180  
  
QY 171 HGMDPDEREVLWRDPSRLAFHVAHRELHPEYKNC 206  
DB 181 hgtedpekeviewrfsdsklafhvharelhpeyykdc 216  
  
RESULT 23  
AAW53113  
ID AAW53113 standard; Protein; 210 AA.  
XX  
XX AAW53113;  
AC  
XX  
DT 25-JUN-1998 (first entry)  
XX  
DE Protein 6 contained in a complete ARV-2 nucleotide sequence.  
XX  
XX ARV-2; enhanced promoter; gene expression; cytomegalovirus;  
KW HIV; AIDS.  
XX

XX Human immunodeficiency virus type 1.  
OS  
XX US5688688-A.  
PN  
XX 18-NOV-1997.  
PD  
XX  
XX 10-AUG-1994; 94US-0288336.  
PF  
XX  
XX 24-DEC-1987; 87US-0138894.  
PR 31-OCT-1984; 84US-0667501.  
PR 30-JAN-1985; 85US-0696534.  
PR 06-SEP-1985; 85US-0773447.  
PR 17-AUG-1992; 92US-0931191.  
PR 28-JUN-1993; 93US-0083391.  
PR 17-AUG-1993; 93US-0107377.  
PR 10-AUG-1994; 94US-0288336.  
XX  
XX (CHIR ) CHIRON CORP.  
PA  
XX  
XX Chapman BS, Dina D, Haigwood NL, Luciw PA, Rosenberg S;  
PI Thayer RM;  
XX  
XX WPI: 1998-007982/01.  
XX  
XX Enhanced promoter for gene expression - comprising Cytomegalovirus  
PT immediate early promoter plus intron  
PT  
XX Example 1; Fig 4C-P; 99pp; English.  
PS  
XX This sequence represents a protein of unspecified function contained in a  
CC complete nucleotide sequence of ARV-2 derived from partial sequences of  
CC several ARV clones. The invention provides a method for construction of a  
CC vector for expression of a polypeptide in a mammalian cell, comprising a  
CC polypeptide coding sequence operably linked downstream of an enhanced  
CC promoter. The enhanced promoter comprises the human cytomegalovirus  
CC immediate early region (HCMV IE1) promoter and the first intron proximate  
CC to the 3' end of the HCMV IE1 promoter. The polypeptide can be any of the  
CC HIV recombinant polypeptides and especially HIV gp120. Expression of HIV  
CC gp120 by COS 7 cells transfected with pcMV6a containing the gp120 coding  
CC region, where pcMV6a is a vector containing the above enhanced promoter,  
CC is increased by a factor of 50-100 compared with the use of a vector  
CC containing the SV40 early promoter.  
XX  
SQ Sequence 210 AA;  
  
Query Match 59.1%; Score 997; DB 19; Length 210;  
Best Local Similarity 85.2%; Pred. No. 8.9e-89;  
Matches 179; Conservative 16; Mismatches 11; Indels 4; Gaps 1;  
  
QY 1 MGKSKSSVVGWPTVRRMR-----RAEPAADGVGAASRDLEKHGAISSNTAATNACA 56  
DB 1 mggkswksrsmggwsalrermrraeapaadvgavsrdrlekghaltsntaatnadca 60  
  
QY 57 WLEAQEEVEGFPVTPQVPLRPMYKAAVDLSHFLKEKGLGLIHSORRQDILDLIYH 116  
DB 61 wleaqeeveegfvrpgvplrpmtkykaavdlsflflekkgleglihsqrqeldliwlyh 120  
  
QY 117 TQGYFPDQNYTPGPGVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMDP 176  
DB 121 tqgyfpdqnytpgpgirylrpltfgwckfklvpepekeveanegenncillhpsmlhgmmeda 180  
  
QY 177 EREVLEWRDPSRLAFHVAHRELHPEYKNC 206  
DB 181 ekevlvwrfdsklafhvharelhpeyykdc 210  
  
RESULT 24  
AAY77299  
ID AAY77299 standard; Protein; 210 AA.  
XX  
XX AAY77299;  
AC

XX DT 22-MAY-2000 (first entry)  
XX DE HIV-1 (ATCC CRL 8597) ORF #3-encoded protein.  
XX KW HIV-1; immunoassay; antigen; pol fragment; p31; recombinant; antibody;  
XX KW detection.  
XX OS Human immunodeficiency virus type 1 'ATCC CRL 8597'.  
XX PN US6013432-A.  
XX PD 11-JAN-2000.  
XX PF 17-MAY-1995; 95US-0443434.  
XX PR 08-JUL-1993; 93US-0089407.  
XX PR 24-DEC-1987; 87US-0138894.  
XX PR 17-AUG-1992; 92US-0931154.  
XX PR 31-OCT-1984; 84US-0667501.  
XX PR 30-JAN-1985; 85US-0696534.  
XX PR 06-SEP-1985; 85US-0773447.  
XX (CHIR ) CHIRON CORP.  
XX PI Luciw PA, Dina D;  
XX DR WPI; 2000-170256/15.  
XX DR N-PSDB; AA290201.  
XX PT Immunoassay for antibodies against human immune deficiency virus, for  
XX PT diagnosing infection, uses an immunogenic fragment of the pol protein  
XX PS as antigen -  
XX PS Example 1; Fig 40-P; 99pp; English.  
XX CC The invention relates to the improvement of HIV-1 immunoassays by the  
XX CC use of an HIV-1 antigen comprising an immunogenic fragment of  
XX CC recombinant or synthetic HIV-1 pol, which is encoded by an approximately  
XX CC 9.7 kb sequence between a BstXI restriction site at position 3006 and an  
XX CC NdeI site at position 5131 of the genome (the proviral DNA sequence is  
XX CC given in AA290201). The immunogenic pol fragment is not immunologically  
XX CC cross-reactive with human T cell lymphotropic viruses I or II. The  
XX CC invention also encompasses the use of p31 as an antigen. The recombinant  
XX CC antigens may be produced in Escherichia coli, Saccharomyces cerevisiae or  
XX CC in mammalian cells. Immunoassays using the recombinant HIV proteins may  
XX CC be used to diagnose and stage HIV-1 infections. Sequences  
XX CC AA27294-Y77299 represent proteins encoded by the genome of HIV-1 (ATCC  
XX CC CRL 8597).  
XX SQ Sequence 210 AA;  
Query Match 59.1%; Score 997; DB 21; Length 210;  
Best Local Similarity 85.2%; Pred. No. 8.9e-89;  
Matches 179; Conservative 16; Mismatches 11; Indels 4; Gaps 1;  
QY 1 MGGKWSKSSVGVGPTVRMR-----RAEPAADGVGAASRDLEKHGAITSNTAATNAACA 56  
Db 1 mggkwsrsmggwsalretrmrtaeapaadgvgavsrdekhgaitssntaataadca 60  
QY 57 WLEAQEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLGLIHSQRQDILDWYH 116  
Db 61 wleaqeeveegfvrpqrpmtykaalishflkekgglegllwsqrqeldlwiyh 120  
QY 117 TQGYFPDQNYTPGCVRYPLTFGWCKLVPEPDKVEEANKGENTSLHHPVSLHGMDDP 176  
Db 121 tqgyfpdqnytpgcvrypltfgwcklvpepekeveeankgentsllhpslghmeda 180  
QY 177 EREVLEWRFDSRLAFHVAHRELHPEYFKNC 206  
Db 181 ekevlwrfdsrlafhvharelhpeyfkdc 210

RESULT 25  
AAE04962  
ID AAE04962 standard; Protein; 217 AA.  
XX AC AAE04962;  
XX DT 10-SEP-2001 (first entry)  
DE HIV-1 jrf1 Nef (G2A, LLAA) mutant protein.  
KW DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV;  
KW cell mediated immune response; cytotoxic T lymphocyte; CTL; mutein.  
KW human immunodeficiency virus-1; HIV-1; jrf1 Nef; mutant; mutein.  
XX OS Human immunodeficiency virus type 1.  
OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Misc-difference 2 /note= "Wild type myristylation site at Gly2 substituted  
XX FT with Ala"  
XX FT Misc-difference 174..175 /note= "Wild type dileucine motif (Leu-Leu) substituted  
XX FT with Ala-Ala"  
XX PN WO200143693-A2.  
XX PD 21-JUN-2001.  
XX PF 15-DEC-2000; 2000WO-US34162.  
XX PR 17-DEC-1999; 99US-0172442.  
XX PA (MERI ) MERCK & CO INC.  
XX PI Shilver JW, Liang X, Fu T;  
XX DR WPI; 2001-417878/44.  
XX DR N-PSDB; AAD09605.  
XX PT Novel DNA vaccine useful for inducing cell mediated immune response  
XX PT against virulent strains of HIV, comprises DNA expression vector, and  
XX PT DNA containing codon optimized open reading frame encoding Nef protein  
XX PS Claim 29; Page 18; 84pp; English.  
XX CC The present invention relates to a DNA vaccine comprising a DNA  
XX CC expression vector, and a DNA molecule containing a codon optimised open  
XX CC reading frame encoding a Nef protein or its immunogenic derivative. The  
XX CC Nef protein or its derivative is expressed and generates an immune  
XX CC response which provides a substantial level of protection against HIV  
XX CC infection, upon administration of to a host. The DNA vaccine is useful  
XX CC for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL)  
XX CC response against infection or disease caused by virulent strains of HIV,  
XX CC by administering the DNA vaccine into the tissue of the vertebrate host,  
XX CC preferably human. It is also useful for lowering transmission rate to  
XX CC previously uninfected individuals and/or for reducing levels of viral  
XX CC loads within an infected individual, so as to prolong the asymptomatic  
XX CC phase of HIV infection. The present sequence is human immunodeficiency  
XX CC virus-1 (HIV-1) jrf1 Nef (G2A, LLAA) mutant protein. The different nef  
XX CC constructs of the invention are used in the exemplification of the  
XX SQ Sequence 217 AA;

Query Match 59.0%; Score 996; DB 22; Length 217;  
Best Local Similarity 82.0%; Pred. No. 1.2e-88;  
Matches 178; Conservative 16; Mismatches 13; Indels 10; Gaps 1;

QY 1 MGGKWSKSSVGVGPTVRMRRAEPAAD-----GVGAASRDLEKHGAITSNTAA 50

Db 1 magkkskrsvpgwstvrermttaepaadvrrtpeaavgavsrldkxhgaitsntaa 60  
QY 51 TNAACAWLEAQEEVEGFVPTQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDIL 110  
Db 61 tnadcawleaqedeefvprpqvplrpmtkygavdlshflkekggleglshsqkrqdl 120  
QY 111 DLWIVHTQCYFPDQWNTYTPGPGVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSL 170  
Db 121 dlwvhtqgyfpdqwnytpgpgvryplrtfgwcfklvppekeveeanegeencaahpmsq 180  
QY 171 HGMDPPEVLEWRFDSRLAFHHVARELHPEYFKNCT 207  
Db 181 hgiedpekevelewfasklafhhvarelhpeyykdc 217

RESULT 26  
AA12262  
ID AA12262 standard; Protein; 210 AA.  
AC AA12262;  
XX 20-AUG-1991 (first entry)  
XX HIV-1 strain OYI open reading frame (ORF) F protein.  
DE HIV-1; AIDS; retroviruses.  
KW HIV-1; AIDS; retroviruses.  
XX Homo sapiens.  
OS Homo sapiens.  
XX US019510-A.  
XX 28-MAY-1991.  
XX 28-OCT-1987; 87US-0113655.  
XX 28-OCT-1987; 87US-0113655.  
XX (INSP ) INST PASTEUR.  
XX Wain-Hobson S, Huet T, Delaporte E, Brun-Vezinet F;  
XX WPI; 1991-177518/24.  
XX Purified human retrovirus - is mutant of HIV-1 having  
XX characteristics of HIV-1 OYI, used in diagnosis of HIV infection  
XX Disclosure; fig 8; 23pp; English.  
XX This sequence constitutes the ORF F protein constituent of a new  
XX strain of HIV-1 retrovirus, OYI. This mutant retroviral strain is  
XX useful in an assay for diagnosing HIV infection. See also AAQ11943  
XX (OYI nucleotide sequence), AA12255-61 (other HIV OYI constituent  
XX proteins).  
XX Sequence 210 AA;

Query Match 58.2%; Score 983; DB 12; Length 210;  
Best Local Similarity 82.5%; Pred. NO. 2e-87;  
Matches 174; Conservative 22; Mismatches 9; Indels 6; Gaps 2;  
QY 1 MGCKSKSSVVGHTVREMRRA-----EPAADGVGAASRDLEKKGAISSNTAATNAAC 55  
Db 1 mggkscsmkmgvptiremrkraelppepaegvgaasrdlekhgaitsntaatnadc 60  
QY 56 AWLEAQEEVEGFVPTQVPLRPMTYKAAVDLSHFLKEKGLGSLHSQRQDILDWIY 115  
Db 61 awleaqedeefvprpqvplrpmtkygavdlshflkekggleglshsqkrqdl-d-wwy 119  
QY 116 HTGQYFPDQWNTYTPGPGVRYPLTFGWCYKLVPEPDKVEEANKGENTSLHPVSLHGMD 175  
Db 120 htggyfpdqwnytpgpgvryplrtfgwcfklvpmdpdqveeanegeenllhplshgmdd 179

QY 176 PEREVLEWRFDSRLAFHHVARELHPEYFKNC 206  
Db 180 pekevlewxfdsrlafhhvarelhpeyykdc 210  
RESULT 27  
AAE04961  
ID AAE04961 standard; Protein; 237 AA.  
XX AAE04961;  
XX 10-SEP-2001 (first entry)  
XX Human tPA leader peptide-HIV-1 jrf1 Nef (opt tpanef) mutant protein.  
XX DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV;  
XX cell mediated immune response; cytotoxic T lymphocyte; CTL;  
XX human immunodeficiency virus-1; HIV-1; human; jrf1 Nef; opt tpanef;  
XX tissue plasminogen activator; tPA; chimeric protein; mutant; mutein.  
XX Chimeric - Human immunodeficiency virus type 1.  
XX Chimeric - Homo sapiens.  
XX Key Location/Qualifiers  
XX Peptide 1..26  
XX /label= Leader\_peptide  
XX /note= "Human tissue plasminogen activator (tPA)  
XX leader sequence"  
XX Protein 27..237  
XX /note= "Mature HIV-1 Nef (6-216aa) protein"  
XX Domain 195..196  
XX /label= Dileucine\_motif  
XX WO200143693-A2.  
XX 21-JUN-2001.  
XX 15-DEC-2000; 2000WO-US34162.  
XX 17-DEC-1999; 99US-0172442.  
XX (MERI ) MERCK & CO INC.  
XX Shiver JW, Liang X, Fu T;  
XX WPI; 2001-417878/44.  
XX N-PSDB; AAD09604.  
XX Novel DNA vaccine useful for inducing cell mediated immune response  
XX against virulent strains of HIV, comprises DNA expression vector, and  
XX DNA containing codon optimized open reading frame encoding Nef protein  
XX Claim 29; Page 17; 84pp; English.

The present invention relates to a DNA vaccine comprising a DNA expression vector, and a DNA molecule containing a codon optimised open reading frame encoding a Nef protein or its immunogenic derivative. The Nef protein or its derivative is expressed and generates an immune response which provides a substantial level of protection against HIV infection, upon administration of to a host. The DNA vaccine is useful for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL) response against infection or disease caused by virulent strains of HIV, by administering the DNA vaccine into the tissue of the vertebrate host, preferably human. It is also useful for lowering transmission rate to previously uninfected individuals and/or for reducing levels of viral loads within an infected individual, so as to prolong the asymptomatic phase of HIV infection. The present sequence is human tissue plasminogen activator (tPA) leader peptide-human immunodeficiency virus-1 (HIV-1) jrf1 Nef (opt tpanef) chimeric mutant protein. The mutation include deletion of the myristylation site (Gly2) in the HIV-1 jrf1 Nef protein. The different codon optimised nef constructs of the invention are used

CC in the exemplification of the invention.

XX Sequence 237 AA;

Query Match 57.9%; Score 978; DB 22; Length 237;

Best Local Similarity 83.4%; Pred. No. 7.4e-87;

Matches 176; Conservative 15; Mismatches 10; Indels 10; Gaps 1;

QY 6 SKSSVVGWPTVRMRRAEPAAD-----GVGAASRDLEKHAITSSNTAATNAAC 55

Db 27 skrspgstvtrmraraeaaadvrrtapaavgavardlekhaitsntaatnadc 86

QY 56 AWLEAEDEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKGGLGSLHSORRQDILDIWY 115

Db 87 awleaqedeegfpvtrpqpvlrptmtykgavdlshflikeggleglihsqrqdlldwy 146

QY 116 HTQGYFPDQWNTYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMD 175

Db 147 htqgyfpdqwnytpgpgirfpltfwgcfklvpvepkveeangennclhpmshgied 206

QY 176 PEREVLWRFDLSLAFHHVARELHPYFKNC 206

Db 207 pekeviewrfdsklafhhvarelhpeyykdc 237

AAE04963

AAE04963 standard; Protein; 237 AA.

AAE04963;

10-SEP-2001 (first entry)

Human tPA leader peptide-HIV-1 jrf1 Nef (LLAA) mutant protein.

DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV;

cell mediated immune response; cytotoxic T lymphocyte; CTL;

human immunodeficiency virus-1; HIV-1; human; jrf1 nef; opt tpanef;

tissue plasminogen activator; tPA; chimeric protein; mutant; mutein.

Chimeric - Human immunodeficiency virus type 1.

Chimeric - Homo sapiens.

Key Location/Qualifiers

Peptide 1..26

/label= Leader\_peptide

/note= "Human tissue plasminogen activator (tPA)

leader sequence"

Protein 27..237

/note= "Mature HIV-1 Nef (6-216aa) protein"

Misc-difference 195..196

/note= "Wild type dileucine motif (Leu-Leu) substituted

with Ala-Ala"

WO200143693-A2.

21-JUN-2001.

15-DEC-2000; 2000WO-US34162.

17-DEC-1999; 99US-0172442.

(MERI ) MERCK & CO INC.

Shiver JW, Liang X, Fu T;

WPI: 2001-417878/44.

N-PSDB; AAD09606.

Novel DNA vaccine useful for inducing cell mediated immune response

PT against virulent strains of HIV, comprises DNA expression vector, and

PT DNA containing codon optimized open reading frame encoding Nef protein

PT

XX

PS

XX

CC

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XX

XX

Sequence 237 AA;

Query Match 57.3%; Score 968; DB 22; Length 237;

Best Local Similarity 82.5%; Pred. No. 7e-86;

Matches 174; Conservative 15; Mismatches 12; Indels 10; Gaps 1;

QY 6 SKSSVVGWPTVRMRRAEPAAD-----GVGAASRDLEKHAITSSNTAATNAAC 55

Db 27 skrspgstvtrmraraeaaadvrrtapaavgavardlekhaitsntaatnadc 86

QY 56 AWLEAEDEEVEGFPVTPQVPLRPMTYKAAVDLSHFLKKGGLGSLHSORRQDILDIWY 115

Db 87 awleaqedeegfpvtrpqpvlrptmtykgavdlshflikeggleglihsqrqdlldwy 146

QY 116 HTQGYFPDQWNTYTPGCVRYPLTFGWCYKLVPEPKVEEANKGENTSLHPVSLHGMD 175

Db 147 htqgyfpdqwnytpgpgirfpltfwgcfklvpvepkveeangennclhpmshgied 206

QY 176 PEREVLWRFDLSLAFHHVARELHPYFKNC 206

Db 207 pekeviewrfdsklafhhvarelhpeyykdc 237

RESULT 29

AAE04963

ID AAE04963 standard; Protein; 206 AA.

XX AAE04963;

AC AAE04963;

XX 20-APR-2001 (first entry)

XX HIV-1 non-subtype B clone 962M651-8 nef protein.

DE HIV-1; human immunodeficiency virus; non-subtype B; gag; pol; env;

KW vpu; vif; vpr; tat; rev; nef; vaccine.

XX Human immunodeficiency virus type 1.

OS WO200026416-A1.

PN 11-MAY-2000.

XX 25-OCT-1999; 99WO-US24837.

XX 02-NOV-1998; 98US-0184418.

XX (UABR-) UAB RES FOUND.

XX Hahn BH, Shaw GM, Gao F;

XX



DR WPI: 2000-365651/31.  
XX  
XX Novel genomic nucleic acids of non-subtype B human immunodeficiency  
PT virus type 1 useful for detecting and treating AIDS comprises a  
PT specific nucleotide sequence  
XX  
XX Claim 41; Fig 22; 131pp; English.  
XX  
XX The present in invention provides the protein and coding sequences for a  
CC number of human immunodeficiency virus (HIV) type 1 non-subtype B  
CC isolates. The sequences shown include the near full-length coding  
CC sequences from each isolate, and the env, pol, vif, vpr, gag, tat,  
CC rev and nef proteins. These can be used to detect the presence of HIV-1  
CC in a sample and to produce antibodies against non-subtype B HIV-1 virus.  
CC These antibodies can be used in vaccines to prevent and treat HIV  
CC infection.  
XX  
XX Sequence 206 AA;  
SQ  
  
Query Match 56.4%; Score 952; DB 21; Length 206;  
Best Local Similarity 81.1%; Pred. No. 2.1e-84;  
Matches 167; Conservative 24; Mismatches 15; Indels 0; Gaps 0;  
  
QY 1 MGCKWSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGALTSSNTAATNAACAWLEA 60  
Db 1 mgckwssivgwpavrerirrtpeaagvgasqldkygaltssntstnaacawlea 60  
  
QY 61 QEEEEVGFVPTQVPLRPMYKAAVDLSHFLKEKGLGLELIHSQRQDILDLYIHTQGY 120  
Db 61 qeeeevgfvpqpvrpmpmtkykaavdlshflkekglegliyskkrqelidlvwyhtqgf 120  
  
QY 121 FPDWQNTPGGVRYPLTFGWCYKLVPEPKVEEANKGENTSLLLHPVSLHGMDDPREV 180  
Db 121 fpdwqntpggvrypltfgwcylkvpdpkveeankgentslldhpsvslhgmdddhrev 180  
  
QY 181 LEWRFSRLAFHHVARELHPEYFKNC 206  
Db 181 lkwkfdshlahkkmarelhpeyykdc 206  
  
RESULT 30  
AAB86169  
ID AAB86169 standard; Protein; 3025 AA.  
XX  
XX AAB86169;  
XX  
XX 21-AUG-2001 (first entry)  
DE  
DE HIV-1 subtype C protein fragment #1.  
XX  
XX Infection; diagnosis; human; humoral immune response; antiviral;  
KW cellular immune response; vaccine; treatment; gene therapy.  
XX  
XX Human immunodeficiency virus type 1.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 1..3025  
FT /label= Xaa  
FT /note= "Xaa represents a stop codon"  
XX  
XX DE10056747-A1.  
XX  
XX 31-MAY-2001.  
XX  
XX 16-NOV-2000; 2000DE-1056747.  
XX  
XX 16-NOV-1999; 99DE-1055089.  
XX  
XX (SHAO/) SHAO Y.  
PA (GENE-) GENEART GMBH GES ANGEWANDTE BIOTECHNOLOG.  
XX  
XX Wagner R, Wolf H, Shao Y, Graf M;  
PI

XX  
DR WPI: 2001-336417/36.  
DR N-PSDB; AAH20870.  
XX  
PT New nucleic acid sequences from a human immune deficiency virus  
PT intersubtype, useful for treatment, prevention and diagnosis of  
PT infection  
XX  
XX Disclosure; Fig 8A-O; 48pp; German.  
PS  
XX This invention describes a novel polynucleotide isolated from human  
CC immunodeficiency virus type 1 subtype C/B' which can be used for the  
CC induction of specific humoral and cellular immune responses. (I) and  
CC polypeptides (II) encoded by them, are useful in pharmaceuticals,  
CC vaccines and diagnostic agents, particularly for treatment or prevention  
CC of human immune deficiency virus-1 (HIV-1) infections, also for rational  
CC design of test or therapeutic reagents, or gene therapy vectors.  
CC Polypeptides, especially antibodies, specifically directed against (II)  
CC are similarly useful as pharmaceutical and diagnostic agents. (I) are  
CC specific for intersubtype C/B' of HIV-1 so are useful in regions  
CC (particularly China and South-East Asia) where this subtype is prevalent.  
CC The products of the invention have antiviral activity. This sequence  
CC represents a protein encoded by the HIV-1 subtype C genome described in  
CC the method of the invention.  
XX  
XX Sequence 3025 AA;  
SQ  
  
Query Match 56.2%; Score 948.5; DB 22; Length 3025;  
Best Local Similarity 70.6%; Pred. No. 1.9e-82;  
Matches 175; Conservative 22; Mismatches 42; Indels 9; Gaps 2;  
  
QY 1 MGCKWSSVVGWPTVRRMRRAEPAADGVGAASRDLEKHGALTSSNTAATNAACAWLEA 60  
Db 2723 mgckwssivgwpalrerirrtpeaagvgavsrldkghaltssntaatnedcawlea 2782  
  
QY 61 QEEEEVGFVPTQVPLRPMYKAAVDLSHFLKEKGLGLELIHSQRQDILDLYIHTQGY 120  
Db 2783 qeeevgfvpqpvrpmpmtkykaavdlshflkekglegliyskkrqelidlvwyhtqgy 2842  
  
QY 121 FPDWQNTPGGVRYPLTFGWCYKLVPEPKVEEANKGENTSLLLHPVSLHGMDDPREV 180  
Db 2843 fpdwqntpggvrypltfgwcylkvpdpkveeankgentslldhpsvslhgmdddhrev 2902  
  
QY 181 LEWRFSRLAFHHVARELHPEYFKNCSTSEPVDPDR-----LEPWKHPGSPKTTACTN 233  
Db 2903 lkwkfdshlahkkmarelhpefykdcxhrrdfrglstgafxevws--ggtgsgqpanaa 2960  
  
QY 234 CKKCCFHC 241  
Db 2961 ykqlfac 2968  
  
Search completed: August 26, 2002, 08:12:25  
Job time: 234 sec

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OM protein - protein search, using sw model

Run on: August 26, 2002, 08:08:31 ; Search time 38.46 Seconds  
(without alignments)  
191.797 Million cell updates/sec

Title: US-09-509-239-13  
Perfect score: 1688  
Sequence: 1 MGGKWSKVGVGPTVRMRM.....QSRGDPGPKETSGHHHHH 302

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2.6/ptodata/2/iaa/5A-COMB.pep.\*  
2: /cgn2.6/ptodata/2/iaa/5B-COMB.pep.\*  
3: /cgn2.6/ptodata/2/iaa/6A-COMB.pep.\*  
4: /cgn2.6/ptodata/2/iaa/6B-COMB.pep.\*  
5: /cgn2.6/ptodata/2/iaa/PTUS-COMB.pep.\*  
6: /cgn2.6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1138	67.4	239	4	US-08-679-493A-76
2	1115	66.1	206	3	US-08-388-353-644
3	1115	66.1	206	3	US-08-488-551B-644
4	971	57.5	206	4	US-08-679-493A-75
5	638	37.8	123	4	US-09-124-900-10
6	498.5	29.5	151	4	US-08-679-493A-74
7	486	28.8	86	1	US-08-450-257-1
8	486	28.8	86	1	US-08-450-246-1
9	486	28.8	86	1	US-08-450-098-1
10	486	28.8	86	1	US-08-451-233-1
11	486	28.8	86	1	US-08-450-236-1
12	486	28.8	86	3	US-07-808-452-1
13	486	28.8	86	3	US-09-030-613-19
14	486	28.8	86	4	US-09-124-900-6
15	486	28.8	86	4	US-09-451-905-19
16	486	28.8	86	4	US-08-235-403-1
17	486	28.8	86	5	PCR-US92-10770-1
18	486	28.8	86	5	PCR-US95-06077-2
19	478.5	28.3	266	3	US-08-815-809-5
20	478.5	28.3	280	2	US-08-816-155B-43
21	478.5	28.3	280	4	US-09-079-587-43
22	470	27.8	86	2	US-08-505-210-1
23	470	27.8	86	4	US-09-099-333-1
24	466	27.6	83	2	US-08-417-210A-96
25	455	27.0	82	1	US-08-053-079A-15
26	430.5	25.5	253	2	US-08-659-251-4
27	430.5	25.5	253	4	US-09-256-490-4

28	430.5	25.5	253	5	PCT-US96-11445-4	Sequence 4, Appl
29	409	24.2	72	3	US-09-030-613-17	Sequence 17, Appl
30	409	24.2	72	4	US-09-451-905-17	Sequence 17, Appl
31	385	22.8	72	2	US-08-893-853-1	Sequence 1, Appl
32	385	22.8	72	4	US-09-113-921-1	Sequence 1, Appl
33	372	22.0	122	6	5304466-3	Patent No. 5304466
34	365.5	21.7	312	1	US-08-094-128A-27	Sequence 27, Appl
35	365.5	21.7	312	1	US-08-455-674-27	Sequence 27, Appl
36	365.5	21.7	312	1	US-08-455-992-27	Sequence 27, Appl
37	365.5	21.7	312	1	US-08-455-972-27	Sequence 27, Appl
38	365.5	21.7	312	5	PCT-US92-00652-27	Sequence 27, Appl
39	362.5	21.5	3025	6	5223423-3	Patent No. 5223423
40	352	20.9	72	1	US-07-910-867B-2	Sequence 2, Appl
41	331	19.6	72	1	US-07-910-867B-5	Sequence 5, Appl
42	325	19.3	72	1	US-07-910-867B-3	Sequence 3, Appl
43	311	18.4	72	1	US-07-910-867B-1	Sequence 1, Appl
44	290	17.2	56	4	US-09-055-075C-48	Sequence 48, Appl
45	277	16.4	56	1	US-08-450-257-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-08-679-493A-76  
; Sequence 76, Application US/08679493A  
; Patent No. 6303295  
; GENERAL INFORMATION:  
; APPLICANT: Taylor, Ethan W.  
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
; FILE REFERENCE: 55-95  
; CURRENT APPLICATION NUMBER: US/08/679,493A  
; CURRENT FILING DATE: 1996-07-12  
; PRIOR APPLICATION NUMBER: 60/001203  
; PRIOR FILING DATE: 1995-07-14  
; PRIOR APPLICATION NUMBER: 60/003,112  
; PRIOR FILING DATE: 1995-09-01  
; NUMBER OF SEQ ID NOS: 216  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 76  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)..(239)  
; OTHER INFORMATION: X os selenocysteine.  
US-08-679-493A-76

Query Match 67.4%; Score 1138; DB 4; Length 239;  
Best Local Similarity 88.7%; Pred. No. 1.2e-108;  
Matches 211; Conservative 2; Mismatches 25; Indels 0; Gaps 0;  
QY 1 MGGKWSKVGVGPTVRMRRAEPAADGVGAASRDLKKGATSSNTAATNAACAWLEA 60  
Db 1 MGGKWSKVGVGPTVRMRRAEPAADGVGAASRDLKKGATSSNTAATNAACAWLEA 60  
QY 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKKGGLIHSQRQDIDLWIYHTQGY 120  
Db 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKKGGLIHSQRQDIDLWIYHTQGY 120  
QY 121 FPDWQNYTPGPGVRYPLTFGWCYKLVPEPDKVVEANKGENTSLLLHPVSLHGMDPEREV 180  
Db 121 FPDWQNYTPGPGVRYPLTFGWCYKLVPEPDKVVEANKGENTSLLLHPVSLHGMDPEREV 180  
QY 181 LEWRFDSRLAFHVAHRELHPEYFNKCTSEPDRLPEFPKHPGSPQKTACTIONCYCKCC 238  
Db 181 LEWRFDSRLAFHVAHRELHPEYFNKCTSEPDRLPEFPKHPGSPQKTACTIONCYCKCC 238

RESULT 2  
US-08-388-353-644

; Sequence 644, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 644:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 206 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-388-353-644

Query Match 66.1%; Score 1115; DB 3; Length 206;  
Best Local Similarity 98.1%; Pred. No. 2.le-106;  
Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGATSSNTAATNAACAWLEA 60  
Db 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGATSSNTAATNAACAWLEA 60

QY 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKKEKGGLEGLHSORRODILDLYHTQGY 120  
Db 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKKEKGGLEGLHSORRODILDLYHTQGY 120

QY 121 FPDQNTPTGPGVRYPLTFGCYKLVPEPDKVEEANKGENTSLHVPVSLHGMDPPERV 180  
Db 121 FPDQNTPTGPGVRYPLTFGCYKLVPEPDKVEEANKGENTSLHVPVSLHGMDPPERV 180

QY 181 LEWRFDRLAFHHVARELHPEYFKNC 206  
Db 181 LEWRFDRLAFHHVARELHPEYFKNC 206

RESULT 3  
US-08-488-551B-644  
; Sequence 644, Application US/08488551B  
; Patent No. 6015661  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Deacon  
; APPLICANT: Dale A. McPhee  
; APPLICANT: David Cooper

; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 841  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 GARDEN CITY PLAZA  
; CITY: GARDEN CITY  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 11530-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,551B  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PM3864 (AU)  
; FILING DATE: 14-FEB-1994  
; APPLICATION NUMBER: PM4002 (AU)  
; FILING DATE: 21-FEB-1994  
; APPLICATION NUMBER: PM0284 (AU)  
; FILING DATE: 23-DEC-1994  
; APPLICATION NUMBER: US 08/388,353  
; FILING DATE: 14-FEB-1995  
; APPLICATION NUMBER: PM3021/95  
; FILING DATE: 17-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FRANK S. DIGIGLIO  
; REFERENCE/DOCKET NUMBER: 9606Z  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; INFORMATION FOR SEQ ID NO: 644:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 206 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-488-551B-644

Query Match 66.1%; Score 1115; DB 3; Length 206;  
Best Local Similarity 98.1%; Pred. No. 2.le-106;  
Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGATSSNTAATNAACAWLEA 60  
Db 1 MGGKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKKGATSSNTAATNAACAWLEA 60

QY 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKKEKGGLEGLHSORRODILDLYHTQGY 120  
Db 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKKEKGGLEGLHSORRODILDLYHTQGY 120

QY 121 FPDQNTPTGPGVRYPLTFGCYKLVPEPDKVEEANKGENTSLHVPVSLHGMDPPERV 180  
Db 121 FPDQNTPTGPGVRYPLTFGCYKLVPEPDKVEEANKGENTSLHVPVSLHGMDPPERV 180

QY 181 LEWRFDRLAFHHVARELHPEYFKNC 206  
Db 181 LEWRFDRLAFHHVARELHPEYFKNC 206

RESULT 4  
US-08-679-493A-75  
; Sequence 75, Application US/08679493A  
; Patent No. 6303295  
; GENERAL INFORMATION:  
; APPLICANT: Taylor, Ethan W.  
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
; FILE REFERENCE: 55-95

;; CURRENT APPLICATION NUMBER: US/08/679,493A  
;; CURRENT FILING DATE: 1996-07-12  
;; PRIOR APPLICATION NUMBER: 60/001203  
;; PRIOR FILING DATE: 1995-07-14  
;; PRIOR APPLICATION NUMBER: 60/003,112  
;; PRIOR FILING DATE: 1995-09-01  
;; NUMBER OF SEQ ID NOS: 216  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 75  
;; LENGTH: 206  
;; TYPE: PRT  
;; ORGANISM: Human immunodeficiency virus type 1  
;; NAME/KEY: VARIANT  
;; LOCATION: (1)..(206)  
;; OTHER INFORMATION: X is selenocysteine.  
US-08-679-493A-75

Query Match 57.5%; Score 971; DB 4; Length 206;  
Best Local Similarity 89.0%; Pred. No. 1.2e-91;  
Matches 186; Conservative 2; Mismatches 15; Indels 6; Gaps 3;  
QY 1 MGCKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60  
Db 1 MGCKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60  
QY 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGG---LEGLIHSORRODILDLWIYHTG 117  
Db 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGGTGRANSLPTKTRYPSVDL--PHT 118  
QY 118 QGVFPDQNTGPGVRYPLTFCGCKVLPVPEPKVEEANKGENTSLHHPVSLHGMDDPE 177  
Db 119 R-LLPQNTGPGVRYPLTFCGCKVLPVPEPKVEEANKGENTSLHHPVSLHGMDDPE 177  
QY 178 REVLWRFDSRLAFHHVARELHPEYFKNC 206  
Db 178 REVLWRFDSRLAFHHVARELHPEYFKNC 206

RESULT 5  
US-09-124-900-10  
;; Sequence 10, Application US/09124900  
;; Patent No. 6268484  
;; GENERAL INFORMATION:  
;; APPLICANT: KATINGER, Hermann  
;; APPLICANT: BUCHACHER, Andrea  
;; APPLICANT: ERNST, Wolfgang  
;; APPLICANT: BALLAUN, Claudia  
;; APPLICANT: PURTSCHER, Martin  
;; APPLICANT: TRKOLA, Alexandra  
;; APPLICANT: PREDL, Renate  
;; APPLICANT: SCHMATZ, Christine  
;; APPLICANT: KLIMA, Annelies  
;; APPLICANT: STEINDL, Franz  
;; APPLICANT: MUSTER, Thomas  
;; TITLE OF INVENTION: HIV-Vaccines  
;; FILE REFERENCE: 1939-112P  
;; CURRENT APPLICATION NUMBER: US/09/124,900  
;; CURRENT FILING DATE: 1998-07-30  
;; PRIOR APPLICATION NUMBER: PCT/EP95/01481  
;; PRIOR FILING DATE: 1995-04-19  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 10  
;; LENGTH: 123  
;; TYPE: PRT  
;; ORGANISM: Human immunodeficiency virus type 1  
US-09-124-900-10

Query Match 37.8%; Score 638; DB 4; Length 123;  
Best Local Similarity 97.6%; Pred. No. 7.3e-58;

Matches 120; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MGCKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60  
Db 1 MGCKWSKSSVVGWPAVRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60  
QY 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGGLEGLIHSORRODILDLWIYHTG 120  
Db 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGGLEGLIHSORRODILDLWIYHTG 120  
QY 121 FPD 123  
Db 121 FPD 123  
RESULT 6  
US-08-679-493A-74  
;; Sequence 74, Application US/08679493A  
;; Patent No. 6303295  
;; GENERAL INFORMATION:  
;; APPLICANT: Taylor, Ethan W.  
;; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
;; FILE REFERENCE: 55-95  
;; CURRENT APPLICATION NUMBER: US/08/679,493A  
;; CURRENT FILING DATE: 1996-07-12  
;; PRIOR APPLICATION NUMBER: 60/001203  
;; PRIOR FILING DATE: 1995-07-14  
;; PRIOR APPLICATION NUMBER: 60/003,112  
;; PRIOR FILING DATE: 1995-09-01  
;; NUMBER OF SEQ ID NOS: 216  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 74  
;; LENGTH: 151  
;; TYPE: PRT  
;; ORGANISM: Human immunodeficiency virus type 1  
;; NAME/KEY: VARIANT  
;; LOCATION: (1)..(151)  
;; OTHER INFORMATION: X is selenocysteine.  
US-08-679-493A-74

Query Match 29.5%; Score 498.5; DB 4; Length 151;  
Best Local Similarity 73.0%; Pred. No. 1.8e-43;  
Matches 103; Conservative 4; Mismatches 7; Indels 27; Gaps 3;  
QY 1 MGCKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60  
Db 1 MGCKWSKSSVVGWPTVRMRRAEPAADGVGAASRDLEKHGAISSNTAATNAACAWLEA 60  
QY 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGG----- 96  
Db 61 QEEVEGFPVTPQVPLRPMTYKAADVLSHFLKEKGGTGRANSLPTKTRYPSVDLPHTRL 120  
QY 97 LEGL--IHSORROD--LDLWI 114  
Db 121 LPXLAEHLTRARGISTDLWM 141

RESULT 7  
US-08-450-257-1  
;; Sequence 1, Application US/08450257  
;; Patent No. 5652122  
;; GENERAL INFORMATION:  
;; APPLICANT: FRANKEL, Alan  
;; APPLICANT: PABO, Carl  
;; APPLICANT: BARSOUM, James G.  
;; APPLICANT: FAWELL, Stephen E.  
;; APPLICANT: PEPINSKY, R. B.  
;; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
;; NUMBER OF SEQUENCES: 69  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: FISH & NEAVE

STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450.257  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235.403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934.375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098.766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454.450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 08/158.015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: human immunodeficiency virus  
STRAIN: type 1  
US-08-450-257-1

Query Match 28.8%; Score 486; DB 1; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.6e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 209 EPVDPRLPEWKHPGSPKPTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 268  
DB 2 EPVDPRLPEWKHPGSPKPTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
QY 269 SOTHQVSLSKQPTSQSRGDPGPK 293  
DB 62 SOTHQVSLSKQPTSQSRGDPGPK 86

RESULT 8  
US-08-450-246-1  
Sequence 1, Application US/08450246  
Patent No. 5670617  
GENERAL INFORMATION:  
APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOU, James G.  
APPLICANT: FAMELL, Stephen E.  
APPLICANT: PEPINSKY, R. B.  
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES

NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450.246  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235.403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934.375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098.766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454.450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636.662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158.015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: human immunodeficiency virus  
STRAIN: type 1  
US-08-450-246-1  
Query Match 28.8%; Score 486; DB 1; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.6e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 209 EPVDPRLPEWKHPGSPKPTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 268  
DB 2 EPVDPRLPEWKHPGSPKPTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
QY 269 SOTHQVSLSKQPTSQSRGDPGPK 293  
DB 62 SOTHQVSLSKQPTSQSRGDPGPK 86  
RESULT 9  
US-08-450-098-1  
Sequence 1, Application US/08450098  
Patent No. 5674980  
GENERAL INFORMATION:  
APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOU, James G.

APPLICANT: FAWELL, Stephen E.  
APPLICANT: PEPINSKY, R. B.  
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,098  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: human immunodeficiency virus  
STRAIN: type 1  
US-08-450-098-1

Query Match 28.8%; Score 486; DB 1; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.6e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 EPVDPRLPEPKHFGSQPKTACTNCYCKKCCFHQVCFITKALGISYGRKKRRRRPPQG 268  
|||||  
Db 2 EPVDPRLPEPKHFGSQPKTACTNCYCKKCCFHQVCFITKALGISYGRKKRRRRPPQG 61  
|||||

QY 269 SQTHQVSLSKQPTSQSRGDPGPK 293  
|||||  
Db 62 SQTHQVSLSKQPTSQSRGDPGPK 86  
|||||

RESULT 10  
US-08-451-233-1  
; Sequence 1, Application US/08451233  
; Patent No. 5747641  
; GENERAL INFORMATION:

APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOUM, James G.  
APPLICANT: FAWELL, Stephen E.  
APPLICANT: PEPINSKY, R. B.  
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451,233  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: human immunodeficiency virus  
STRAIN: type 1  
US-08-451-233-1

Query Match 28.8%; Score 486; DB 1; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.6e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 EPVDPRLPEPKHFGSQPKTACTNCYCKKCCFHQVCFITKALGISYGRKKRRRRPPQG 268  
|||||  
Db 2 EPVDPRLPEPKHFGSQPKTACTNCYCKKCCFHQVCFITKALGISYGRKKRRRRPPQG 61  
|||||

QY 269 SQTHQVSLSKQPTSQSRGDPGPK 293  
|||||  
Db 62 SQTHQVSLSKQPTSQSRGDPGPK 86  
|||||

RESULT 11  
US-08-450-236-1

Sequence 1, Application US/08450236  
Patent No. 5804604  
GENERAL INFORMATION:  
APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOUM, James G.  
APPLICANT: FAWELL, Stephen E.  
APPLICANT: PEPINSKY, R. B.  
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,236  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: human immunodeficiency virus  
STRAIN: type 1  
US-08-450-236-1

Query Match 28.8%; Score 486; DB 1; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.6e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 209 EPVDPRLPEWKHPGSPKTKACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRPPQG 268  
Db 2 EPVDPRLPEWKHPGSPKTKACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
QY 269 SQTHQVLSKQPTSQSRGDPGTGPKE 293  
Db 62 SQTHQVLSKQPTSQSRGDPGTGPKE 86

RESULT 12  
US-07-808-452-1  
Sequence 1, Application US/07808452  
Patent No. 6063612  
GENERAL INFORMATION:  
APPLICANT: Jayasena, Sumedha D.  
APPLICANT: Johnston, Brian H.  
TITLE OF INVENTION: Antiviral Reagents Based on  
TITLE OF INVENTION: RNA-Binding Proteins  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Peter Dehlinger  
STREET: 350 Cambridge Avenue, Suite 300  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/808,452  
FILING DATE: 19911213  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 8255-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: the sequence of the TAT protein of  
INDIVIDUAL ISOLATE: HIV-1  
US-07-808-452-1  
Query Match 28.8%; Score 486; DB 3; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.6e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 209 EPVDPRLPEWKHPGSPKTKACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRPPQG 268  
Db 2 EPVDPRLPEWKHPGSPKTKACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
QY 269 SQTHQVLSKQPTSQSRGDPGTGPKE 293  
Db 62 SQTHQVLSKQPTSQSRGDPGTGPKE 86  
RESULT 13  
US-09-030-613-19  
Sequence 19, Application US/09030613  
Patent No. 6083706  
GENERAL INFORMATION:  
APPLICANT: Florlewicz, Robert Z.  
APPLICANT: Baird, J. Andrew  
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue

```

; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/030.613
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083706tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.418C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-030-613-19

Query Match 28.8%; Score 486; DB 3; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.6e-42;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 EPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFTKALGISYGRKKRRRPPQG 268
Db 2 EPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFTKALGISYGRKKRRRPPQG 61

QY 269 SOTHQVSLSKOPTSQRGDPGPK 293
Db 62 SOTHQVSLSKOPTSQRGDPGPK 86

RESULT 14
US-09-124-900-6
; Sequence 6, Application US/09124900
; Patent No. 6268484
; GENERAL INFORMATION:
; APPLICANT: KATINGER, Hermann
; APPLICANT: BUCHACHER, Andrea
; APPLICANT: ERNST, Wolfgang
; APPLICANT: BALLAUN, Claudia
; APPLICANT: PURTSCHER, Martin
; APPLICANT: TRKOLA, Alexandra
; APPLICANT: PREDL, Renate
; APPLICANT: SCHMATZ, Christine
; APPLICANT: KLIMA, Annelies
; APPLICANT: STEINDL, Franz
; APPLICANT: MUSTER, Thomas
; TITLE OF INVENTION: HIV-vaccines
; FILE REFERENCE: 1939-112P
; CURRENT APPLICATION NUMBER: US/09/124,900
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: PCT/EP95/01481
; PRIOR FILING DATE: 1995-04-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-124-900-6

; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/030.613
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083706tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.418C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-030-613-19

Query Match 28.8%; Score 486; DB 3; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.6e-42;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 EPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFTKALGISYGRKKRRRPPQG 268
Db 2 EPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFTKALGISYGRKKRRRPPQG 61

QY 269 SOTHQVSLSKOPTSQRGDPGPK 293
Db 62 SOTHQVSLSKOPTSQRGDPGPK 86

RESULT 14
US-09-124-900-6
; Sequence 6, Application US/09124900
; Patent No. 6268484
; GENERAL INFORMATION:
; APPLICANT: KATINGER, Hermann
; APPLICANT: BUCHACHER, Andrea
; APPLICANT: ERNST, Wolfgang
; APPLICANT: BALLAUN, Claudia
; APPLICANT: PURTSCHER, Martin
; APPLICANT: TRKOLA, Alexandra
; APPLICANT: PREDL, Renate
; APPLICANT: SCHMATZ, Christine
; APPLICANT: KLIMA, Annelies
; APPLICANT: STEINDL, Franz
; APPLICANT: MUSTER, Thomas
; TITLE OF INVENTION: HIV-vaccines
; FILE REFERENCE: 1939-112P
; CURRENT APPLICATION NUMBER: US/09/124,900
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: PCT/EP95/01481
; PRIOR FILING DATE: 1995-04-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-124-900-6

; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/030.613
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083706tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.418C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-030-613-19

Query Match 28.8%; Score 486; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.6e-42;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 EPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFTKALGISYGRKKRRRPPQG 268
Db 2 EPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFTKALGISYGRKKRRRPPQG 61

QY 269 SOTHQVSLSKOPTSQRGDPGPK 293
Db 62 SOTHQVSLSKOPTSQRGDPGPK 86

RESULT 15
US-09-451-905-19
; Sequence 19, Application US/09451905
; Patent No. 6306613
; GENERAL INFORMATION:
; APPLICANT: Robert Z. Florkiewicz
; APPLICANT: Andrew Baird
; APPLICANT: Dale E. Warnock
; TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT
; FILE REFERENCE: 200124.402C4
; CURRENT APPLICATION NUMBER: US/09/451,905
; CURRENT FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-451-905-19

Query Match 28.8%; Score 486; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.6e-42;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 EPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFTKALGISYGRKKRRRPPQG 268
Db 2 EPVDPRLPEPKHGPSQPKTACTNCYCKKCCFHCQVCFTKALGISYGRKKRRRPPQG 61

QY 269 SOTHQVSLSKOPTSQRGDPGPK 293
Db 62 SOTHQVSLSKOPTSQRGDPGPK 86

RESULT 16
US-08-235-403-1
; Sequence 1, Application US/08235403
; Patent No. 6316003
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOU, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/235.403  
FILING DATE: 13-DEC-1991  
CLASSIFICATION: 514  
PRIOR APPLICATION NUMBER: US 07/934.375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098.766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454.450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636.662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158.015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: human immunodeficiency virus  
STRAIN: type 1  
US-08-235-403-1

Query Match 28.8%; Score 486; DB 4; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.6e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 EPVDRLEPWKHPGSGPKTACTNCYKCCFHCQVCFITKALGISYGRKKRRRPPQG 268  
Db 2 EPVDRLEPWKHPGSGPKTACTNCYKCCFHCQVCFITKALGISYGRKKRRRPPQG 61  
QY 269 SOTHQVLSKQPTQSRSRGDPTGPK 293  
Db 62 SOTHQVLSKQPTQSRSRGDPTGPK 86

RESULT 17  
PCT-US92-10770-1  
Sequence 1, Application PC/TUS9210770  
GENERAL INFORMATION:  
APPLICANT: Jayasena, Suredha D.  
APPLICANT: Johnston, Brian H.  
TITLE OF INVENTION: Antiviral Reagents Based on  
TITLE OF INVENTION: RNA-Binding Proteins  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SRI International  
STREET: 333 Ravenswood Avenue  
CITY: Menlo Park  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10770  
FILING DATE: 19921211

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808.452  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: P-2962  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 859-4550  
TELEFAX: (415) 859-3880  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: the sequence of the TAT protein of  
INDIVIDUAL ISOLATE: HIV-1  
PCT-US92-10770-1

Query Match 28.8%; Score 486; DB 5; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.6e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 EPVDRLEPWKHPGSGPKTACTNCYKCCFHCQVCFITKALGISYGRKKRRRPPQG 268  
Db 2 EPVDRLEPWKHPGSGPKTACTNCYKCCFHCQVCFITKALGISYGRKKRRRPPQG 61  
QY 269 SOTHQVLSKQPTQSRSRGDPTGPK 293  
Db 62 SOTHQVLSKQPTQSRSRGDPTGPK 86

RESULT 18  
PCT-US93-06077-2  
Sequence 2, Application PC/TUS9306077  
GENERAL INFORMATION:  
APPLICANT: Immunobiology Research, Institute Inc.  
TITLE OF INVENTION: Vaccine Interdiction of Extracellular  
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus  
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar  
TITLE OF INVENTION: Intercellular Transactivating Strategies  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr, PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06077  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/247.991  
FILING DATE: 23-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: IRI44PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200

TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-06077-2

Query Match 28.8%; Score 486; DB 5; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.6e-42;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 EPVDPRLPEWKHPGSPKPTACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRPPQG 268  
Db 2 EPVDPRLPEWKHPGSPKPTACTNCYCKKCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
QY 269 SOTHQVSLSKQPTSQSRGDPGPK 293  
Db 62 SOTHQVSLSKQPTSQSRGDPGPK 86

RESULT 19  
US-08-815-809-5  
Sequence 5, Application US/08815809  
Patent No. 6004777  
GENERAL INFORMATION:  
APPLICANT: TARTAGLIA, James  
APPLICANT: GOEBEL, Scott J.  
APPLICANT: COX, William I.  
APPLICANT: GETTIG, Russell R.  
APPLICANT: PINCUS, Steven E.  
APPLICANT: PAOLETTI, Enzo  
APPLICANT: JACOBS, Bertram L.  
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND METHODS OF  
FILE REFERENCE: 454310-3010  
CURRENT APPLICATION NUMBER: US/08/815,809  
CURRENT FILING DATE: 1997-03-12  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 266  
TYPE: PRP  
ORGANISM: Vaccinia virus  
US-08-815-809-5

Query Match 28.3%; Score 478.5; DB 3; Length 266;  
Best Local Similarity 77.3%; Pred. No. 4.5e-41;  
Matches 92; Conservative 4; Mismatches 6; Indels 17; Gaps 4;

QY 66 VGFPVTPQVPLRPMTYKAAVDLSHFLKEGGLIHSQRQDILDWIYHTQGYFPDQW 125  
Db 136 VGFPVTPQVPLRPMTYKAAVDLSHFLKEGGLIHSQRQDILDWIYHTQGYFPDQW 195  
QY 126 NYTPGPGVRYPLTFGWCYKLVPEPKVEANKGENTSLHLPVSLH-GMDDPEREVLW 183  
Db 196 NYTPGPGVRYPLTFGWCYKLVPM-----IETV-----PVKLPKMGDGP--KVKQW 238

RESULT 20  
US-08-816-155B-43  
Sequence 43, Application US/08816155B  
Patent No. 5990091  
GENERAL INFORMATION:  
APPLICANT: TARTAGLIA, JAMES  
APPLICANT: COX, WILLIAM I.  
APPLICANT: GETTIG, RUSSELL R.  
APPLICANT: MARTINEZ, HECTOR  
APPLICANT: PAOLETTI, ENZO  
APPLICANT: PINCUS, STEVEN E.

TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND  
METHODS OF MAKING AND USES THEREOF  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP  
STREET: 745 FIFTH AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10151  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND  
METHODS OF MAKING AND USES THEREOF  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP  
STREET: 745 FIFTH AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10151  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

Query Match 28.3%; Score 478.5; DB 2; Length 280;  
Best Local Similarity 77.3%; Pred. No. 4.8e-41;  
Matches 92; Conservative 4; Mismatches 6; Indels 17; Gaps 4;

QY 66 VGFPVTPQVPLRPMTYKAAVDLSHFLKEGGLIHSQRQDILDWIYHTQGYFPDQW 125  
Db 150 VGFPVTPQVPLRPMTYKAAVDLSHFLKEGGLIHSQRQDILDWIYHTQGYFPDQW 209  
QY 126 NYTPGPGVRYPLTFGWCYKLVPEPKVEANKGENTSLHLPVSLH-GMDDPEREVLW 183  
Db 210 NYTPGPGVRYPLTFGWCYKLVPM-----IETV-----PVKLPKMGDGP--KVKQW 252

RESULT 21  
US-09-079-587-43  
Sequence 43, Application US/09079587  
Patent No. 6130066  
GENERAL INFORMATION:  
APPLICANT: TARTAGLIA, JAMES  
APPLICANT: COX, WILLIAM I.  
APPLICANT: GETTIG, RUSSELL R.  
APPLICANT: MARTINEZ, HECTOR  
APPLICANT: PAOLETTI, ENZO  
APPLICANT: PINCUS, STEVEN E.  
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND  
METHODS OF MAKING AND USES THEREOF  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP  
STREET: 745 FIFTH AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10151  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/079,587  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/816,155  
;; FILING DATE: 12-MAR-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: KOWALSKI, THOMAS J.  
;; REGISTRATION NUMBER: 32,147  
;; REFERENCE/DOCKET NUMBER: 454310-2990  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212-588-0800  
;; TELEFAX: 212-588-0500  
;; INFORMATION FOR SEQ ID NO: 43:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 280 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: n/a  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: amino acid  
US-09-079-587-43

Query Match 28.3%; Score 478.5; DB 4; Length 280;  
Best Local Similarity 77.3%; Pred. No. 4.8e-41;  
Matches 92; Conservative 4; Mismatches 6; Indels 17; Gaps 4;  
  
QY 66 VGFPPVTPVPLRPMTYKAAVDLSHFLKKGGLGHSRRQDILDLWIYHTQGYFPDQW 125  
|||||  
DB 150 VGFPPVTPVPLRPMTYKAAVDLSHFLKKGGLGHSRRQDILDLWIYHTQGYFPDQW 209  
|||||  
  
QY 126 NYTPGGVRYPLTFGCYKLVPEPKVEANKGENTSLLPVSLH-GMDDPEREVLEW 183  
|||||  
DB 210 NYTPGGVRYPLTFGCYKLVPEPKVEANKGENTSLLPVSLH-GMDDPEREVLEW 252  
|||||

RESULT 22  
US-08-505-210-1  
;; Sequence 1, Application US/08505210  
;; Patent No. 5981258  
;; GENERAL INFORMATION:  
;; APPLICANT: MEHTALI, Majid  
;; APPLICANT: GUSS, Tania  
;; TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS  
;; TITLE OF INVENTION: OF VIRAL PROTEINS FOR OBTAINING AN ANTIVIRAL EFFECT  
;; NUMBER OF SEQUENCES: 7  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
;; STREET: 1737 King Street, Suite 500  
;; CITY: Alexandria  
;; STATE: Virginia  
;; COUNTRY: United States  
;; ZIP: 22314-2756  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/505,210  
;; FILING DATE: 14-AUG-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/215,248  
;; FILING DATE: 21-MAR-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/FR94/01457  
;; FILING DATE: 13-DEC-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Dadio, Susan M.

;; REGISTRATION NUMBER: 40,373  
;; REFERENCE/DOCKET NUMBER: 017753-066  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703) 836-6620  
;; TELEFAX: (703) 836-2021  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 86 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Human immunodeficiency virus type 1  
;; STRAIN: Lai  
;; INDIVIDUAL ISOLATE: sequence of the TAT protein of HIV-1  
US-08-505-210-1

Query Match 27.8%; Score 470; DB 2; Length 86;  
Best Local Similarity 96.5%; Pred. No. 7.1e-41;  
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 209 EPVDPRLPEPKHPSQPKTACTNCKYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 268  
|||||  
DB 2 EPVDPRLPEPKHPSQPKTACTNCKYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
|||||  
  
QY 269 SOTHQVSLSKQPTSQSRGDPGTGPK 293  
|||||  
DB 62 SOTHQVSLSKQPTSQSRGDPGTGPK 86  
|||||

RESULT 23  
US-09-099-333-1  
;; Sequence 1, Application US/09099333A  
;; Patent No. 6228369  
;; GENERAL INFORMATION:  
;; APPLICANT: MEHTALI, Majid  
;; APPLICANT: GUSS, Tania  
;; TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS OF VIRAL  
;; TITLE OF INVENTION: PROTEINS FOR OBTAINING AN ANTI-VIRAL EFFECT  
;; FILE REFERENCE: 017753-091  
;; CURRENT APPLICATION NUMBER: US/09/099,333A  
;; CURRENT FILING DATE: 1998-06-18  
;; EARLIER APPLICATION NUMBER: FR 93 14914  
;; EARLIER FILING DATE: 1993-12-13  
;; EARLIER APPLICATION NUMBER: US 08/215,248  
;; EARLIER FILING DATE: 1994-03-21  
;; EARLIER APPLICATION NUMBER: US 08/505,210  
;; EARLIER FILING DATE: 1995-08-14  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 1  
;; LENGTH: 86  
;; TYPE: PRT  
;; ORGANISM: Human immunodeficiency virus type 1  
US-09-099-333-1

Query Match 27.8%; Score 470; DB 4; Length 86;  
Best Local Similarity 96.5%; Pred. No. 7.1e-41;  
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 209 EPVDPRLPEPKHPSQPKTACTNCKYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 268  
|||||  
DB 2 EPVDPRLPEPKHPSQPKTACTNCKYCKKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
|||||  
  
QY 269 SOTHQVSLSKQPTSQSRGDPGTGPK 293  
|||||  
DB 62 SOTHQVSLSKQPTSQSRGDPGTGPK 86  
|||||

RESULT 24  
US-08-417-210A-96  
; Sequence 96, Application US/08417210A  
; Patent No. 5863542  
; GENERAL INFORMATION:  
; APPLICANT: PAOLETTI, ENZO  
; APPLICANT: TARTAGLIA, JAMES  
; APPLICANT: COX, WILLIAM I.  
; TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS  
; NUMBER OF SEQUENCES: 148  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.  
; STREET: 530 FIFTH AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/417,210A  
; FILING DATE: 05-APR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOWALSKI, THOMAS J.  
; REGISTRATION NUMBER: 32,147  
; REFERENCE/DOCKET NUMBER: 454310-2690  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-840-3333  
; INFORMATION FOR SEQ ID NO: 96:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 83 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: amino acid  
US-08-417-210A-96

Query Match 27.6%; Score 466; DB 2; Length 83;  
Best Local Similarity 100.0%; Pred. No. 1.7e-40;  
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 VGFVPTQVPLRPMYKAAVDLSHFLKEGGLGSLHSQRQDILDWYHTQGYFFPDWQ 125  
Db 2 VGFVPTQVPLRPMYKAAVDLSHFLKEGGLGSLHSQRQDILDWYHTQGYFFPDWQ 61

Qy 126 NYTPGVRVPLTFGCYKLVLP 147  
Db 62 NYTPGVRVPLTFGCYKLVLP 83

RESULT 25  
US-08-053-079A-15  
; Sequence 15, Application US/08053079A  
; Patent No. 5606026  
; GENERAL INFORMATION:  
; APPLICANT: Rodman  
; TITLE OF INVENTION: Natural Human IgM Antibodies  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby  
; STREET: 805 Third Ave.  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,079A  
; FILING DATE: 26-APR-1993  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robinson, Joseph, R.  
; REGISTRATION NUMBER: 33,448  
; REFERENCE/DOCKET NUMBER: 4436/16060US4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)527-7700  
; TELEFAX: (212)753-6237  
; TELEX: 236687  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 82  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-053-079A-15

Query Match 27.0%; Score 455; DB 1; Length 82;  
Best Local Similarity 98.8%; Pred. No. 2.3e-39;  
Matches 80; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 209 EPVDPRLPEPKHSGSQPTACTNCYCKKCFHCQVCFITKALGTSYGRKKRRRRPQ 268  
Db 2 EPVDPRLPEPKHSGSQPTACTNCYCKKCFHCQVCFITKALGTSYGRKKRRRRPQ 61

Qy 269 SQTHQVSLSKQPTSQSRGDPT 289  
Db 62 SQTHQVSLSKQPTSQSRGDPT 82

RESULT 26  
US-08-659-251-4  
; Sequence 4, Application US/08659251  
; Patent No. 5883081  
; GENERAL INFORMATION:  
; APPLICANT: Kraus, Guenter  
; APPLICANT: Wong-Staal, Flossie  
; APPLICANT: Talbott, Randy  
; APPLICANT: Poschla, Eric  
; TITLE OF INVENTION: Isolation of No. 5883081el HIV-2 Proviruses  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/659,251  
; FILING DATE: No. 5883081 yet assigned  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001,441  
; FILING DATE: 26-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Garrett-Wackowski, Eugenia  
; REGISTRATION NUMBER: 37,330  
; REFERENCE/DOCKET NUMBER: 02307E-056410US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200

```
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 253 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   FEATURE:
;   NAME/KEY: Protein
;   LOCATION: 1..253
;   OTHER INFORMATION: /note= "nef protein encoded by HIV-2kr"
US-08-659-251-4

Query Match          25.5%; Score 430.5; DB 2; Length 253;
Best Local Similarity 39.4%; Pred. No. 3.4e-36;
Matches 99; Conservative 29; Mismatches 82; Indels 41; Gaps 6;

QY 1 MGKWKSSVVGWPTVVRMRRAEPAADG---VGAASRDLE-KHGATSSNTAATNAA-- 54
   || || || || || || || || || || || || || || || || || || ||
Db 1 MGASGSKKCSRSLOGLRRLRARGETCGGQWDGSAGEYLQFQEGSGRGONLPSCEGQY 60

QY 55 -----CAW-----LEAQEEEEVEGFPVTPQVPLRPMYKAAVDLS 88
   || || || || || || || || || || || || || || || || || || ||
Db 61 QQGDFMNTPWRTPAAGREGTLYKQNNDDVDADNDNLIGVPTPRVPLRAMTYKLAVDIS 120

QY 89 HFLKEKGLGLHSQRQDILDWIYHTOGYFPDQNYTPGCGVRYPLTFGWCYKLPVP 148
   || || || || || || || || || || || || || || || || || || ||
Db 121 HFLNEKGLDGMYSERHRILDIYMEKEGIIIPDQNYTHGCGVRYPKFPGWLKLPVP 180

QY 149 EPDKVEANKGENTSLHHPVSLHGMDDPEREVLEWRDLSLAFHHVARELHPEYFKNCTS 208
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 DVPQGE-----EDHCLLHPAQTSDDPHGETLMWRDPRLAYETAFNRYPEFGYKSG 235

QY 209 EPVDPRLPEPWK 219
   | | | | |
Db 236 LPE-----EWWK 242
```

## RESULT 27

```
US-09-256-490-4
; Sequence 4, Application US/09256490
; Patent No. 6235881
; GENERAL INFORMATION:
; APPLICANT: Kraus, Guenter
; APPLICANT: Wong-Staal, Flossie
; APPLICANT: Taibott, Randy
; APPLICANT: Poeschla, Eric
; TITLE OF INVENTION: Isolation of No. 6235881el HIV-2 Proviruses
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/256,490
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/659,251
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
```

```
; REFERENCE/DOCKET NUMBER: 02307E-056410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 253 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   FEATURE:
;   NAME/KEY: Protein
;   LOCATION: 1..253
;   OTHER INFORMATION: /note= "nef protein encoded by HIV-2kr"
US-09-256-490-4

Query Match          25.5%; Score 430.5; DB 4; Length 253;
Best Local Similarity 39.4%; Pred. No. 3.4e-36;
Matches 99; Conservative 29; Mismatches 82; Indels 41; Gaps 6;

QY 1 MGKWKSSVVGWPTVVRMRRAEPAADG---VGAASRDLE-KHGATSSNTAATNAA-- 54
   || || || || || || || || || || || || || || || || || || ||
Db 1 MGASGSKKCSRSLOGLRRLRARGETCGGQWDGSAGEYLQFQEGSGRGONLPSCEGQY 60

QY 55 -----CAW-----LEAQEEEEVEGFPVTPQVPLRPMYKAAVDLS 88
   || || || || || || || || || || || || || || || || || || ||
Db 61 QQGDFMNTPWRTPAAGREGTLYKQNNDDVDADNDNLIGVPTPRVPLRAMTYKLAVDIS 120

QY 89 HFLKEKGLGLHSQRQDILDWIYHTOGYFPDQNYTPGCGVRYPLTFGWCYKLPVP 148
   || || || || || || || || || || || || || || || || || || ||
Db 121 HFLNEKGLDGMYSERHRILDIYMEKEGIIIPDQNYTHGCGVRYPKFPGWLKLPVP 180

QY 149 EPDKVEANKGENTSLHHPVSLHGMDDPEREVLEWRDLSLAFHHVARELHPEYFKNCTS 208
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 DVPQGE-----EDHCLLHPAQTSDDPHGETLMWRDPRLAYETAFNRYPEFGYKSG 235

QY 209 EPVDPRLPEPWK 219
   | | | | |
Db 236 LPE-----EWWK 242
```

## RESULT 28

```
PCF-US96-11445-4
; Sequence 4, Application PC/TUS9611445
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Isolation of Novel HIV-2 Proviruses
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11445
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-399C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
```

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 253 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..253  
OTHER INFORMATION: /note= "nef protein encoded by HIV-2KR"  
PCT-US96-11445-4

Query Match 25.5%; Score 430.5; DB 5; Length 253;  
Best Local Similarity 39.4%; Pred. No. 3.4e-36;  
Matches 99; Conservative 29; Mismatches 82; Indels 41; Gaps 6;  
QY 1 MGKSKSVGWPVTRMRRAEPAADG---VGAARDLE-KHGAITSSNTAATNAA-- 54  
DB 1 MGASGKCSRLQGLRERLLRARGTCGGQWDGSGAGEYLQFOEGSGRQNLPSCEGQRY 60  
QY 55 -----CAW-----LEAQEEVEGFPVTPQVPLRPMTYKAAVDLS 88  
DB 61 QQGFDMNTWRTPAAGRECTLYKQNMDDVDADNDNLIGVPTPRVPLRAMTYKLAVDIS 120  
QY 89 HFLKEGGLGLHSGRRDIDLWYHTQGYFPDQWNTPGGVRYPLTFGWCYKLVVPV 148  
DB 121 HFLNKGGLDGMYSERRRIIDYMEKEGIPDQWNTHTGPGVRYPKFFGWLKLVVPV 180  
QY 149 EPDKVEEANKGENTSLHPVLSLGHGMDPEREVLWRFDLSRLAFHVAHELHPEYFNKCTS 208  
DB 181 DVPQGE-----EDHCLLHPAQTSGGDDPHGELTLMRFDRLAYEYATFNRYPEEFGYKSG 235  
QY 209 EPVDPRLPEPK 219  
DB 236 LPE-----EEWK 242

RESULT 29  
US-09-030-613-17  
; Sequence 17, Application US/09030613  
; Patent No. 6083706  
; GENERAL INFORMATION:  
; APPLICANT: Florckiewicz, Robert Z.  
; APPLICANT: Baird, J. Andrew  
; TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,613  
; FILING DATE: 25-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6083706tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 760100.418C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 72 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-030-613-17

Query Match 24.2%; Score 409; DB 3; Length 72;  
Best Local Similarity 100.0%; Pred. No. 9.7e-35;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 209 EPVDPRLPEPKHPSQPKTACTNCTCYKCCFHCQVCFITKALGISYGRKKRRRRPPQG 268  
DB 2 EPVDPRLPEPKHPSQPKTACTNCTCYKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
QY 269 SOTHQVSLSKQ 279  
DB 62 SOTHQVSLSKQ 72

RESULT 30  
US-09-451-905-17  
; Sequence 17, Application US/09451905  
; Patent No. 6306613  
; GENERAL INFORMATION:  
; APPLICANT: Robert Z. Florckiewicz  
; APPLICANT: Andrew Baird  
; APPLICANT: Dale E. Warnock  
; TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT  
; FILE REFERENCE: 200124.402C4  
; CURRENT APPLICATION NUMBER: US/09/451,905  
; CURRENT FILING DATE: 1999-12-01  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 72  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-451-905-17

Query Match 24.2%; Score 409; DB 4; Length 72;  
Best Local Similarity 100.0%; Pred. No. 9.7e-35;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 209 EPVDPRLPEPKHPSQPKTACTNCTCYKCCFHCQVCFITKALGISYGRKKRRRRPPQG 268  
DB 2 EPVDPRLPEPKHPSQPKTACTNCTCYKCCFHCQVCFITKALGISYGRKKRRRRPPQG 61  
QY 269 SOTHQVSLSKQ 279  
DB 62 SOTHQVSLSKQ 72

Search completed: August 26, 2002, 08:10:39  
Job time: 128 sec